



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number 114289

TO: Lorraine Spector  
Location: REM/4D55/4C70  
Art Unit: 1647  
Monday, February 23, 2004

Case Serial Number: 10/063671

From: Toby Port  
Location: Biotech-Chem Library  
Remsen 1A59  
Phone: 571-272-2523

[toby.port@uspto.gov](mailto:toby.port@uspto.gov)

### Search Notes

Dear Examiner Spector,

Here are the results of your search.  
Please feel free to contact me if you have any questions.

Toby Port

score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

Result	No
--------	----

1

UN

47

00

21

13

16

18 19

20  
2122  
23

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452	Homo sapiens (human)		1	Eston, D. L., Filvaroff, E., Gerritsen, M. E., Goddard, A., and
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452	Homo sapiens		2	Godwin, B. T., Oxenblatt, C. I., Gurvey, A. I., Watanabe, C. K. and
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		3	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		4	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			5	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			6	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			7	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			8	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			9	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			10	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			11	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			12	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			13	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			14	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			15	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			16	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			17	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			18	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			19	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			20	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			21	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			22	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			23	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			24	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			25	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			26	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			27	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			28	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			29	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			30	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			31	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			32	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			33	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			34	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			35	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:13444452			36	
AX092276	AX092276	Sequence 7 from Patent WO0116318.	AX092276	AX092276	GI:134444				



TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 016318-A 7 08-MAR-2001;  
Genentech, Inc. (US)  
FEATURES  
Source Location/Qualifiers  
1. 2586  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 631 a 679 c 703 g 573 t  
ORIGIN  
Query Match 100.0%; Score 2586; DB 6; Length 2586;  
Best Local Similarity 100.0%; Pired. No. 0;  
Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGCCGCGCTCCCGACCCGCGCGCCGCGCCGCGCTCCGCGCATCTGACACCCGACG 60  
Db 1 CGCCGCGCTCCCGACCCGCGCGCCGCGCCGCGCTCCGCGCATCTGACACCCGACG 60  
QY 61 CCGGCGGCTCCCGCGCGGAGCGAGATCCAGTCCGCGCCGCGACGCACTCGGTCA 120  
Db 61 CCGGCGGCTCCCGCGCGGAGCGAGATCCAGTCCGCGCCGCGACGCACTCGGTCA 120  
QY 121 GTGGGGGCGGCGGCTGGGGGCGAGAGATGACGGGCTTGGGGGCGACCTGCTGT 180  
Db 121 GTGGGGGCGGCGGCTGGGGGCGAGAGATGACGGGCTTGGGGGCGACCTGCTGT 180  
QY 181 GCGTGTCTGGCGCGCGGCTCCGACGCGCCCGCGCGCGCTCCGACGCGCGCTCG 240  
Db 181 GCGTGTCTGGCGCGCGGCTCCGACGCGCCCGCGCGCGCTCCGACGCGCGCTCG 240  
QY 241 CTCGAGTCAGCCCGCGCGGCTCTCAGCTACCCGCGAGAGAGGCGCCCTCAATGAA 300  
Db 241 CTCGAGTCAGCCCGCGCGGCTCTCAGCTACCCGCGAGAGAGGCGCCCTCAATGAA 300  
QY 301 TGTTCGCGAGGTGAGGAACTGATGAGGACACGACCAATTGCGAGCGCGGTGG 360  
Db 301 TGTTCGCGAGGTGAGGAACTGATGAGGACACGACCAATTGCGAGCGCGGTGG 360  
QY 361 AAGAGATGAGGCGAAGAACTGCTCTTAAGCATATCAAAATGAACTTGGCAA 420  
Db 361 AAGAGATGAGGCGAAGAACTGCTCTTAAGCATATCAAAATGAACTTGGCAA 420  
QY 421 TACCTCCAGCTATCAATGAGACCAACAGACAGAGTTGGAAATATACCATCC 480  
Db 421 TACCTCCAGCTATCAATGAGACCAACAGACAGAGTTGGAAATATACCATCC 480  
QY 481 ATGTGCAACCGAATTCACAAATTAACAACCACTGAGCAAAATGCTTTTTCAG 540  
Db 481 ATGTGCAACCGAATTCACAAATTAACAACCACTGAGCAAAATGCTTTTTCAG 540  
QY 541 AGACAGTTATCATCTGTGGGAGACGAGAGAGGAGAGAGGCGACGAGTGCATATG 600  
Db 541 AGACAGTTATCATCTGTGGGAGACGAGAGAGGAGAGAGGCGACGAGTGCATATG 600  
QY 601 ACGAGACTGTGGGCGCGAGATGTATGCGCAATTTGCACTTCACTACCTGCAG 660  
Db 601 ACGAGACTGTGGGCGCGAGATGTATGCGCAATTTGCACTTCACTACCTGCAG 660  
QY 661 CATTCGCGGCGAGAGATGCTGTGACCCGCGAGAGTGTGTGTGTGTGTGTGTGTGT 720  
Db 661 CATTCGCGGCGAGAGATGCTGTGACCCGCGAGAGTGTGTGTGTGTGTGTGTGTGT 720  
QY 721 GTGTCTGGGCTCACTGACCAAAATGCGCAACAGGGGCACTATGGGACATCTGTGAC 780  
Db 721 GTGTCTGGGCTCACTGACCAAAATGCGCAACAGGGGCACTATGGGACATCTGTGAC 780  
QY 781 ACCGAGAGAGTGTGACAGCGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840  
Db 781 ACCGAGAGAGTGTGACAGCGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840  
QY 841 TGTGACAGACCCCTGCGGTGAGGGCGAGCTTTGTCATGACCCCGGACGCGCTTCTG 900

Db 841 TGTGACAGACCCCTGCGGTGAGGGCGAGCTTTGTCATGACCCCGGACGCGCTTCTG 900  
QY 901 ACCTCATACCTGGAGCTTAAGCCTGATGAGCCTTGGACCGATGCCCTTGTGCACTG 960  
Db 901 ACCTCATACCTGGAGCTTAAGCCTGATGAGCCTTGGACCGATGCCCTTGTGCACTG 960  
QY 961 GCGTCCCTGCGAGCGCCACAGCCACACCGCGGTGTATGTGTGCAAGCGCACTTCTG 1020  
Db 961 GCGTCCCTGCGAGCGCCACAGCCACACCGCGGTGTATGTGTGCAAGCGCACTTCTG 1020  
QY 1021 GGAGCGCTGACCAAGATGGGAGATCCTGCTGCCAGAGAGTCCCGATGATGAAAG 1080  
Db 1021 GGAGCGCTGACCAAGATGGGAGATCCTGCTGCCAGAGAGTCCCGATGATGAAAG 1080  
QY 1081 TTGGAGCTTCAATGAGAGAGTGGCGCGAGCTGAGAGACCTGAGAGAGAGCCTGACTG 1140  
Db 1081 TTGGAGCTTCAATGAGAGAGTGGCGCGAGCTGAGAGACCTGAGAGAGAGCCTGACTG 1140  
QY 1141 AAGAGATGGCGCTGGGGAGCCTGCGGCTGCGCGCTGCACTGCTGGAGAGGAGAGA 1200  
Db 1141 AAGAGATGGCGCTGGGGAGCCTGCGGCTGCGCGCTGCACTGCTGGAGAGGAGAGA 1200  
QY 1201 TTTAGATCTGACACAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCA 1260  
Db 1201 TTTAGATCTGACACAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCA 1260  
QY 1261 GGTGTGTCTTTAGCGGTGAGGCTGACAGAGCTTCTCTCATCTTCTCCAGTAAGTT 1320  
Db 1261 GGTGTGTCTTTAGCGGTGAGGCTGACAGAGCTTCTCTCATCTTCTCCAGTAAGTT 1320  
QY 1321 TCCCTCTGCTTGAACAGATGAGGTGTGTGCAATTTGTAGCTCCCGGAGCTGTCT 1380  
Db 1321 TCCCTCTGCTTGAACAGATGAGGTGTGTGCAATTTGTAGCTCCCGGAGCTGTCT 1380  
QY 1381 CCAGGCTTCAAGCTGTGGCTTGGAGAGTGCAGAGGCTTCTCTCATCTTCTCCAGTAAGTT 1440  
Db 1381 CCAGGCTTCAAGCTGTGGCTTGGAGAGTGCAGAGGCTTCTCTCATCTTCTCCAGTAAGTT 1440  
QY 1441 GCCACCTCTGTCCAGATTAATGCTGCTTGTCTTCACTGAGTGGCAGACGCGTTGT 1500  
Db 1441 GCCACCTCTGTCCAGATTAATGCTGCTTGTCTTCACTGAGTGGCAGACGCGTTGT 1500  
QY 1501 TCTACATGGCTTGAATTAATGTTTGAAGGAGAGAGTGAATGATGAGTGTCTCCCTC 1560  
Db 1501 TCTACATGGCTTGAATTAATGTTTGAAGGAGAGAGTGAATGATGAGTGTCTCCCTC 1560  
QY 1561 TGAATGCTTTGGGAGAAATGTGAGAGAGTGCCTGTGTGCAACATCACTGGCAA 1620  
Db 1561 TGAATGCTTTGGGAGAAATGTGAGAGAGTGCCTGTGTGCAACATCACTGGCAA 1620  
QY 1621 AAATGCAACAAATGAATTTTCAAGCAGTTCTTCAATGGGCAATGAGTGAAGCTT 1680  
Db 1621 AAATGCAACAAATGAATTTTCAAGCAGTTCTTCAATGGGCAATGAGTGAAGCTT 1680  
QY 1681 CAGCTGTGCAATGAATTTTCAAGCAGTTCTTCAATGGGCAATGAGTGAAGCTT 1740  
Db 1681 CAGCTGTGCAATGAATTTTCAAGCAGTTCTTCAATGGGCAATGAGTGAAGCTT 1740  
QY 1741 GTGTGCTCAGCTCTCACTGTGCGAGAGGAGACATTTTCAATGCAAGTCAATTTCC 1800  
Db 1741 GTGTGCTCAGCTCTCACTGTGCGAGAGGAGACATTTTCAATGCAAGTCAATTTCC 1800  
QY 1801 TCTCTCAGACAGCTGGGAGAGGAGGATTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1860  
Db 1801 TCTCTCAGACAGCTGGGAGAGGAGGATTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1860  
QY 1861 GCTCAGACAGCTGAGAGGCTGTGCGAGAGTCAACAGTGAAGACAGAGAGTTTC 1920  
Db 1861 GCTCAGACAGCTGAGAGGCTGTGCGAGAGTCAACAGTGAAGACAGAGAGTTTC 1920  
QY 1921 ATCTGTGTGACTTAAGTCAAGTGTCTCTCTCACTACCCACAGAGCTTGTGTGCA 1980

Db	1921	ATCTGCTTGAGACTCTAAGCTCAATGGCTCTCTCCACTACCCACACACAGCCTTG9TGCA	1980
Qy	1981	CCAAAAGTGTCTCCCCAAAAGGAGAGATGGGATTTTCTTTGAGGCAATGCACATCTGGA	2040
Db	1981	CCAAAAGTGTCTCCCCAAAAGGAGAGATGGGATTTTCTTTGAGGCAATGCACATCTGGA	2040
Qy	2041	ATTAAAGTGCAACTAATTTCTCACATGCCCTCTAAAGTAACTAATCTGTATGAGAACAGCAGT	2100
Db	2041	ATTAAAGTGCAACTAATTTCTCACATGCCCTCTAAAGTAACTAATCTGTATGAGAACAGCAGT	2100
Qy	2101	GTTCCTCACAGTGTGGGAGCCGCTCTTTCTAATGAGAACAAATGATATTGACACTGTCCCT	2160
Db	2101	GTTCCTCACAGTGTGGGAGCCGCTCTTTCTAATGAGAACAAATGATATTGACACTGTCCCT	2160
Qy	2161	CTTTGGCAGCTGCACNTACTAATCTTTGAAAGGATATGACTAGAGCTACATACAGGTTAA	2220
Db	2161	CTTTGGCAGCTGCACNTACTAATCTTTGAAAGGATATGACTAGAGCTACATACAGGTTAA	2220
Qy	2221	CTTCGAGAAACAGTACTATTAGGTAATTGTAGGGCGAGATTAATAATGAAATTTGCAAAAT	2280
Db	2221	CTTCGAGAAACAGTACTATTAGGTAATTGTAGGGCGAGATTAATAATGAAATTTGCAAAAT	2280
Qy	2281	CACCTTAGACGCACTGGAAGACATTTATCAACCACTGAGAGAAATCAACCGAGAGGGC	2340
Db	2281	CACCTTAGACGCACTGGAAGACATTTATCAACCACTGAGAGAAATCAACCGAGAGGGC	2340
Qy	2341	TGTGTGAAACACATGGTGTATATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAA	2400
Db	2341	TGTGTGAAACACATGGTGTATATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAA	2400
Qy	2401	TGATGTTTTCAGGTGTCATGACCTGTGGCCACCATGATATTCATCCAGATTTCTTAAAGTT	2460
Db	2401	TGATGTTTTCAGGTGTCATGACCTGTGGCCACCATGATATTCATCCAGATTTCTTAAAGTT	2460
Qy	2461	TAAAGTGCACATGATGTGTATATAGCATCTTTCTTGGATTTTAATATATGATATTAACAT	2520
Db	2461	TAAAGTGCACATGATGTGTATATAGCATCTTTCTTGGATTTTAATATATGATATTAACAT	2520
Qy	2521	AAGTGTGCATTTAGAAATCAAGCATTAATCACTTCAACTGCACAAAAA	2580
Db	2521	AAGTGTGCATTTAGAAATCAAGCATTAATCACTTCAACTGCACAAAAA	2580
Qy	2581	AAAAAA 2586	
Db	2581	AAAAAA 2586	
RESULT 2			
LOCUS	AX54464	2586 bp	DNA linear
DEFINITION	Sequence 49 from Patent WO0208284.		
ACCESSION	AX54464		
VERSION	AX54464.1	GI:21713856	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Masters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W.		
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis		
JOURNAL	Patent: WO 0208284-A 49 31-JAN-2002, Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Masters, Scott A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)		

FEATURES		Location/Qualifiers
source	1..2586	
	/organism="Homo sapiens"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:9606"	
BASE COUNT	631 a 679 c 703 g 573 t	
ORIGIN		
Query Match	100.0%; Score 2586; DB 6; Length 2586;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 2586; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
QY	1 CGCGCGCTCCCGCACCCGCGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCGACG	60
Db	1 CGCGCGGCTCCCGCACCCGCGCCCGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCGACG	60
QY	61 CGCGCGGCTCCCGCGCGGAGCGAGCAGCATCTCGGCGCCGACAGCGGACCTCGGTCGA	120
Db	61 CGCGCGGCTCCCGCGCGGAGCGAGCAGCATCTCGGCGCCGACAGCGGACCTCGGTCGA	120
QY	121 GTGCGGCGCGCGGCTCGCGGCGCGAGCGGAGATGACAGCGGCTTTGGGCGCCACCTGCTGT	180
Db	121 GTGCGGCGCGCGGCTCGCGGCGCGAGCGGAGATGACAGCGGCTTTGGGCGCCACCTGCTGT	180
QY	181 GCCTGCTGCTGGCGCGGCGGCTGCCACGCGCCCGCGCCGCTTCGACGCGGACCTCGG	240
Db	181 GCCTGCTGCTGGCGCGGCGGCTGCCACGCGCCCGCGCCGCTTCGACGCGGACCTCGG	240
QY	241 CTTCAGTCAAGCGCGCGCGCGGCTCACTCACTCCGCGAGAGAGAGGCGCACCTCAATGAGA	300
Db	241 CTTCAGTCAAGCGCGCGCGCGGCTCACTCACTCCGCGAGAGAGAGGCGCACCTCAATGAGA	300
QY	301 TGTTCGCGAGGTTGAGAACTGATGAGAGCACGCGACGCAAAATTGCGCGCGGTGG	360
Db	301 TGTTCGCGAGGTTGAGAACTGATGAGAGCACGCGACGCAAAATTGCGCGCGGTGG	360
QY	361 AAAGATGAGAGCGAAGAAAGCTGTGTTAAGATCATAGAAAGTGAACCTGCGAAACT	420
Db	361 AAAGATGAGAGCGAAGAAAGCTGTGTTAAGATCATAGAAAGTGAACCTGCGAAACT	420
QY	421 TACCTCCAGCTATCAATGAGACCAACAGACAGAGAAAGTTGGAATATACCATCC	480
Db	421 TACCTCCAGCTATCAATGAGACCAACAGACAGAGAAAGTTGGAATATACCATCC	480
QY	481 ATGTGCAACCGAAGAAATTCAAGAAATACCAACACAGACTGACAAATGGTCTTTTCAG	540
Db	481 ATGTGCAACCGAAGAAATTCAAGAAATACCAACACAGACTGACAAATGGTCTTTTCAG	540
QY	541 AGACAGTTATCATCTGTGGGAGCGAAGAAAGCAGAAAGAGCCAGATGTGCATATCG	600
Db	541 AGACAGTTATCATCTGTGGGAGCGAAGAAAGCAGAAAGAGCCAGATGTGCATATCG	600
QY	601 ACGAGGACTGTGGGCCCGAGCATGTATCTGCCAGTTTGCAAGTTTCAATACCTGCGACG	660
Db	601 ACGAGGACTGTGGGCCCGAGCATGTATCTGCCAGTTTGCAAGTTTCAATACCTGCGACG	660
QY	661 CAGCGCGGCGCGAGAGATGCTCTGCACCCGCGGACAGTAGAGTGCTGTGGAGACAAGCTGT	720
Db	661 CAGCGCGGCGCGAGAGATGCTCTGCACCCGCGGACAGTAGAGTGCTGTGGAGACAAGCTGT	720
QY	721 GTGTCTGGGGTCACTGCACCAAAATGGCCACACAGGCGCGAGCAATGAGACCATCTGTGACA	780
Db	721 GTGTCTGGGGTCACTGCACCAAAATGGCCACACAGGCGCGAGCAATGAGACCATCTGTGACA	780
QY	781 ACGAGAGGAGCTGCGCAGCGCGGCGGTGAGCTTCCAGAGAGGCGCTGTGTCCTG	840
Db	781 ACGAGAGGAGCTGCGCAGCGCGGCGGTGAGCTTCCAGAGAGGCGCTGTGTCCTG	840
QY	841 TGTGCAACCCCTGCGCGGTGAGAGGCGAGCTTTGCAATGACCCCGCAGCGCGGCTTCTGG	900
Db	841 TGTGCAACCCCTGCGCGGTGAGAGGCGAGCTTTGCAATGACCCCGCAGCGCGGCTTCTGG	900
QY	901 ACCTCATCACTCGGAGGCTTAGAGCCTGATGAGACCTTGGACCATGTGCTTGTGCGAGTG	960

```

Db 901 ACCCTACCTGAGGAGCTGAGGCTGATGAGGCTTGGACCGATGCTTGTGCGCAGTG 960
Qy 961 GCCCTCTCTCCAGAGCCCGACAGCCAGAGCTGTGTATGTGTGCAAGCCGACCTTGTGTG 1020
Db 961 GCCCTCTCTCCAGAGCCCGACAGCCAGAGCTGTGTGTGTGTGCAAGCCGACCTTGTGTG 1020
Qy 1021 GAGAGCGGTGACCAAGATGGGGAGATCCTGTGCGCCAGAGAGGTGCCCCGATGATAGTAAG 1080
Db 1021 GAGAGCGGTGACCAAGATGGGGAGATCCTGTGCGCCAGAGAGGTGCCCCGATGATAGTAAG 1080
Qy 1081 TTGGCAGCTTCATGAGAGAGGTGTGCGCCAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAG 1140
Db 1081 TTGGCAGCTTCATGAGAGAGGTGTGCGCCAGAGAGAGCTGTGAGAGAGAGAGAGAGAGAG 1140
Qy 1141 AAGAGATGGCGCTGGGGAGAGCTTGGCGCTGCGCGCTGCACTGTGTGGAGGGAGAGAGA 1200
Db 1141 AAGAGATGGCGCTGGGGAGAGCTTGGCGCTGCGCGCTGCACTGTGTGGAGGGAGAGAGA 1200
Qy 1201 TTTCAGCTCTGAGCAGAGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCA 1260
Db 1201 TTTCAGCTCTGAGCAGAGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCA 1260
Qy 1261 GGTGTGTGCTTTAGGCGGTGGGTGAGCCAGAGCTTCTTCAATCTTCTTCCAGTAAGTT 1320
Db 1261 GGTGTGTGCTTTAGGCGGTGGGTGAGCCAGAGCTTCTTCAATCTTCTTCCAGTAAGTT 1320
Qy 1321 TCCCTCTGTGCTGACAGCATGAGAGGTGTGTGCAATTTGTTCAAGTCCCCAGAGCTGTCT 1380
Db 1321 TCCCTCTGTGCTGACAGCATGAGAGGTGTGTGCAATTTGTTCAAGTCCCCAGAGCTGTCT 1380
Qy 1381 CCAGGCTTCACAGTCTGTGTGTGGAGAGTCAAGGAGGTAACTGCGAGAGAGAGTT 1440
Db 1381 CCAGGCTTCACAGTCTGTGTGTGGAGAGTCAAGGAGGTAACTGCGAGAGAGAGTT 1440
Qy 1441 GCCACCCCTGTCAGATTAATGCTGTGCTTGGCTCTTCAAGAGTTGGCAGAGAGAGCTTGT 1500
Db 1441 GCCACCCCTGTCAGATTAATGCTGTGCTTGGCTCTTCAAGAGTTGGCAGAGAGAGCTTGT 1500
Qy 1501 TCTACATGAGCTTTGATATGTTGTTGAGGGAGAGAGATGAGAAACAATGTGAGTCTCCCT 1560
Db 1501 TCTACATGAGCTTTGATATGTTGTTGAGGGAGAGAGATGAGAAACAATGTGAGTCTCCCT 1560
Qy 1561 TGATGTGTTTGGGGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Db 1561 TGATGTGTTTGGGGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Qy 1621 AAATGCAACAATGATTTTCCAGCAGATCTTTCATGAGAGAGAGAGAGAGAGAGAGAG 1680
Db 1621 AAATGCAACAATGATTTTCCAGCAGATCTTTCATGAGAGAGAGAGAGAGAGAGAGAG 1680
Qy 1681 CAGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 CAGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Qy 1741 GTGTGTGCTCAGAGCTCTCTGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Db 1741 GTGTGTGCTCAGAGCTCTCTGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Qy 1801 TCTCTCAGCAGAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Db 1801 TCTCTCAGCAGAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Qy 1861 GCTCAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Db 1861 GCTCAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Qy 1921 ATCTGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db 1921 ATCTGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Qy 1981 CCAAAAGTGTCTCCCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040

```

```

Db 1981 CCAAAAGTGTCTCCCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
Qy 2041 ATTAAGGTCAAACTAATTTCTCACTCCCTTAAAGTAAGTAAGTAAGTAAGTAAGTAAG 2100
Db 2041 ATTAAGGTCAAACTAATTTCTCACTCCCTTAAAGTAAGTAAGTAAGTAAGTAAGTAAG 2100
Qy 2101 GTTCTCAGAGGTGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Db 2101 GTTCTCAGAGGTGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Qy 2161 CTTTGGCAGTTGCACTTAACTTTGAAAGGTATATGACTGAGAGAGAGAGAGAGAGAGAG 2220
Db 2161 CTTTGGCAGTTGCACTTAACTTTGAAAGGTATATGACTGAGAGAGAGAGAGAGAGAGAG 2220
Qy 2221 CCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
Db 2221 CCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
Qy 2281 CACTTAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
Db 2281 CACTTAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
Qy 2341 TGTGTGAAACAATGTGTGTAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
Db 2341 TGTGTGAAACAATGTGTGTAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
Qy 2401 TGATGTGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
Db 2401 TGATGTGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
Qy 2461 TAAAGTGTGCACTGATTTGTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
Db 2461 TAAAGTGTGCACTGATTTGTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
Qy 2521 AAGTGTGCACTTGAAGATCAACATTAATCACTTCACTGCAAGAGAGAGAGAGAGAGAG 2580
Db 2521 AAGTGTGCACTTGAAGATCAACATTAATCACTTCACTGCAAGAGAGAGAGAGAGAGAG 2580
Qy 2581 AAAAAA 2586
Db 2581 AAAAAA 2586

RESULT 3
AX490942
LOCUS AX490942 2586 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 49 from Patent WO200690.
ACCESSION AX490942
VERSION AX490942.1 GI:22323808
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gunney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Pavoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0200690-A 49 03-JAN-2002;
Genentech, Inc. (US)
FEATURES
source
1..2586
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 631 a 673 c 703 g 573 t
ORIGIN
Query Match 100.0%; Score 2586; DB 6; Length 2586;
Best Local Similarity 100.0%; Pred. No. 0;

```

Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGCGCTCCCGCACCAGCGCCCGCCACCGCGCGCTCCGCACTGTCACCCGAGC 60  
Db 1 CGCGGCGCTCCCGCACCAGCGCCCGCCACCGCGCGCTCCGCACTGTCACCCGAGC 60  
QY 61 CGCGGCGCTCCCGCGGAGCGAGCAAGATCCAGTCCGCGCCGAGCGCAATCTGCTCA 120  
Db 61 CGCGGCGCTCCCGCGGAGCGAGCAAGATCCAGTCCGCGCCGAGCGCAATCTGCTCA 120  
QY 121 GTCGCGGCGCGCGCTGCGGCGCGAGCGAGATGCAAGCGCTTGGGGCCACCCCTGTGT 180  
Db 121 GTCGCGGCGCGCGCTGCGGCGCGAGCGAGATGCAAGCGCTTGGGGCCACCCCTGTGT 180  
QY 181 GCTGCTGCTGCGCGCGCGGCTCCCAAGCGCCCGCGCCGCTCCGAGCGGCACTCGG 240  
Db 181 GCTGCTGCTGCGCGCGCGGCTCCCAAGCGCCCGCGCCGCTCCGAGCGGCACTCGG 240  
QY 241 CTCGAGTCAGCGCGCGCGCGCTCTCAGCTAACCGCGAGGAGGCGCACCCCTGAATGAG 300  
Db 241 CTCGAGTCAGCGCGCGCGCGCTCTCAGCTAACCGCGAGGAGGCGCACCCCTGAATGAG 300  
QY 301 TGTTCGCGAGGTTGAGGAACTGATGAGAGCAAGAGCAAAATTCGAGCGCGTGG 360  
Db 301 TGTTCGCGAGGTTGAGGAACTGATGAGAGCAAGAGCAAAATTCGAGCGCGTGG 360  
QY 361 AAGAGATGAGAGCGAGAAAGCTGCTGTAAGATCATGAAAGTGAACCTGGCAACT 420  
Db 361 AAGAGATGAGAGCGAGAAAGCTGCTGTAAGATCATGAAAGTGAACCTGGCAACT 420  
QY 421 TACCTCCAGCTATCAGATGAGACCAAGAGCAAGAGTTGGAATATATACATCC 480  
Db 421 TACCTCCAGCTATCAGATGAGACCAAGAGCAAGAGTTGGAATATATACATCC 480  
QY 481 ATGTGCAACCGAGAAATTCAGAGTAAACAACAACGAGCTGCAAAATGCTTTTCAG 540  
Db 481 ATGTGCAACCGAGAAATTCAGAGTAAACAACAACGAGCTGCAAAATGCTTTTCAG 540  
QY 541 AGAGATGATACATCTGTGGGAGACGAGAGGCAAGAGGCAAGAGTGAATGATG 600  
Db 541 AGAGATGATACATCTGTGGGAGACGAGAGGCAAGAGGCAAGAGTGAATGATG 600  
QY 601 ACGAGACTGTGGGCGCAGCATGTACTGCGAGTTGCGAGCTTCAGTACACCTGCCAGC 660  
Db 601 ACGAGACTGTGGGCGCAGCATGTACTGCGAGTTGCGAGCTTCAGTACACCTGCCAGC 660  
QY 661 CATGCCGGGCGCAAGAGATGCTTGCACCCGGGACAGTGAAGTGTGGAGACCAAGTGT 720  
Db 661 CATGCCGGGCGCAAGAGATGCTTGCACCCGGGACAGTGAAGTGTGGAGACCAAGTGT 720  
QY 721 GTGTCTGGGAGTCACTGCAACCAAAATGGCCACAGGGGCAAGAAATGGGACCATCTGTGACA 780  
Db 721 GTGTCTGGGAGTCACTGCAACCAAAATGGCCACAGGGGCAAGAAATGGGACCATCTGTGACA 780  
QY 781 ACCAGAGGAACTGCAAGCCGGGGCTGTGCTGTGCTTCAGAGAGGCTGTGCTGCTG 840  
Db 781 ACCAGAGGAACTGCAAGCCGGGGCTGTGCTGTGCTTCAGAGAGGCTGTGCTGCTG 840  
QY 841 TGTGCAACACCCCTGCGCGGAGGCGAGCTTTGSCATGACCCCGCAGCGGCTTCTGG 900  
Db 841 TGTGCAACACCCCTGCGCGGAGGCGAGCTTTGSCATGACCCCGCAGCGGCTTCTGG 900  
QY 901 ACCTCATCACTGAGAGCTAGAGCTTGAAGCTTGAACCGATGCTTGTGCGAGT 960  
Db 901 ACCTCATCACTGAGAGCTAGAGCTTGAAGCTTGAACCGATGCTTGTGCGAGT 960  
QY 961 GCTCTCTGCGAGCGCCACAGCAGCAGCTGTGTATGTGTGCAAGCGCAGCTTGTG 1020  
Db 961 GCTCTCTGCGAGCGCCACAGCAGCAGCTGTGTATGTGTGCAAGCGCAGCTTGTG 1020  
QY 1021 GGAAGCGTGACCAAGATGGGAGATCTGTGCGCCAGAGAGTCCCGATGAGTAAAG 1080  
Db 1021 GGAAGCGTGACCAAGATGGGAGATCTGTGCGCCAGAGAGTCCCGATGAGTAAAG 1080

QY 1081 TTGCAAGCTTCAATGAGAGAGTGCGCCAGAGCTGAGAGACCTGAGAGAGCTGAC 1140  
Db 1081 TTGCAAGCTTCAATGAGAGAGTGCGCCAGAGCTGAGAGACCTGAGAGAGCTGAC 1140  
QY 1141 AAGAGATGCGCTGGGGAGAGCTGCGGCTGCGCGCTGCGCACTGTGGAGAGGAGAGA 1200  
Db 1141 AAGAGATGCGCTGGGGAGAGCTGCGGCTGCGCGCTGCGCACTGTGGAGAGGAGAGA 1200  
QY 1201 TTTAGATCTGAGCAAGAGCTGTGGGAGATGATGCAATAGAAATAGCTATTTATCCCA 1260  
Db 1201 TTTAGATCTGAGCAAGAGCTGTGGGAGATGATGCAATAGAAATAGCTATTTATCCCA 1260  
QY 1261 GGTGTGTCTTTAGGCGGTGGGCTGACAGGCTTCTTCTACATCTTCTTCCAGTAACT 1320  
Db 1261 GGTGTGTCTTTAGGCGGTGGGCTGACAGGCTTCTTCTACATCTTCTTCCAGTAACT 1320  
QY 1321 TCCCTCTGCGCTTGAACAGATAGAGGTGTGTGCAATTTGTAGAGTCCCGCGGCTTCT 1380  
Db 1321 TCCCTCTGCGCTTGAACAGATAGAGGTGTGTGCAATTTGTAGAGTCCCGCGGCTTCT 1380  
QY 1381 CCAGGCTTCAAGCTGTGAGTGTGGAGAGTCAAGCAGGTTAACTGACAGAGCAGTTT 1440  
Db 1381 CCAGGCTTCAAGCTGTGAGTGTGGAGAGTCAAGCAGGTTAACTGACAGAGCAGTTT 1440  
QY 1441 GCGACCCCTGTCCAGATTTATGCTGCTTGTGCTTACAGTGTGGCAGACAGCGTTGT 1500  
Db 1441 GCGACCCCTGTCCAGATTTATGCTGCTTGTGCTTACAGTGTGGCAGACAGCGTTGT 1500  
QY 1501 TCTACATGCTTGAATATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCCTC 1560  
Db 1501 TCTACATGCTTGAATATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCCTC 1560  
QY 1561 TGATTGCTTTGGGAAATGTGAGAGAGTCCCTGCTTTGCAAAATCAACCTGGCA 1620  
Db 1561 TGATTGCTTTGGGAAATGTGAGAGAGTCCCTGCTTTGCAAAATCAACCTGGCA 1620  
QY 1621 AATGCAACAAATGAATTTTCCAGCAGTCTTTCATGGGAGATGATGAGTGTGCTT 1680  
Db 1621 AATGCAACAAATGAATTTTCCAGCAGTCTTTCATGGGAGATGATGAGTGTGCTT 1680  
QY 1681 CAGCTGTGCAAGTAAATGTTCTGTTCACCCGTGATTAATGTTATTCATCAGCA 1740  
Db 1681 CAGCTGTGCAAGTAAATGTTCTGTTCACCCGTGATTAATGTTATTCATCAGCA 1740  
QY 1741 GGTGTGCTCAGCTCTTACCTGTGCGCAGGGAGAGATTTTCAATCAAGATCAATCC 1800  
Db 1741 GGTGTGCTCAGCTCTTACCTGTGCGCAGGGAGAGATTTTCAATCAAGATCAATCC 1800  
QY 1801 TCTCTCAGACAGCCTGGGAGAGGGGTCAATGTTCTCTCGGCCATCAGGAGTCCAGAG 1860  
Db 1801 TCTCTCAGACAGCCTGGGAGAGGGGTCAATGTTCTCTCGGCCATCAGGAGTCCAGAG 1860  
QY 1861 GCTCAGAGCTGCAAGCTGCTTGGCCAAAGTCAACAAGTGAAGAGACCAAGCAGTTTC 1920  
Db 1861 GCTCAGAGCTGCAAGCTGCTTGGCCAAAGTCAACAAGTGAAGAGACCAAGCAGTTTC 1920  
QY 1921 ATCTGGTGTGACTTAAGCTCAGTGTCTCTCCACTAACCCCAACAGCCTTGTGTGCA 1980  
Db 1921 ATCTGGTGTGACTTAAGCTCAGTGTCTCTCCACTAACCCCAACAGCCTTGTGTGCA 1980  
QY 1981 CCAAAAGTCTCCCAAAAGAGAGAAATGGGATTTTCTTGAAGCATGCAATCTGGA 2040  
Db 1981 CCAAAAGTCTCCCAAAAGAGAGAAATGGGATTTTCTTGAAGCATGCAATCTGGA 2040  
QY 2041 ATTAAGTCAAACTAATCTCAATCCTCTTAAAGTAACTACTGTGAGAAACAGAGT 2100  
Db 2041 ATTAAGTCAAACTAATCTCAATCCTCTTAAAGTAACTACTGTGAGAAACAGAGT 2100  
QY 2101 GTTCTCAAGTGTGGGAGCGGCTTCTTAAATGAAGCAATGATTTGAACACTGTCCCT 2160  
Db 2101 GTTCTCAAGTGTGGGAGCGGCTTCTTAAATGAAGCAATGATTTGAACACTGTCCCT 2160

QY 2161 CTTGGCAGTTCATTAGTAAGTTCGAAAGTATATGACTGAGCGTATGACAGGTTAA 2220  
DB 2161 CTTGGCAGTTCATTAGTAAGTTCGAAAGTATATGACTGAGCGTATGACAGGTTAA 2220  
QY 2221 CTTGGCAGTTCATTAGTAAGTTCGAAAGTATATGACTGAGCGTATGACAGGTTAA 2280  
DB 2221 CTTGGCAGTTCATTAGTAAGTTCGAAAGTATATGACTGAGCGTATGACAGGTTAA 2280  
QY 2281 CATTAGCAGCACTGAAAGCAATTTATCAACCACTGAGAGAAATCAACCGAGCAGGCG 2340  
DB 2281 CATTAGCAGCACTGAAAGCAATTTATCAACCACTGAGAGAAATCAACCGAGCAGGCG 2340  
QY 2341 TGTGTGAAACATGTTGTATATGCGACTGCGAACAACCTGACCTTACGCCACTCCAGAA 2400  
DB 2341 TGTGTGAAACATGTTGTATATGCGACTGCGAACAACCTGACCTTACGCCACTCCAGAA 2400  
QY 2401 TGTATGTTTCAAGGTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460  
DB 2401 TGTATGTTTCAAGGTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460  
QY 2461 TAAAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
DB 2461 TAAAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
QY 2521 AAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580  
DB 2521 AAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580  
QY 2581 AAAAAA 2586  
DB 2581 AAAAAA 2586

RESULT 4  
AX697644 2586 bp DNA linear PAT 02-APR-2003  
LOCUS AX697644  
DEFINITION Sequence 235 from Patent WO0104311.  
ACCESSION AX697644  
VERSION AX697644.1 GI:29498737  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Ashkenazi, A.J., Borstein, D., Desnoyers, L., Baton, D.L., Ferrara, N.,  
Rilivartoff, E., Fong, S., Geo, W.Q., Gerber, H., Gertsen, M.E.,  
Goddard, A., Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Hillan, K.J.,  
Klavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, W.A.,  
Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.  
Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0104311-A 235 18-JAN-2001;  
Genentech Inc. (US)  
Location/Qualifiers  
1..2586  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 631 a 679 c 703 g 573 t

ORIGIN  
Query Match 100.0%; Score 2586; DB 6; Length 2586;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGCGCTCCCGACCG 60  
DB 1 CGCCGCGCTCCCGACCG 60  
QY 61 CGCGCGCTCCCGACCG 120  
DB 61 CGCGCGCTCCCGACCG 120

QY 121 GTCCGCGCGCGCGCTGCG 180  
DB 121 GTCCGCGCGCGCGCTGCG 180  
QY 181 GCTTGTCTGCG 240  
DB 181 GCTTGTCTGCG 240  
QY 241 CTCAGTCAAGCCCG 300  
DB 241 CTCAGTCAAGCCCG 300  
QY 301 TGTTCGCGAGGTTGAGGAACTGATGAGGAACTGATGAGGAACTGATGAGGAACTGATGAGG 360  
DB 301 TGTTCGCGAGGTTGAGGAACTGATGAGGAACTGATGAGGAACTGATGAGGAACTGATGAGG 360  
QY 361 AAGAGTGAAGGCGAAGAACTGCTGTAAGATGATGATGATGATGATGATGATGATGATGAT 420  
DB 361 AAGAGTGAAGGCGAAGAACTGCTGTAAGATGATGATGATGATGATGATGATGATGATGAT 420  
QY 421 TACCTCCAGCTTATCAATGAGCAACACAGACAGAGAGTTGAAATTAATACATCC 480  
DB 421 TACCTCCAGCTTATCAATGAGCAACACAGACAGAGAGTTGAAATTAATACATCC 480  
QY 481 ATGTGACCGGAAATTCAGAAATTAACCAACAGAGAGTTGAAATTAATACATCC 540  
DB 481 ATGTGACCGGAAATTCAGAAATTAACCAACAGAGAGTTGAAATTAATACATCC 540  
QY 541 AGACAGTTATCATCTGTGAG 600  
DB 541 AGACAGTTATCATCTGTGAG 600  
QY 601 ACGAGAGCTGTGCG 660  
DB 601 ACGAGAGCTGTGCG 660  
QY 661 CATGCGCGCGCGCGAG 720  
DB 661 CATGCGCGCGCGCGAG 720  
QY 721 GTGTGCGCGCGCGAG 780  
DB 721 GTGTGCGCGCGCGAG 780  
QY 781 ACCAGAGGAGCTGCG 840  
DB 781 ACCAGAGGAGCTGCG 840  
QY 841 TGTGACACACCCCTGCG 900  
DB 841 TGTGACACACCCCTGCG 900  
QY 901 ACCATCATACCTGCGAG 960  
DB 901 ACCATCATACCTGCGAG 960  
QY 961 GCTTCTTGTGCG 1020  
DB 961 GCTTCTTGTGCG 1020  
QY 1021 GAGAGCGGAGCGAAG 1080  
DB 1021 GAGAGCGGAGCGAAG 1080  
QY 1081 TTGAGAGCTTCAATGAG 1140  
DB 1081 TTGAGAGCTTCAATGAG 1140  
QY 1141 AAGAGATGCGCTGCG 1200  
DB 1141 AAGAGATGCGCTGCG 1200



QY 1201 TTATGATCTGACAGGCTGTGGGATGATGTGCAATAGAAATAGTATTTATTTCCCA 1260  
 DB 1201 TTATGATCTGACAGGCTGTGGGATGATGTGCAATAGAAATAGTATTTATTTCCCA 1260  
 QY 1261 GGTGTGCTTTAGGCGTGGGCTGACAGGCTTTCTCTCAATCTTTCTCCAGTAAGT 1320  
 DB 1261 GGTGTGCTTTAGGCGTGGGCTGACAGGCTTTCTCTCAATCTTTCTCCAGTAAGT 1320  
 QY 1321 TCCCTCTGCTGACAGCATAGAGTGTGTGCAATTTGTCACTCCCGAGCTGTCT 1380  
 DB 1321 TCCCTCTGCTGACAGCATAGAGTGTGTGCAATTTGTCACTCCCGAGCTGTCT 1380  
 QY 1321 TCCCTCTGCTGACAGCATAGAGTGTGTGCAATTTGTCACTCCCGAGCTGTCT 1380  
 DB 1321 TCCCTCTGCTGACAGCATAGAGTGTGTGCAATTTGTCACTCCCGAGCTGTCT 1380  
 QY 1381 CCAGGCTTCAAGTGTGTGCTTTGGAGAGTCAAGGAGGTTAACTGACAGGACAGTTT 1440  
 DB 1381 CCAGGCTTCAAGTGTGTGCTTTGGAGAGTCAAGGAGGTTAACTGACAGGACAGTTT 1440  
 QY 1441 GGCACCCCTGTGCAAGTATTTGGGCTGTTCCTTCAAGTGGGAGAGCGGCTGT 1500  
 DB 1441 GGCACCCCTGTGCAAGTATTTGGGCTGTTCCTTCAAGTGGGAGAGCGGCTGT 1500  
 QY 1501 TCTACATGCTTTGATTAATTTGTGAGGAGAGATGGAACAATGTGAGTCTCCCTC 1560  
 DB 1501 TCTACATGCTTTGATTAATTTGTGAGGAGAGATGGAACAATGTGAGTCTCCCTC 1560  
 QY 1561 TGATTTGCTTTGGGAAATGTGAGAGAGAGTCCCTGCTTTGCAAAATCACTGGCAA 1620  
 DB 1561 TGATTTGCTTTGGGAAATGTGAGAGAGAGTCCCTGCTTTGCAAAATCACTGGCAA 1620  
 QY 1621 AAATGCAACAATGATTTTCCAGCAGTCTTTTCAATGGGATAGTAAAGCTGTGCTT 1680  
 DB 1621 AAATGCAACAATGATTTTCCAGCAGTCTTTTCAATGGGATAGTAAAGCTGTGCTT 1680  
 QY 1681 CAGCTGTGACAGATGAAATGTTCTGTTCACCTGATTAACATGCTTTATTCACGCA 1740  
 DB 1681 CAGCTGTGACAGATGAAATGTTCTGTTCACCTGATTAACATGCTTTATTCACGCA 1740  
 QY 1741 GGTGCTCAGCTCCTACCTCTGTTCACGAGGAGATTTTCAATGCAAGTCAATCCG 1800  
 DB 1741 GGTGCTCAGCTCCTACCTCTGTTCACGAGGAGATTTTCAATGCAAGTCAATCCG 1800  
 QY 1801 TCTCTCAGCAAGCTGTGGGAGGGGCTCATTTGTTCTCTGCTCATGAGGATCTCAG 1860  
 DB 1801 TCTCTCAGCAAGCTGTGGGAGGGGCTCATTTGTTCTCTGCTCATGAGGATCTCAG 1860  
 QY 1861 GCTCAGAGCTGCAAGCTGTGGGAGGGGCTCATTTGTTCTCTGCTCATGAGGATCTCAG 1920  
 DB 1861 GCTCAGAGCTGCAAGCTGTGGGAGGGGCTCATTTGTTCTCTGCTCATGAGGATCTCAG 1920  
 QY 1921 ATCTGCTGTGACTCTAGCTCAGTGTCTCTCCACTACCCCAAGCAGGCTTGTGCTCA 1980  
 DB 1921 ATCTGCTGTGACTCTAGCTCAGTGTCTCTCCACTACCCCAAGCAGGCTTGTGCTCA 1980  
 QY 1981 CCAAAAAGCTGCTCCCAAAAGGAGGAAATGGGATTTTCTTGAAGGATGACATCTGGA 2040  
 DB 1981 CCAAAAAGCTGCTCCCAAAAGGAGGAAATGGGATTTTCTTGAAGGATGACATCTGGA 2040  
 QY 2041 ATTAAGCTCAACTAATCTCACAATCCCTCTAAAGTAACTACTGCTTAGAGACAGAGT 2100  
 DB 2041 ATTAAGCTCAACTAATCTCACAATCCCTCTAAAGTAACTACTGCTTAGAGACAGAGT 2100  
 QY 2101 GTTCTCAGAGTGTGGGAGCGCTCTCTTAATGAGCAATGATTAATGACATGCTCCCT 2160  
 DB 2101 GTTCTCAGAGTGTGGGAGCGCTCTCTCTTAATGAGCAATGATTAATGACATGCTCCCT 2160  
 QY 2161 CTTTGGCAGTTGCAATTAATCTTGAAGGATATGACTGAGGCTGACATGAGTTAA 2220  
 DB 2161 CTTTGGCAGTTGCAATTAATCTTGAAGGATATGACTGAGGCTGACATGAGTTAA 2220  
 QY 2221 CCTGCAAGAAAGTAATCTTAGGTAATGTAGGCGAGGATTAATAATGAAATTTGCAAAAT 2280  
 DB 2221 CCTGCAAGAAAGTAATCTTAGGTAATGTAGGCGAGGATTAATAATGAAATTTGCAAAAT 2280  
 QY 2281 CACTTAGCAGCACTGAAGCAATTAATCAACAGCTGAGAGAAATCAAAACGAGCAGGGC 2340

DB 2281 CACTTAGCAGCACTGAAGCAATTAATCAACAGCTGAGAGAAATCAAAACGAGCAGGGC 2340  
 QY 2341 TGTGTAACCATGCTTTGTAATTTGACCTGCGAACAACGAACTTACGCACTCCACAA 2400  
 DB 2341 TGTGTAACCATGCTTTGTAATTTGACCTGCGAACAACGAACTTACGCACTCCACAA 2400  
 QY 2401 TGAATTTTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460  
 DB 2401 TGAATTTTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460  
 QY 2461 TAAAGTTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
 DB 2461 TAAAGTTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
 QY 2521 AAGTTGCAATTTGAATCAAGATTAATCACTTCACTGCACTGCACTGCACTGCACT 2580  
 DB 2521 AAGTTGCAATTTGAATCAAGATTAATCACTTCACTGCACTGCACTGCACTGCACT 2580  
 QY 2581 AAAAAA 2586  
 DB 2581 AAAAAA 2586  
 RESULT 5  
 BD075562  
 LOCUS  
 DEFINITION  
 BD075562  
 Secretory and transmembrane polypeptide and nucleic acid encoding  
 the same.  
 ACCESSION  
 BD075562  
 VERSION  
 BD075562.1 GI:22621165  
 KEYWORDS  
 JP 2001516580-A/195.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 2586)  
 Wood, W.I., Gurney, A.L., Goddard, A., Penica, D., Chen, J. and Yuan, J.  
 Secretory and transmembrane polypeptide and nucleic acid encoding  
 the same  
 JOURNAL  
 Patent: JP 2001516580-A 195 02-OCT-2001;  
 GENENTECH INC  
 OS Homo sapiens (human)  
 PN JP 2001516580-A/195  
 PD 02-OCT-2001  
 PR 16-SEP-1998 JP 2000511867  
 PR 17-SEP-1997 US 60/059112,17-SEP-1997 US 60/059117 PR  
 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR  
 17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR  
 18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR  
 17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR  
 21-OCT-1997 US 60/062486,24-OCT-1997 US 60/062816 PR  
 24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR  
 24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR  
 24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR  
 27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR  
 28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR  
 28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR  
 28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063546 PR  
 29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063728 PR  
 29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063735 PR  
 29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063745 PR  
 29-OCT-1997 US 60/064103,31-OCT-1997 US 60/063870 PR  
 30-NOV-1997 US 60/064248,07-NOV-1997 US 60/064809 PR  
 12-NOV-1997 US 60/065186,17-NOV-1997 US 60/065846 PR  
 18-NOV-1997 US 60/065693,21-NOV-1997 US 60/066120 PR  
 21-NOV-1997 US 60/066364,24-NOV-1997 US 60/066772 PR  
 24-NOV-1997 US 60/066466,24-NOV-1997 US 60/066770 PR  
 24-NOV-1997 US 60/066511,24-NOV-1997 US 60/066453 PR  
 25-NOV-1997 US 60/066840  
 PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDLEY GODDARD,DIANE PENICA, PI  
 JEAN CHEN,

PI JEAN YUAN  
PC C12N15/09, C07K14/47, C07K14/705, C07K16/18, C07K16/28, C07K19/00,  
PC C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12P21/08, C12Q1/02, C12P21/08, PC  
C12R1/31,  
PC C12N15/00, C12N5/00  
CC secretory and transmembrane polypeptide and nucleic acid CC  
FH Key Location/Qualifiers  
FT source 1. 2586  
FT Location/Qualifiers  
1. 2586  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 631 a 679 c 703 g 573 t

ORIGIN

Query Match 100.0%; Score 2586; DB 6; Length 2586;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGCCGCGCTCCCGACCCGCGGCGCCGACCGCGCGCTCCCGCATCTGCAACCGGCAAG 60  
1 CGCCGCGCTCCCGACCCGCGGCGCCGACCGCGCGCTCCCGCATCTGCAACCGGCAAG 60  
61 CCGGCGGCTCCCGCGCGGAGCGAGATCCAGTCCGCGCGCGCATCTGCAACCGGCAAG 120  
61 CCGGCGGCTCCCGCGCGGAGCGAGATCCAGTCCGCGCGCGCATCTGCAACCGGCAAG 120  
121 GTGGGGGCGGCGCTGGGGGCGGAGCGGAGATGCAAGCGGCTTGGGGGCAACCTCTCTGT 180  
121 GTGGGGGCGGCGCTGGGGGCGGAGCGGAGATGCAAGCGGCTTGGGGGCAACCTCTCTGT 180  
121 GTGGGGGCGGCGCTGGGGGCGGAGCGGAGATGCAAGCGGCTTGGGGGCAACCTCTCTGT 180  
181 GCGTGTCTGTGGGCGGCGGATCCCAAGCGCGCGCGCGCTCCGACGCGGCACTCGG 240  
181 GCGTGTCTGTGGGCGGCGGATCCCAAGCGCGCGCGCGCTCCGACGCGGCACTCGG 240  
241 CTCGAGTCAAGCCCGCGCGCTTCTCAGTACCCGCGAGAGAGGCGCATCTTAATGA 300  
241 CTCGAGTCAAGCCCGCGCGCTTCTCAGTACCCGCGAGAGAGGCGCATCTTAATGA 300  
301 TGTTCGCGAGGTTGAGGAAGTGTATGAGGAGCAAGCATCATCAAGTGAACCTGGCAACT 420  
301 TGTTCGCGAGGTTGAGGAAGTGTATGAGGAGCAAGCATCATCAAGTGAACCTGGCAACT 420  
361 AAGAGATGAGGCGAGAGAGTGTCTTAAGCATCATCAAGTGAACCTGGCAACT 420  
361 AAGAGATGAGGCGAGAGAGTGTCTTAAGCATCATCAAGTGAACCTGGCAACT 420  
421 TACTTCCAGTATCAATGAGCAACAGACAGACAGAGTTGAGAAATTAATACATCC 480  
421 TACTTCCAGTATCAATGAGCAACAGACAGACAGAGTTGAGAAATTAATACATCC 480  
481 ATGTGACCGAGAAATTCACAAAGTAACCAACAGACAGTGAACAATGTCTTTTCAG 540  
481 ATGTGACCGAGAAATTCACAAAGTAACCAACAGACAGTGAACAATGTCTTTTCAG 540  
541 AAGAGTTATCAATCTGTGGAGAGCAAGAGGCGAGAGAACCCAGATGATCATG 600  
541 AAGAGTTATCAATCTGTGGAGAGCAAGAGGCGAGAGAACCCAGATGATCATG 600  
601 ACGAGGACTGTGGGCCAGATGATGCGCAGTTTGCACTTCCAGTACACTGCGAG 660  
601 ACGAGGACTGTGGGCCAGATGATGCGCAGTTTGCACTTCCAGTACACTGCGAG 660  
661 CATGCCGCGGCGAGAGATGCTGTGCAACCGGAGCAATGAGTCTGTGAGACCACTGT 720  
661 CATGCCGCGGCGAGAGATGCTGTGCAACCGGAGCAATGAGTCTGTGAGACCACTGT 720  
721 GTGTCTGGGCTCACTGCAACCAAAATGCGCACAGGGGCAACAATGGGACCATCTGTGACA 780

DB 721 GTGTCTGGGCTCACTGCAACCAAAATGCGCACAGGGGCAACAATGGGACCATCTGTGACA 780  
QY ACCAGAGGACTGTGCGAGCCGCGGCGTGTGCTGTGCTTCCAGAGAGGCGCTGTCTCTG 840  
QY 781 ACCAGAGGACTGTGCGAGCCGCGGCGTGTGCTGTGCTTCCAGAGAGGCGCTGTCTCTG 840  
DB 841 TGTGCAACCCCTGCGCGGAGGCGAGCTTTTGCATGACCCCGGACGCGGCTTCTG 900  
QY 841 TGTGCAACCCCTGCGCGGAGGCGAGCTTTTGCATGACCCCGGACGCGGCTTCTG 900  
DB 841 TGTGCAACCCCTGCGCGGAGGCGAGCTTTTGCATGACCCCGGACGCGGCTTCTG 900  
QY 841 TGTGCAACCCCTGCGCGGAGGCGAGCTTTTGCATGACCCCGGACGCGGCTTCTG 900  
DB 901 ACCATATACCTGAGAGTATGAGGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 960  
QY 901 ACCATATACCTGAGAGTATGAGGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 960  
DB 901 ACCATATACCTGAGAGTATGAGGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 960  
QY 901 ACCATATACCTGAGAGTATGAGGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 960  
DB 961 GCTCTCTGCGAGCCCGACAGCCAGACGCTGTATGATGATGAGACCGACCTTCTG 1020  
QY 961 GCTCTCTGCGAGCCCGACAGCCAGACGCTGTATGATGATGAGACCGACCTTCTG 1020  
DB 961 GCTCTCTGCGAGCCCGACAGCCAGACGCTGTATGATGATGAGACCGACCTTCTG 1020  
QY 1021 GAGAGCGTGAACCAAGATGAGGAGATCTGTCTGCGCCAGAGAGTCCCGATGATGATGAG 1080  
DB 1021 GAGAGCGTGAACCAAGATGAGGAGATCTGTCTGCGCCAGAGAGTCCCGATGATGATGAG 1080  
QY 1081 TTGGAGCTTATGAGAGAGGATGAGGCGGAGAGCTGAGAGAGCTTGAAGAGAGCTGAG 1140  
DB 1081 TTGGAGCTTATGAGAGAGGATGAGGCGGAGAGCTGAGAGAGCTTGAAGAGAGCTGAG 1140  
QY 1141 AAGAGATGCGGCTGAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1200  
DB 1141 AAGAGATGCGGCTGAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1200  
QY 1201 TTTAGATGAGACAGGCTGAGGAGTATGAGAAATGAGAAATGAGAAATGAGAAATGAG 1260  
DB 1201 TTTAGATGAGACAGGCTGAGGAGTATGAGAAATGAGAAATGAGAAATGAGAAATGAG 1260  
QY 1261 GATGTGTCTTTAGGCGTGAACAAGCTTCTTCTCATCATCTTCTTCTCATCATCTT 1320  
DB 1261 GATGTGTCTTTAGGCGTGAACAAGCTTCTTCTCATCATCTTCTTCTCATCATCTT 1320  
QY 1321 TCCCTCTGCTTGAACAGATGAGTGTGTGCAATTTGCAAGTCCCGGAGGCTTCT 1380  
DB 1321 TCCCTCTGCTTGAACAGATGAGTGTGTGCAATTTGCAAGTCCCGGAGGCTTCT 1380  
QY 1381 CAGGCTTCAAGTCTGAGTGTGTGCAATTTGCAAGTCCCGGAGGCTTCT 1440  
DB 1381 CAGGCTTCAAGTCTGAGTGTGTGCAATTTGCAAGTCCCGGAGGCTTCT 1440  
QY 1441 GCGACCCCTGTCAGATTAATGAGTGTGTGCAATTTGCAAGTCCCGGAGGCTTCT 1500  
DB 1441 GCGACCCCTGTCAGATTAATGAGTGTGTGCAATTTGCAAGTCCCGGAGGCTTCT 1500  
QY 1501 TCTCATGAGCTTGAATTTGAGGAGGAGAGTGAAGCAATGAGTGAAGTGAAGTGAAG 1560  
DB 1501 TCTCATGAGCTTGAATTTGAGGAGGAGAGTGAAGCAATGAGTGAAGTGAAGTGAAG 1560  
QY 1561 TGAATGTTTGGGAAATGAGGAGAGTGTGTGCAATTTGCAAGTCCCGGAGGCTTCT 1620  
DB 1561 TGAATGTTTGGGAAATGAGGAGAGTGTGTGCAATTTGCAAGTCCCGGAGGCTTCT 1620  
QY 1621 AATGCAACCAATGAAATTTTCAAGCAGTCTTCTCAATGAGGCAATGAGTGAAGTGAAG 1680  
DB 1621 AATGCAACCAATGAAATTTTCAAGCAGTCTTCTCAATGAGGCAATGAGTGAAGTGAAG 1680  
QY 1681 CAGCTGTGAGATGAATGTTCTGTGTCAACCTGATTAATGAGTGAATGAGTGAAGTGAAG 1740  
DB 1681 CAGCTGTGAGATGAATGTTCTGTGTCAACCTGATTAATGAGTGAATGAGTGAAGTGAAG 1740  
QY 1741 GTGTGCTCAGCTCTTCACTGTGTGCAAGGAGGAGATTTTCAATCAATCAATCAATCC 1800  
DB 1741 GTGTGCTCAGCTCTTCACTGTGTGCAAGGAGGAGATTTTCAATCAATCAATCAATCC 1800  
QY 1801 TCTCTGAGCAGGCTGAGGAGGAGGAGTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCT 1860  
DB 1801 TCTCTGAGCAGGCTGAGGAGGAGGAGTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCT 1860

QY	1861	GCTCAGAGACATCGCAAGCGCTTGCCCAAGTCAACAGCTATGSAAGCACAGAGAGTTCC	1920
Db	1861	GCTCAGAGACATCGCAAGCGCTTGCCCAAGTCAACAGCTATGSAAGCACAGAGAGTTCC	1920
QY	1921	ATCTGTTGTGACTCTAAGCTCAAGTCTCTCTCCACTACCCACACAGCCTTGATGCCA	1980
Db	1921	ATCTGTTGTGACTCTAAGCTCAAGTCTCTCTCCACTACCCACACAGCCTTGATGCCA	1980
QY	1981	CCAAAGAAGTCCCCCAAAAGAGAGAAATGGGAATTTTCTTGAGGAGATGACATCTGGA	2040
Db	1981	CCAAAGAAGTCCCCCAAAAGAGAGAAATGGGAATTTTCTTGAGGAGATGACATCTGGA	2040
QY	2041	ATTAAAGTCAAACTAATTTCTGCATCCCTCTAAAGTAACTACTGTTAGGAACAGAGT	2100
Db	2041	ATTAAAGTCAAACTAATTTCTGCATCCCTCTAAAGTAACTACTGTTAGGAACAGAGT	2100
QY	2101	GTTTCTCAAGTGGGGGAGCGCGCTTCTATAGACAAATGATATTGACATCTGCCCT	2160
Db	2101	GTTTCTCAAGTGGGGGAGCGCGCTTCTATAGACAAATGATATTGACATCTGCCCT	2160
QY	2161	CTTTCGACGTTGCATTAGTAATTTGAAAGGTAATGACTGAGCGTACATACAGGTTAA	2220
Db	2161	CTTTCGACGTTGCATTAGTAATTTGAAAGGTAATGACTGAGCGTACATACAGGTTAA	2220
QY	2221	CTTCGACAGAAACAGTACTTAAGTAAATTTGAGGGCGAGATTATTAATGAAATTTGCCAAAT	2280
Db	2221	CTTCGACAGAAACAGTACTTAAGTAAATTTGAGGGCGAGATTATTAATGAAATTTGCCAAAT	2280
QY	2281	CACCTTACGACGAATGGAAGAACATTAATCAACAGTGGAGAAATCAAAACCGACAGGGC	2340
Db	2281	CACCTTACGACGAATGGAAGAACATTAATCAACAGTGGAGAAATCAAAACCGACAGGGC	2340
QY	2341	TGTGTGAAACATGCTTTGTAATATGCGACTGCGAAACATGAACTTAGCGCCTCACAAA	2400
Db	2341	TGTGTGAAACATGCTTTGTAATATGCGACTGCGAAACATGAACTTAGCGCCTCACAAA	2400
QY	2401	TGATGTTTTCAGTGTGTCATGAGTGTGGCCACGACATGATATCATCGAGTTCTTAAAGTT	2460
Db	2401	TGATGTTTTCAGTGTGTCATGAGTGTGGCCACGACATGATATCATCGAGTTCTTAAAGTT	2460
QY	2461	TAAAGTTGCACATATGTAATAGACATGCTTTCTTGATTTAAATTATGTAATAACAT	2520
Db	2461	TAAAGTTGCACATATGTAATAGACATGCTTTCTTGATTTAAATTATGTAATAACAT	2520
QY	2521	AAGTTGCATTTAGAAATCAAGCATAAATCACTTCAACGCAAAAAA	2580
Db	2521	AAGTTGCATTTAGAAATCAAGCATAAATCACTTCAACGCAAAAAA	2580
QY	2581	AAAAAA 2586	
Db	2581	AAAAAA 2586	
RESULT 6			
BD172422			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
GENBANK			

[illegible]



QY 301 TGTTCGGCAGGTTGAGAACTGANTGAGAGACAACGACGACAAATTTGCGACGCGGTGG 360  
DB 301 TGTTCGGCAGGTTGAGAACTGANTGAGAGACACGACGACAAATTTGCGACGCGGTGG 360  
QY 361 AAGAGATGAGAGGAGAGAAAGCTGTCTTAAGGACATCAGAAAGTGAACCTGGGAACT 420  
DB 361 AAGAGATGAGAGGAGAGAAAGCTGTCTTAAGGACATCAGAAAGTGAACCTGGGAACT 420  
QY 421 TACCTCCAGCTATCACAATGAGACCAACAGACAGAAAGTTGAAATTAATCATCC 480  
DB 421 TACCTCCAGCTATCACAATGAGACCAACAGACAGAAAGTTGAAATTAATCATCC 480  
QY 481 ATGTGACCGAGAAATTTCAACAATTAACAAACCAACGATGAGAAATGCTTTTCA 540  
DB 481 ATGTGACCGAGAAATTTCAACAATTAACAAACCAACGATGAGAAATGCTTTTCA 540  
QY 541 AGACAGTTATCAATCTGTGGAGACGAAGAGGAGAGAGAGACGAGTGCATCATCG 600  
DB 541 AGACAGTTATCAATCTGTGGAGACGAAGAGGAGAGAGAGACGAGTGCATCATCG 600  
QY 601 ACAGAGACTGTGGGCCCCAGATGTAATGCGAGTTTCCAGCTTCCAGTACACCTGCACG 660  
DB 601 ACAGAGACTGTGGGCCCCAGATGTAATGCGAGTTTCCAGCTTCCAGTACACCTGCACG 660  
QY 661 CATGCCGAGGAGAGATGCTGTGACACCGGAGACAGTGAAGTGTGAGACAGCTGT 720  
DB 661 CATGCCGAGGAGAGATGCTGTGACACCGGAGACAGTGAAGTGTGAGACAGCTGT 720  
QY 721 GTGTCTGGGGTCACTGACCAAAATGAGCAACAGGGGAGCAATGGGACATCTGTGACA 780  
DB 721 GTGTCTGGGGTCACTGACCAAAATGAGCAACAGGGGAGCAATGGGACATCTGTGACA 780  
QY 781 ACCAGAGGAGACTGCGACCGGGGCTGTGCTGTGCTTCCAGAGAGGCTGTGCTTCCG 840  
DB 781 ACCAGAGGAGACTGCGACCGGGGCTGTGCTGTGCTTCCAGAGAGGCTGTGCTTCCG 840  
QY 841 TGTGACACACCCCTGCGGTGAGAGGAGGAGGCTTTGCCATGACCCCGCAGCTTCTGG 900  
DB 841 TGTGACACACCCCTGCGGTGAGAGGAGGAGGCTTTGCCATGACCCCGCAGCTTCTGG 900  
QY 901 ACCTCAATCACTGGAGAGCTTGAAGACCTGATGAGACCTTGAACCGATGCTTGTGCAAG 960  
DB 901 ACCTCAATCACTGGAGAGCTTGAAGACCTGATGAGACCTTGTGACCGATGCTTGTGCAAG 960  
QY 961 GCCTCCTGTGCGACGCCCAACGACGACGCTGTGTATGTGTGCAAGCGACCTTGTGG 1020  
DB 961 GCCTCCTGTGCGACGCCCAACGACGACGCTGTGTATGTGTGCAAGCGACCTTGTGG 1020  
QY 1021 GAGACCGTGAACCAAGTGGGAGATCTGTGCTGCCAGAGAGGTTCCCGATGATGAAG 1080  
DB 1021 GAGACCGTGAACCAAGTGGGAGATCTGTGCTGCCAGAGAGGTTCCCGATGATGAAG 1080  
QY 1081 TTGGCAGCTTCAAGAGAGAGTGTGCGACAGGAGCTGAGAGACCTGAGAGAGAGAGCTG 1140  
DB 1081 TTGGCAGCTTCAAGAGAGAGTGTGCGACAGGAGCTGAGAGAGCTGAGAGAGAGAGCTG 1140  
QY 1141 AAGAGATGCGCTGGGGAGACCTGTGCGCTGCGCGCTGCACTGTGAGAGGAGAGAGAGA 1200  
DB 1141 AAGAGATGCGCTGGGGAGACCTGTGCGCTGCGCGCTGCACTGTGAGAGGAGAGAGAGA 1200  
QY 1201 TTATGATCTGAGACAGGCTGTGGGTAGATGTGCAATGAAATGCAATTTATTTCCCA 1260  
DB 1201 TTATGATCTGAGACAGGCTGTGGGTAGATGTGCAATGAAATGCAATTTATTTCCCA 1260  
QY 1261 GGTGTGTCTTTAAGCGGTGAGACAGGCTTCTTCTAATCTTTTCCAGTAAGTT 1320  
DB 1261 GGTGTGTCTTTAAGCGGTGAGACAGGCTTCTTCTAATCTTTTCCAGTAAGTT 1320  
QY 1321 TCCCTCTGCTTGAAGAGCTGAGAGTGTGATTTGTTGAGCTGCTGAGAGCTTCT 1380  
DB 1321 TCCCTCTGCTTGAAGAGCTGAGAGTGTGATTTGTTGAGCTGCTGAGAGCTTCT 1380

QY 1381 CCAGGCTTCAACAGTGTGCTTGGAGAGTCAAGGAGGTTAACTGACAGAGCACTTT 1440  
DB 1381 CCAGGCTTCAACAGTGTGCTTGGAGAGTCAAGGAGGTTAACTGACAGAGCACTTT 1440  
QY 1441 GCGACCCCTGTCCAGATTAATTTGGCTGTGCTTACAGCTTGGAGAGAGGCTTGT 1500  
DB 1441 GCGACCCCTGTCCAGATTAATTTGGCTGTGCTTACAGCTTGGAGAGAGGCTTGT 1500  
QY 1501 TCTACATGCTTGTATTAATTTTGAAGGAGAGAGATGAAACATATGTGAGTCTCCCTC 1560  
DB 1501 TCTACATGCTTGTATTAATTTTGAAGGAGAGAGATGAAACATATGTGAGTCTCCCTC 1560  
QY 1561 TGATGTGTTTTGGGAAATGTGAGAAAGATGACCTGCTTGTGCAACATCACTGGCAA 1620  
DB 1561 TGATGTGTTTTGGGAAATGTGAGAAAGATGACCTGCTTGTGCAACATCACTGGCAA 1620  
QY 1621 AAATGCAACAAATGAAATTTTCAAGCAGTCTTCCATGGGCAATAGTAAGTGTGCTT 1680  
DB 1621 AAATGCAACAAATGAAATTTTCAAGCAGTCTTCCATGGGCAATAGTAAGTGTGCTT 1680  
QY 1681 CAGCTGTGAGAGTGAATGTTCTGTGACACCTGCAATTAATGTTTATTCATCCAGCA 1740  
DB 1681 CAGCTGTGAGAGTGAATGTTCTGTGACACCTGCAATTAATGTTTATTCATCCAGCA 1740  
QY 1741 GTGTGTGCTCAGCTCTCTCTGTGCGAGGAGCAATTTTCATATCCAGATCAATCCC 1800  
DB 1741 GTGTGTGCTCAGCTCTCTCTGTGCGAGGAGCAATTTTCATATCCAGATCAATCCC 1800  
QY 1801 TCTCTCAGCAGCTGTGGGAGGGGGTCAATTTCTCTCTGTGCTATAGGATCTCAGAG 1860  
DB 1801 TCTCTCAGCAGCTGTGGGAGGGGGTCAATTTCTCTCTGTGCTATAGGATCTCAGAG 1860  
QY 1861 GCTCAGAGACTGCAAGCTGTGCTGCCCAAGTCAACAGCTAGTGAAGACAGAGAGTTTC 1920  
DB 1861 GCTCAGAGACTGCAAGCTGTGCTGCCCAAGTCAACAGCTAGTGAAGACAGAGAGTTTC 1920  
QY 1921 ATCTGTGTGACTTAAGCTCAGTGTCTCTGCTCACTAATCCCAACAGCTTGTGCGCA 1980  
DB 1921 ATCTGTGTGACTTAAGCTCAGTGTCTCTGCTCACTAATCCCAACAGCTTGTGCGCA 1980  
QY 1981 CCAGAGTGTGCTCCCAAGAGAGAGAGAGATGGGATTTTCTTGGAGATGACATCTGGA 2040  
DB 1981 CCAGAGTGTGCTCCCAAGAGAGAGAGAGATGGGATTTTCTTGGAGATGACATCTGGA 2040  
QY 2041 ATTAAGTCAAACTAATTTCTCAATCCCTTAAAGTAACTAAGTAAAGAGAGAGT 2100  
DB 2041 ATTAAGTCAAACTAATTTCTCAATCCCTTAAAGTAACTAAGTAAAGAGAGAGT 2100  
QY 2101 GTTCTCAAGTGGGAGGAGCGGCTTCTTAAGAGACATGATTAACATGCTGCT 2160  
DB 2101 GTTCTCAAGTGGGAGGAGCGGCTTCTTAAGAGACATGATTAACATGCTGCT 2160  
QY 2161 CTTTGGCAGTTGCTTGTAACTTTGAAGATATGATGAGAGGTGATACAGTTAA 2220  
DB 2161 CTTTGGCAGTTGCTTGTAACTTTGAAGATATGATGAGAGGTGATACAGTTAA 2220  
QY 2221 CTTGCAAAACAGTACTTAAGTAAATGTAGGCGAGATTTTAAATTAATTTGCAAAAT 2280  
DB 2221 CTTGCAAAACAGTACTTAAGTAAATGTAGGCGAGATTTTAAATTAATTTGCAAAAT 2280  
QY 2281 CACTTACAGCACTGAAGCAATTAATCAACAGCTGAGAGAAATCAACAGAGAGG 2340  
DB 2281 CACTTACAGCACTGAAGCAATTAATCAACAGCTGAGAGAAATCAACAGAGAGG 2340  
QY 2341 TGTGTAAACATGTTGTATATGCGAGCTGCGAACCTGAATCTTACAGCACTTCAAAA 2400  
DB 2341 TGTGTAAACATGTTGTATATGCGAGCTGCGAACCTGAATCTTACAGCACTTCAAAA 2400  
QY 2401 TGATGTTTTGAGGTGATGAGCTGTGCGACAGATGATTCATCCAGAGTCTTAAAGTT 2460  
DB 2401 TGATGTTTTGAGGTGATGAGCTGTGCGACAGATGATTCATCCAGAGTCTTAAAGTT 2460  
QY 2461 TAAAGTTGACATGATGATTAAGCATGCTTTCTTGAAGTTTAAATTAATTAATTAAT 2520

Db	2461	TTAAGTCCACATGATTGTTATAGCATGCTTCTTCTTGAGTTTAATTATGATTAACAT	2520
OY	2521	AAAGTGCACTTAGAAATCAAGCATTAATCACTTCACCTGCAAAAAAAAAAAAAA	2586
Db	2521	AAAGTGCACTTAGAAATCAAGCATTAATCACTTCACCTGCAAAAAAAAAAAAAA	2586
OY	2581	AAAAAA 2586	
Db	2581	AAAAAA 2586	
RESULT 7			
BD172741			
LOCUS			
DEFINITION	BD172741	2586 bp	DNA
	Secreted and transmembrane polypeptides and nucleic acids encoding the same.		linear
ACCESSION	BD172741		
VERSION	BD172741.1	GI:28414045	
KEYWORDS	JP 2002238586-A/195.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1 (bases 1 to 2586)		
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: JP 2002238586-A 195 27-AUG-2002;		
COMMENT	GENENTECH INC. OS Homo sapiens (human) PN JP 2002238586-A/195 PD 27-AUG-2002 PF 18-DEC-2001 JP 2001385205 PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR 17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR 60/059119,18-SEP-1997 US 60/059263 PR 18-SEP-1997 US 60/059266,18-SEP-1997 US 60/062125 PR 17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR 21-OCT-1997 US 60/062486,21-OCT-1997 US 60/062816 PR 24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR 24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR 24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR 27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR 28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR 28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR 28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR 29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR 29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063735 PR 29-OCT-1997 US 60/064215,29-OCT-1997 US 60/064213 PR 29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064208 PR 31-OCT-1997 US 60/063870,31-OCT-1997 US 60/064428 PR 07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR 07-NOV-1997 US 60/065844,18-NOV-1997 US 60/065653 PR 21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR 24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR 24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR 24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI JIAN ZHENG, PI JEAN YUAN PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC C12N5/10, C12N5/10, PC C12P21/02//C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19) , PC (C12N5/10, C12R1:91), (C12P21/02, C12R1:91), (C12P21/02, C12R1:645), PC (C12P21/02, C12R1:19), (C12P21/08, C12R1:91), C12N15/00, C12N5/00, PC (C12N5/10, C12R1:91) CC Secreted and transmembrane polypeptides and nucleic CC acids encoding the same FH Key Location/Qualifiers		

FEATURES	source	FT	source	1. .2586	/organism='Homo sapiens (human)'	Location/Qualifiers
				1. .2586		
					/organism="Homo sapiens"	
					/mol_type="genomic DNA"	
					/db_xref="taxon:9606"	
BASE COUNT			631 a	679 c	703 g	573 t
ORIGIN						
Query Match			100.0%;	Score 2586;	DB 6;	Length 2586;
Best Local Similarity			100.0%;	Pred. No. 0;		
Matches 2586;			Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1	CGCCGCGCTCCCGACCCCGGGGCCCCCGCCACCGCGCGCGCTCCCGCACTGTGACCCCGACG	60			
Db	1	CGCGCGCTCCCGACCCCGGGGCCCCCGCCACCGCGCGCTCCCGCACTGTGACCCCGACG	60			
OY	61	CCGCGCGCTCCCGCGCGGAGACGAGCAGATCCAGTCGCGGCGCGGACGCGCAACTGCTCCA	120			
Db	61	CCGCGCGCTCCCGCGCGGAGACGAGCAGATCCAGTCGCGGCGCGGACGCGCAACTGCTCCA	120			
OY	121	GTCGCGGCGCGGCTGCGGCGCGACAGCGGAGATGCAGCGGCTTTGGGCGCACTCTGCTGT	180			
Db	121	GTCGCGGCGCGGCTGCGGCGCGACAGCGGAGATGCAGCGGCTTTGGGCGCACTCTGCTGT	180			
OY	181	GCCGCTGCTGCGCGCGCGCGGCTCCCGACGGCCCCCGCGCGCTCCGACGACGACTCTCGG	240			
Db	181	GCCGCTGCTGCGCGCGCGCGGCTCCCGACGGCCCCCGCGCGCTCCGACGACGACTCTCGG	240			
OY	241	CTCCAGTCGAAGCCCGCGCGCTCTCGACTACCCCGCAGAGAGAGGCCACCTCCATGAGA	300			
Db	241	CTCCAGTCGAAGCCCGCGCGCTCTCGACTACCCCGCAGAGAGAGGCCACCTCCATGAGA	300			
OY	301	TGTTCCCGCGAGTTGAAGAACTATGAGAGACACGACGACCAATTGGCGAGCGCGGTGG	360			
Db	301	TGTTCCCGCGAGTTGAAGAACTATGAGAGACACGACGACCAATTGGCGAGCGCGGTGG	360			
OY	361	AAGAGATGAGGCGAGAGAACTGCTGCTTAAGCATCATGAGAAGTGAACTCGCAAACT	420			
Db	361	AAGAGATGAGGCGAGAGAACTGCTGCTTAAGCATCATGAGAAGTGAACTCGCAAACT	420			
OY	421	TACCTCCAGCTATCACAATGAGACCAACACAGACAGAAAGTTGGAAATATACATCC	480			
Db	421	TACCTCCAGCTATCACAATGAGACCAACACAGACAGAAAGTTGGAAATATACATCC	480			
OY	481	ATGTGCACCGGAAATTCACAAGATTAACAACAACGATGGAACAATGGTCTTTCAAG	540			
Db	481	ATGTGCACCGGAAATTCACAAGATTAACAACAACAAGTGAACAATGGTCTTTCAAG	540			
OY	541	AGACAGTTATCACTCTGTGGGAGACGAGAGGCGAGAGAGGACACGAGTGATCATCG	600			
Db	541	AGACAGTTATCACTCTGTGGGAGACGAGAGGCGAGAGAGGACACGAGTGATCATCG	600			
OY	601	ACGAGGACTGTGGGCCCCAGACATGATACAGATTTGCACTTCCAGTACACCTGCCAGC	660			
Db	601	ACGAGGACTGTGGGCCCCAGACATGATACAGATTTGCACTTCCAGTACACCTGCCAGC	660			
OY	661	CATCCCGGCGCGAGAGATGCTCTGCACCCCGGACAGATGATGTGTGTGAGACCAAGCTGT	720			
Db	661	CATCCCGGCGCGAGAGATGCTCTGCACCCCGGACAGATGATGTGTGTGAGACCAAGCTGT	720			
OY	721	GTCGTCGGGCTCACTGACCAAAATGGCCACAGAGGCGACCAATGGGACCATCTGTGACA	780			
Db	721	GTCGTCGGGCTCACTGACCAAAATGGCCACAGAGGCGACCAATGGGACCATCTGTGACA	780			
OY	781	ACCAAGAGGACTGCGACGCGGCTGTGCTGTCTTCCAGAGAGGCTCTGTCTCTG	840			
Db	781	ACCAAGAGGACTGCGACGCGGCTGTGCTGTCTTCCAGAGAGGCTCTGTCTCTG	840			
OY	841	TGTGCACACCTCTGCGCTGTGAGAGGCGAGCTTTGGCATGACCCCGCCAGCGGCTTCTGG	900			
Db	841	TGTGCACACCTCTGCGCTGTGAGAGGCGAGCTTTGGCATGACCCCGCCAGCGGCTTCTGG	900			

Qy	90	ACCTCATACCTGGAGGCTTAGAGACCTGATGAGGACCTTGAGACCAATGCGCTTGTCGCAAGG	96
Dp	901	ACCTCATACCTGGAGGCTTAGAGACCTGATGAGGACCTTGAGACCAATGCGCTTGTCGCAAGG	960
Qy	961	GCTCTCTCTGCAAGCCCCACAGCTCAAGCTGTGTATGTGTCAAGCTTCTGTGG	1021
Dp	961	GCTCTCTCTGCAAGCCCCACAGCTCAAGCTGTGTATGTGTCAAGCTTCTGTGG	1021
Qy	1021	GAGAGCGTGACCAAGATGAGGAGAGATCTGTGCCCAAGAGAGTCCCGATGAGATGAAG	1081
Dp	1021	GAGAGCGTGACCAAGATGAGGAGAGATCTGTGTGCCCAAGAGAGTCCCGATGAGATGAAG	1081
Qy	1081	TTGGCAAGCTTCAATGAGAGAGTGTGCGCAGAGAGCTGTGAAGACTGTGAAGCTTGA	1141
Dp	1081	TTGGCAAGCTTCAATGAGAGAGTGTGCGCAGAGAGCTGTGAAGACTGTGAAGCTTGA	1141
Qy	1201	TTTATGATCTGAGACCAAGGCTGTGGATGATGTGTCAATAGAAATAGCTAATTTATTTCCCA	1261
Dp	1201	TTTATGATCTGAGACCAAGGCTGTGGATGATGTGTCAATAGAAATAGCTAATTTATTTCCCA	1261
Qy	1261	GATGTGTCTTTAGAGGAGTGTGGCTGACCAAGGCTTCTTCCATATTTCTTCCAGTAAGTT	1321
Dp	1261	GATGTGTCTTTAGAGGAGTGTGGCTGACCAAGGCTTCTTCCATATTTCTTCCAGTAAGTT	1321
Qy	1321	TCCCTCTGTGCTTGAACAGATAGAGTGTGTGCAATTTGTTCAGCTCCCAAGGCTGTCT	1381
Dp	1321	TCCCTCTGTGCTTGAACAGATAGAGTGTGTGCAATTTGTTCAGCTCCCAAGGCTGTCT	1381
Qy	1381	CCAGGCTTCAAGTCTGTGCTTGGAGAGTCAAGGCAAGGTTAACTGAGAGAGCAAGTT	1441
Dp	1381	CCAGGCTTCAAGTCTGTGCTTGGAGAGTCAAGGCAAGGTTAACTGAGAGAGCAAGTT	1441
Qy	1441	GCCACCCCTGTGCCAATTTATTTGGCTGTGCTCTACAGTTGTGCAAGACGCCGTTGT	1501
Dp	1441	GCCACCCCTGTGCCAATTTATTTGGCTGTGCTCTACAGTTGTGCAAGACGCCGTTGT	1501
Qy	1501	TCTACATGCTTGTGAATAATTTGATGAGGAGAGATGGAACAATGTGAGTCTCCCTC	1561
Dp	1501	TCTACATGCTTGTGAATAATTTGATGAGGAGAGATGGAACAATGTGAGTCTCCCTC	1561
Qy	1561	TGATTTGCTTTGGGGAAATGTGGAAGAGTGCCTGTTCGCAAAATCAACTGTGCAA	1621
Dp	1561	TGATTTGCTTTGGGGAAATGTGGAAGAGTGCCTGTTCGCAAAATCAACTGTGCAA	1621
Qy	1621	AAATGCAACAATGATTTTCCACGCAAGTCTTTTCATGTGGCATAGGTAAAGTGTGCTT	1681
Dp	1621	AAATGCAACAATGATTTTCCACGCAAGTCTTTTCATGTGGCATAGGTAAAGTGTGCTT	1681
Qy	1681	CAGCTGTGTGCATGAAATGTTCTGTTCACCTGTCAATCACTGTGTTATTTATTCACAGA	1741
Dp	1681	CAGCTGTGTGCATGAAATGTTCTGTTCACCTGTCAATCACTGTGTTATTTATTCACAGA	1741
Qy	1741	GTTTGTCTCAGCTCCATCCTGTGTCCAGAGGAGATTTATATCCAAATCAATTTCC	1801
Dp	1741	GTTTGTCTCAGCTCCATCCTGTGTGTCCAGAGGAGATTTATATCCAAATCAATTTCC	1801
Qy	1801	TCTCTCAGCAAGCTGTGGAGAGGGAGTCAATTTCTCTGTCCAATAGGAATCTCAAG	1861
Dp	1801	TCTCTCAGCAAGCTGTGGAGAGGGAGTCAATTTCTCTGTCCAATAGGAATCTCAAG	1861
Qy	1861	GCTCAGAGACTGCAAGCTGTGCCCAAGTCAACAGCTAATGAAGACAGAGAGATTT	1921
Dp	1861	GCTCAGAGACTGCAAGCTGTGCCCAAGTCAACAGCTAATGAAGACAGAGAGATTT	1921
Qy	1921	ATCTGATTTGATCTTAAGCTCAAGTGTCTCTCCACTACCCCAACAAGCTTGTGTGCA	1981
Dp	1921	ATCTGATTTGATCTTAAGCTCAAGTGTCTCTCTCCACTACCCCAACAAGCTTGTGTGCA	1981

OY		1981	CCAAAGTGCCTCCCAAAAAGAAAGAAATGGGATTTTCTTAGGACATCACACTCGGA	2040
Db		1981	CCAAAGTGCTCCCCAAAAGAAAGAAATGGGATTTTCTTAGGACATCACACTCGGA	2040
OY		2041	ATTAAAGTCAAACTAATTTCTCACATCCCCTCTTAAGAATACTGTTAGAACACGAGT	2100
Db		2041	ATTAAAGTCAAACTAATTTCTCACATCCCCTCTTAAGAATACTGTTAGAACACGAGT	2100
OY		2101	GTTCTCACAGTGTGGGACGCCGCTTCTTAATGAACACATGATTTGACACGTGCTCT	2160
Db		2101	GTTCTCACAGTGTGGGACGCCGCTTCTTAATGAACACATGATTTGACACGTGCTCT	2160
OY		2161	CTTTGGCAGTTTGCATTAGTACTTTGAAGATATATACCTGAGCGTGTACACAGTTTAA	2220
Db		2161	CTTTGGCAGTTTGCATTAGTACTTTGAAGATATATACCTGAGCGTGTACACAGTTTAA	2220
OY		2221	CCTGCAGAAAAACAGTACTAGGTAAATTTGTAGGGCAGAGATTATAATGAATTTTGCAAAT	2280
Db		2221	CCTGCAGAAAAACAGTACTAGGTAAATTTGTAGGGCAGAGATTATAATGAATTTTGCAAAT	2280
OY		2281	CACCTTAGCAGCAATGTGAAGACATTAATTCACACAGTGTGAAGAAAATCAACCAGACAGGC	2340
Db		2281	CACCTTAGCAGCAATGTGAAGACATTAATTCACACAGTGTGAAGAAAATCAACCAGACAGGC	2340
OY		2341	TGTGTGAACACATGTTGTGAATATATGCGACTGCGAACACTGAACCTCTACGCCACTCCACAA	2400
Db		2341	TGTGTGAACACATGTTGTGAATATATGCGACTGCGAACACTGAACCTCTACGCCACTCCACAA	2400
OY		2401	TGATGTTTTCAAGGTGTCAATGACCTGTGGCCACCATGTATTCATCCAGAGTCTTAAAGTT	2460
Db		2401	TGATGTTTTCAAGGTGTCAATGACCTGTGGCCACCATGTATTCATCCAGAGTCTTAAAGTT	2460
OY		2461	TAAAGTGCACATGATTTGTATTAAGCAGCTCTTCTTGAGTTTAAATATATGTATTAACAT	2520
Db		2461	TAAAGTGCACATGATTTGTATTAAGCAGCTCTTCTTGAGTTTAAATATATGTATTAACAT	2520
OY		2521	AAGTTGCATTTAGAAATCAAGCACTAATTCACCTTCACTGCAAAAAAAAAAAAAAAAAAAAA	2580
Db		2521	AAGTTGCATTTAGAAATCAAGCACTAATTCACCTTCACTGCAAAAAAAAAAAAAAAAAAAAA	2580
OY		2581	AAAAAA 2586 	
Db		2581	AAAAAA 2586 	
RESULT 8				
BD173060				
LOCUS				
DEFINITION	BD173060	2586 bp	DNA	linear PAT 18-FEB-2003
ACCESSION	BD173060			
VERSION	BD173060.1	GI:28414366		
KEYWORDS	JP 2002238587-A/195.			
ORGANISM	Homo sapiens (human)			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 2586) Wood,N.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,T. and Yuan,J. Secreted and transmembrane polypeptides and nucleic acids encoding the same. Patent: JP 2002238587-A 195 27-AUG-2002;			
JOURNAL	GENENTECH INC			
COMMENT	OS Homo sapiens (human) PN JP 2002238587-A/195 PD 27-AUG-2002 PF 18-DEC-2001 JP 2001385248 PR 17-SEP-1997 US 60/059115 17-SEP-1997 US 60/059184 PR 17-SEP-1997 US 60/059122 17-SEP-1997 US 60/059121 PR 17-SEP-1997 US 60/059113 17-SEP-1997 US 60/059123 PR 17-SEP-1997 US 60/059119 18-SEP-1997 US 60/059263 PR 18-SEP-1997 US 60/059266 15-OCT-1997 US 60/063125 PR			



Db 1501 TCTACATGGCTTGAATATGTTGAGGGGAGAGATGAAAATGTTGAGATCTCCCTC 1560  
 QY 1561 TGAATGGTTTGGGGAATATGAGAGAGAGTCCCTGCTTTGCAAAATCATACCTGGCAA 1620  
 Db 1561 TGAATGGTTTGGGGAATATGAGAGAGAGTCCCTGCTTTGCAAAATCATACCTGGCAA 1620  
 QY 1621 AAATGCAACAAATGAATTTTCCACGAGATCTTTCCATGGGAGATAGTAACTGTCCTT 1680  
 Db 1621 AAATGCAACAAATGAATTTTCCACGAGATCTTTCCATGGGAGATAGTAACTGTCCTT 1680  
 QY 1681 CAGCTGTGAGATGAATATTTCTGTTCACTCCCTCACTCAATGTTTATTCATCCAGA 1740  
 Db 1681 CAGCTGTGAGATGAATATTTCTGTTCACTCCCTCACTCAATGTTTATTCATCCAGA 1740  
 QY 1741 GTGTTGCTAGCTCTCACTCTGTGCGAGGAGAGATTTTCATATCCAGATCATATCCC 1800  
 Db 1741 GTGTTGCTAGCTCTCACTCTGTGCGAGGAGAGATTTTCATATCCAGATCATATCCC 1800  
 QY 1801 TCTCTCAGCAGACCTCTGCTGCGAGGAGAGATTTTCATATCCAGATCATATCCC 1860  
 Db 1801 TCTCTCAGCAGACCTCTGCTGCGAGGAGAGATTTTCATATCCAGATCATATCCC 1860  
 QY 1861 GCTCAGAGACTGCAAGCTGCTTCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1920  
 Db 1861 GCTCAGAGACTGCAAGCTGCTTCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1920  
 QY 1921 ATCTGTTGTTGACTCTAAGTCTAAGTCTAAGTCTAAGTCTAAGTCTAAGTCTAAGT 1980  
 Db 1921 ATCTGTTGTTGACTCTAAGTCTAAGTCTAAGTCTAAGTCTAAGTCTAAGTCTAAGT 1980  
 QY 1981 CCAAAAGTGTCCCAAAAGAGAGAGATTTTCTGAGGAGAGATTTTCTGAGGAGAGAT 2040  
 Db 1981 CCAAAAGTGTCCCAAAAGAGAGAGATTTTCTGAGGAGAGATTTTCTGAGGAGAGAT 2040  
 QY 2041 ATTAAGTCAAACTAAATTTCTCAATCTCTTAAAGTCAAACTAAATTTCTGAGGAGAG 2100  
 Db 2041 ATTAAGTCAAACTAAATTTCTCAATCTCTTAAAGTCAAACTAAATTTCTGAGGAGAG 2100  
 QY 2101 GTTCTCAAGTGTGGGAGAGAGATTTTCTGAGGAGAGATTTTCTGAGGAGAGATTT 2160  
 Db 2101 GTTCTCAAGTGTGGGAGAGAGATTTTCTGAGGAGAGATTTTCTGAGGAGAGATTT 2160  
 QY 2161 CTTTGGAGTGTGATTAATTTGAAAGTATGATGAGGAGATTTTCTGAGGAGAGATTT 2220  
 Db 2161 CTTTGGAGTGTGATTAATTTGAAAGTATGATGAGGAGATTTTCTGAGGAGAGATTT 2220  
 QY 2221 CTTGCAAGTGTGATTAATTTGAAAGTATGATGAGGAGATTTTCTGAGGAGAGATTT 2280  
 Db 2221 CTTGCAAGTGTGATTAATTTGAAAGTATGATGAGGAGATTTTCTGAGGAGAGATTT 2280  
 QY 2281 CACTTGGAGAGATTAATTTGAAAGTATGATGAGGAGATTTTCTGAGGAGAGATTT 2340  
 Db 2281 CACTTGGAGAGATTAATTTGAAAGTATGATGAGGAGATTTTCTGAGGAGAGATTT 2340  
 QY 2341 TGTGTGAATGATGATTAATTTGAAAGTATGATGAGGAGATTTTCTGAGGAGAGATTT 2400  
 Db 2341 TGTGTGAATGATGATTAATTTGAAAGTATGATGAGGAGATTTTCTGAGGAGAGATTT 2400  
 QY 2401 TGAATGTTTGAAGTGTGATTAATTTGAAAGTATGATGAGGAGATTTTCTGAGGAGAG 2460  
 Db 2401 TGAATGTTTGAAGTGTGATTAATTTGAAAGTATGATGAGGAGATTTTCTGAGGAGAG 2460  
 QY 2461 TAAAGTGTGATGATTAATTTGAAAGTATGATGAGGAGATTTTCTGAGGAGAGATTT 2520  
 Db 2461 TAAAGTGTGATGATTAATTTGAAAGTATGATGAGGAGATTTTCTGAGGAGAGATTT 2520  
 QY 2521 AAGTGTGATTAATTTGAAAGTATGATGAGGAGATTTTCTGAGGAGAGATTTTCTGAGGAG 2580  
 Db 2521 AAGTGTGATTAATTTGAAAGTATGATGAGGAGATTTTCTGAGGAGAGATTTTCTGAGGAG 2580  
 QY 2581 AAAAAA 2586  
 Db 2581 AAAAAA 2586

Db 2581 AAAAAA 2586  
 RESULT 9  
 BD173379  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 OS Homo sapiens (human)  
 PN JP 2002238588-A/195  
 PD 27-AUG-2002  
 PF 18-DEC-2001 JP 2001385315  
 PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059117 PR  
 17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059121 PR  
 17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059126 PR  
 17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR  
 18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR  
 18-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR  
 21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/063216 PR  
 24-OCT-1997 US 60/062814, 24-OCT-1997 US 60/063127 PR  
 24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR  
 24-OCT-1997 US 60/063045, 24-OCT-1997 US 60/063128 PR  
 27-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063327 PR  
 28-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063541 PR  
 28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063542 PR  
 28-OCT-1997 US 60/063544, 28-OCT-1997 US 60/063546 PR  
 29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063738 PR  
 29-OCT-1997 US 60/063704, 29-OCT-1997 US 60/063735 PR  
 29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/064103 PR  
 29-OCT-1997 US 60/063732, 31-OCT-1997 US 60/064248 PR  
 31-OCT-1997 US 60/063870, 03-NOV-1997 US 60/064248 PR  
 07-NOV-1997 US 60/064809, 12-NOV-1997 US 60/065693 PR  
 17-NOV-1997 US 60/065846, 18-NOV-1997 US 60/065846 PR  
 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120 PR  
 24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066772 PR  
 24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066511 PR  
 60/066453, 25-NOV-1997 US 60/066840 PI  
 WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI  
 JIAN ZHENG,  
 PI JEAN YUEN  
 PC C12N15/09, C07K14/435, C07K16/19, C07K19/00, C12N1/19, C12N1/21, PC  
 C12N5/10, C12P21/02, C12P21/08, C12N1/19, C12R1/645, C12N1/21, C12R1/19, PC  
 PC C12N5/10, C12R1/91, C12N15/00, C12N5/00, C12N5/30, C12R1/91 CC  
 Secreted and transmembrane polypeptides and nucleic acids  
 encoding the same  
 PH Key  
 FT source  
 FT source  
 FEATURES  
 source  
 location/Qualifiers  
 1..2586  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 BASE COUNT  
 631 a 679 c 703 g 573 t  
 ORIGIN  
 Query Match 100.0%; Score 2586; DB 6; Length 2586;  
 Best Local Similarity 100.0%; Pred. No. 0;



Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CGCGGAGCTCCCGGACCCGCGGCGCCGACCGCGGCGCTCCGCAATCTTGACACCGGACG 60
Db 1 CGCGGAGCTCCCGGACCCGCGGCGCCGACCGCGGCGCTCCGCAATCTTGACACCGGACG 60
QY 61 CGCGGAGCTCCCGGAGCGGAGCGAGGATCCAGTCCGCGCGCGGACGCAATCTCGTCCA 120
Db 61 CGCGGAGCTCCCGGAGCGGAGCGAGGATCCAGTCCGCGCGCGGACGCAATCTCGTCCA 120
QY 121 GTGCGGAGCGGAGCTGCGGAGCGGAGGATGCAAGCGGCTTTGGGCGCAACCTGCTGT 180
Db 121 GTGCGGAGCGGAGCTGCGGAGCGGAGGATGCAAGCGGCTTTGGGCGCAACCTGCTGT 180
QY 181 GCGTGTGCTGCGCGCGCGGCTCCCGACGCGCGCGCGCGCGCTCCGACGCGGCTCGG 240
Db 181 GCGTGTGCTGCGCGCGCGGCTCCCGACGCGCGCGCGCGCGCTCCGACGCGGCTCGG 240
QY 241 CTCCAGTCAAGCCCGGCGCGGCTTCACTAACCCGACGAGGAGGCGCACTTCAATGAGA 300
Db 241 CTCCAGTCAAGCCCGGCGCGGCTTCACTAACCCGACGAGGAGGCGCACTTCAATGAGA 300
QY 301 TGTTCGCGAGGTTGAGAGACTGATGAGGAGCAGCAGCAATTTGCGCAGCGCGGTGG 360
Db 301 TGTTCGCGAGGTTGAGAGACTGATGAGGAGCAGCAGCAATTTGCGCAGCGCGGTGG 360
QY 361 AAGAGATGAGGCGAGAGAAAGCTGCTGCTAAGCATCATCAAGATGAACTTGGCAACT 420
Db 361 AAGAGATGAGGCGAGAGAAAGCTGCTGCTAAGCATCATCAAGATGAACTTGGCAACT 420
QY 421 TACTCCGACTATCAATGAGACCAAGACAGACGAGGTTGAAATTAATACATCC 480
Db 421 TACTCCGACTATCAATGAGACCAAGACAGACGAGGTTGAAATTAATACATCC 480
QY 481 ATGTGACCGGAGAAATTCACAGATTAACAACAACGAGCTGACCAATGGTCTTTTCAG 540
Db 481 ATGTGACCGGAGAAATTCACAGATTAACAACAACGAGCTGACCAATGGTCTTTTCAG 540
QY 541 AAGACGTTATCAATCTGTGGGAGAGAGAAAGGACAGAGGACCAAGTGCATCATG 600
Db 541 AAGACGTTATCAATCTGTGGGAGAGAGAGAAAGGACCAAGTGCATCATG 600
QY 601 ACGAGACTGTGGGCGCGGACGATGCTACTGCGAGTTTGGCAGCTTCACTACCTGCGAC 660
Db 601 ACGAGACTGTGGGCGCGGACGATGCTACTGCGAGTTTGGCAGCTTCACTACCTGCGAC 660
QY 661 CATGCCGCGGCGCAGAGAGATGCTGTGACCCGCGGACAGTGAAGTGTGAGAGCAAGCTGT 720
Db 661 CATGCCGCGGCGCAGAGAGATGCTGTGACCCGCGGACAGTGAAGTGTGAGAGCAAGCTGT 720
QY 721 GTGTCTGAGGCTCACTGACCAAAATGAGGACACAGGCGGACGATGGAGCAATCTTGACA 780
Db 721 GTGTCTGAGGCTCACTGACCAAAATGAGGACACAGGCGGACGATGGAGCAATCTTGACA 780
QY 781 ACCAGAGGAGCTGCGCAGCGCGGCTGTGTCTGCTTCCAGAGAGGCTGTGCTCCCTG 840
Db 781 ACCAGAGGAGCTGCGCAGCGCGGCTGTGTCTGCTTCCAGAGAGGCTGTGCTCCCTG 840
QY 841 TGTGCAACACCCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db 841 TGTGCAACACCCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 901 ACCTCATCACTTGGAGCTGAGAGCTGATGAGACCTTGAACCGATGCGCTTGGCCAGTG 960
Db 901 ACCTCATCACTTGGAGCTGAGAGCTGATGAGACCTTGAACCGATGCGCTTGGCCAGTG 960
QY 961 GCGTCTGCTGCGCAGCGGACAGGCAAGCGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Db 961 GCGTCTGCTGCGCAGCGGACAGGCAAGCGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
QY 1021 GAGAGCGTGAACCAAGATGAGGAGATCTGTGCGCAGAGAGGTCGCCGATGATGAAG 1080
Db 1021 GAGAGCGTGAACCAAGATGAGGAGATCTGTGCGCAGAGAGGTCGCCGATGATGAAG 1080
```

```
QY 1081 TTGGAGCTTGATGAGAGAGGTGCGCCAGAGCTGAGAGCACTGGAGAGGAGCGCTGACTG 1140
Db 1081 TTGGAGCTTGATGAGAGAGGTGCGCCAGAGCTGAGAGCACTGGAGAGGAGCGCTGACTG 1140
QY 1141 AAGAGATGAGCGTGGGAGAGCGCTGCGGCTGCGCGCTGCACTGTGGAGAGGAGAGAGA 1200
Db 1141 AAGAGATGAGCGTGGGAGAGCGCTGCGGCTGCGCGCTGCACTGTGGAGAGGAGAGAGA 1200
QY 1201 TTTAGATGAGACAGAGCTGTGGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
Db 1201 TTTAGATGAGACAGAGCTGTGGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
QY 1261 GGTGTGCTTTAGGCTGTGGGCTGACAGGCGCTTCTTCAATCTTCTCCAGATAGTT 1320
Db 1261 GGTGTGCTTTAGGCTGTGGGCTGACAGGCGCTTCTTCTTCAATCTTCTCCAGATAGTT 1320
QY 1321 TCCCTCTGGCTTGACAGCAGTGAAGGTGTTGTGCAATTTGTCACTCCCGCAGGCTGTCT 1380
Db 1321 TCCCTCTGGCTTGACAGCAGTGAAGGTGTTGTGCAATTTGTCACTCCCGCAGGCTGTCT 1380
QY 1381 CCAGGCTTCAAGTCTGCTGCGGAGAGTCAAGGAGGTTAACTGACAGAGAGATT 1440
Db 1381 CCAGGCTTCAAGTCTGCTGCGGAGAGTCAAGGAGGTTAACTGACAGAGAGATT 1440
QY 1441 GCGACCCCTGTGACAGATTTATTTGCTTGTGCTTCTTCACTGAGTGGCAGACAGCGTTGT 1500
Db 1441 GCGACCCCTGTGACAGATTTATTTGCTTGTGCTTCTTCACTGAGTGGCAGACAGCGTTGT 1500
QY 1501 TCTACATGCTTTGATTTATTTGTTGAGGAGGAGAGATGGAACAATGTGAGTCTCCCTC 1560
Db 1501 TCTACATGCTTTGATTTATTTGTTGAGGAGGAGAGATGGAACAATGTGAGTCTCCCTC 1560
QY 1561 TGATTGTTTGGGAGAAATGTGAGAGAGTCCCTGCTTTCAGAAATCAACCTGGCAA 1620
Db 1561 TGATTGTTTGGGAGAAATGTGAGAGAGTCCCTGCTTTCAGAAATCAACCTGGCAA 1620
QY 1621 AAATGCCAACAAATGAAATTTTCCAGCAGTCTTTCACATGGGCAATGATGAGTGTGCTT 1680
Db 1621 AAATGCCAACAAATGAAATTTTCCAGCAGTCTTTCACATGGGCAATGATGAGTGTGCTT 1680
QY 1681 CAGCTGTGACAGATGAAATGTTCTGTTCAACCTGATTAATGATGATTAATCAACAGCA 1740
Db 1681 CAGCTGTGACAGATGAAATGTTCTGTTCAACCTGATTAATGATGATTAATCAACAGCA 1740
QY 1741 GTGTGCTCACTCTTACCTGTGTCAGAGGAGAGATTTTATATCCAAATCAATTTCC 1800
Db 1741 GTGTGCTCACTCTTACCTGTGTCAGAGGAGAGATTTTATATCAAAATTTCC 1800
QY 1801 TCTCTCAGCAGAGCTGGGAGGAGGAGTCAATGTTCTGCTGTCATCAGGAGTCTCAGAG 1860
Db 1801 TCTCTCAGCAGAGCTGGGAGGAGGAGTCAATGTTCTGCTGTCATCAGGAGTCTCAGAG 1860
QY 1861 GCTCAGAGACTGCAAGCTGCTTCCAAAGTCAACACATGATGAAGACAGAGAGATTTTC 1920
Db 1861 GCTCAGAGACTGCAAGCTGCTTCCAAAGTCAACACATGATGAAGACAGAGAGATTTTC 1920
QY 1921 ATCTGTTGTGACTCTAAGCTCAAGTCAAGTCTCTCACTACCCACAGAGCTTGTGCGCA 1980
Db 1921 ATCTGTTGTGACTCTAAGCTCAAGTCAAGTCTCTCACTACCCACAGAGCTTGTGCGCA 1980
QY 1981 CCAAAAGTGTCCCAAAAGAGAGAGATGGAATTTTCTTGAAGCATGCAATCTGGA 2040
Db 1981 CCAAAAGTGTCCCAAAAGAGAGAGATGGAATTTTCTTGAAGCATGCAATCTGGA 2040
QY 2041 AATTAAGGCAAACTAATTTCTCAATCCCTCTAAGAACTAATCTGTTAGGAAAGAGAGT 2100
Db 2041 AATTAAGGCAAACTAATTTCTCAATCCCTCTAAGAACTAATCTGTTAGGAAAGAGAGT 2100
QY 2101 GTTCTCAAGTGTGGGAGAGCGGCTCTTCAATGAAGCAATGATATGACACTGTCCCT 2160
Db 2101 GTTCTCAAGTGTGGGAGAGCGGCTCTTCAATGAAGCAATGATATGACACTGTCCCT 2160
```

QY	2161	TTTTGGCAGCTGCATTGTAGTACTCTTGGAAAGGTATATGCTAGCGGTGACATACAGGTTAA	2225
Db	2161	CTTTGGCAGCTTGCATTAGTAACTTTGGAAAGGTATATGCTAGCGGTGACATACAGGTTAA	2220
QY	2221	CTTGCAGAAACAGTACTTAGTGAATTTGTAGGGCGAGATTATTAATGAAATTTGCAAAAT	2280
Db	2221	CTTGCAGAAACAGTACTTAGTGAATTTGTAGGGCGAGATTATTAATGAAATTTGCAAAAT	2280
QY	2281	CAGTTAGCAGCACTGAAAGCAATATATCAACCAAGTGCAGAAATTCAAACCGACAGAGGC	2340
Db	2281	CAGTTAGCAGCACTGAAAGCAATATATCAACCAAGTGCAGAAATTCAAACCGACAGAGGC	2340
QY	2341	TGTGTGAAACATGTTGTTGTAATATGCGACTGCGAACACTGAACTCTACGCACTCCACAA	2400
Db	2341	TGTGTGAAACATGTTGTTGTAATATGCGACTGCGAACACTGAACTCTACGCACTCCACAA	2400
QY	2401	TGATGTTTTCAGGTGTGCATGAGACGTGTCGCAACATGATTCATCCAGAGTTCTTAAAGTT	2460
Db	2401	TGATGTTTTCAGGTGTGCATGAGACGTGTCGCAACATGATTCATCCAGAGTTCTTAAAGTT	2460
QY	2461	TAAAGTGCACATGATTTGTATATGACGATCTTCTTGTAGTTTAAATATATGATTAACAT	2520
Db	2461	TAAAGTGCACATGATTTGTATATGACGATCTTCTTGTAGTTTAAATATATGATTAACAT	2520
QY	2521	AAGTGCATTATAGAAATCAAGCATTAATCATCTCACTGCAGCAAAAAAAAAAAAAAAAAA	2580
Db	2521	AAGTGCATTATAGAAATCAAGCATTAATCATCTCACTGCAGCAAAAAAAAAAAAAAAAAA	2580
QY	2581	AAAAAA 2586	
Db	2581	AAAAAA 2586	
RESULT 10			
BD175413			
LOCUS	BD175413	2586 bp	DNA linear
DEFINITION	Secretory and transmembrane polypeptide and nucleic acid encoding the same.		PAT 18-MAR-2003
ACCESSION	BD175413		
VERSION	BD175413.1	GI:29121109	
KEYWORDS	JP 2002253280-A/195.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.		
TITLE	Secretory and transmembrane polypeptide and nucleic acid encoding the same		
JOURNAL	GENENTECH INC		
COMMENT	OS Homo sapiens (human) PN JP 2002253280-A/195 PD 10-SEP-2002 PF 18-DEC-2001 JP 2001385319 PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR 17-SEP-1997 US 60/059112, 17-SEP-1997 US 60/059117 PR 17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR 17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR 18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/063325 PR 17-OCT-1997 US 60/063287, 17-OCT-1997 US 60/063285 PR 21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR 24-OCT-1997 US 60/062814, 24-OCT-1997 US 60/063127 PR 24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR 24-OCT-1997 US 60/063045, 24-OCT-1997 US 60/063128 PR 27-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063327 PR 28-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063541 PR 28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063542 PR 28-OCT-1997 US 60/063544, 28-OCT-1997 US 60/063564 PR 29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063738 PR 29-OCT-1997 US 60/063704, 29-OCT-1997 US 60/063745 PR 29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063735 PR		

[illegible]

Qy	541	AGACAGTTATCATCTCTGTGAGAGCGAAGAGGACAGAGGATGATCATCTG	600
Db	541	AGACAGTTATCATCTCTGTGAGAGCGAAGAGGACAGAGGATGATCATCTG	600
Qy	601	ACGAGGACTGTGGGCCCCAGCATGTACTGCAAGTTTGCACTTCCAGTACACTGCGAC	660
Db	601	ACGAGGACTGTGGGCCCCAGCATGTACTGCAAGTTTGCACTTCCAGTACACTGCGAC	660
Qy	661	CATGCGGGGGCAGAGAGTCTCTGCAACCCGAGCAGTGAAGTGTGAGACAGCTGT	720
Db	661	CATGCGGGGGCAGAGAGTCTCTGCAACCCGAGCAGTGAAGTGTGAGACAGCTGT	720
Qy	721	GTGTCTGGGGTCACTGCAACCAAAATGCGCACACGAGGGCAGCAATGAGAACATCTGAGCA	780
Db	721	GTGTCTGGGGTCACTGCAACCAAAATGCGCACACGAGGGCAGCAATGAGAACATCTGAGCA	780
Qy	781	ACGAGAGGACTGCGACGCGGGGCTGTGTGCTTCCAGAGAGGCTGTCTCCCTG	840
Db	781	ACGAGAGGACTGCGACGCGGGGCTGTGTGCTTCCAGAGAGGCTGTCTCCCTG	840
Qy	841	TGTGCAACACCCCTGCGCGTGGAGGGCGAGCTTTGCAATGACCCCGCAGCGCTTCTGG	900
Db	841	TGTGCAACACCCCTGCGCGTGGAGGGCGAGCTTTGCAATGACCCCGCAGCGCTTCTGG	900
Qy	901	ACCTCATCACCTGGAGCTAGAGCTGATGAGAGCTTGACCGATGCTTGTGCGCAGTG	960
Db	901	ACCTCATCACCTGGAGCTAGAGCTGATGAGAGCTTGACCGATGCTTGTGCGCAGTG	960
Qy	961	GCTCTCTGTGCAAGCCCAACAGCCAGCGCTGTGTATGTGTGCAAGCCGACCTTGTGG	1020
Db	961	GCTCTCTGTGCAAGCCCAACAGCCAGCGCTGTGTATGTGTGCAAGCCGACCTTGTGG	1020
Qy	1021	GGAGCCGTGACCAAGATGGGGAGATCTGTGCTGCCAAGAGATGCCGATGATGAGAA	1080
Db	1021	GGAGCCGTGACCAAGATGGGGAGATCTGTGCTGCCAAGAGATGCCGATGATGAGAA	1080
Qy	1081	TTGGCAGCTTCAATGAGAGAGGTGCGCAGAGAGCTGAGAGACTGAGAGAGGCTGACTG	1140
Db	1081	TTGGCAGCTTCAATGAGAGAGGTGCGCAGAGAGCTGAGAGACTGAGAGAGGCTGACTG	1140
Qy	1141	AAGAGATGGCGCTGGGGAGGCTGTGCGCTGCGCTGCACTGTGCGAGGGGAGAGAGA	1200
Db	1141	AAGAGATGGCGCTGGGGAGGCTGTGCGCTGCGCTGCACTGTGCGAGGGGAGAGAGA	1200
Qy	1201	TTTATGATCTGGACAGGCTGTGGGTAGATGTGCAATGAAATAGCTAATTTATTTCCCA	1260
Db	1201	TTTATGATCTGGACAGGCTGTGGGTAGATGTGCAATGAAATAGCTAATTTATTTCCCA	1260
Qy	1261	GGTGTGTCTTTAGGCGTGGCTGACAGAGCTTCTTCTCAATCTTCTCCAGTAAGTT	1320
Db	1261	GGTGTGTCTTTAGGCGTGGCTGACAGAGCTTCTTCTCAATCTTCTCCAGTAAGTT	1320
Qy	1321	TCCCTCTGAGTTTCAAGCATGAGAGTGTGCAATTTGTTCAAGTCCCGCAGGCTGTCT	1380
Db	1321	TCCCTCTGAGTTTCAAGCATGAGAGTGTGCAATTTGTTCAAGTCCCGCAGGCTGTCT	1380
Qy	1381	CCAGGCTTCAAGCTGTGCTTGGAGAGTCAAGGCTTAACTGCAAGAGAGCTTT	1440
Db	1381	CCAGGCTTCAAGCTGTGCTTGGAGAGTCAAGGCTTAACTGCAAGAGAGCTTT	1440
Qy	1441	GCCACCCCTGTCCAGATTTATGAGCTTGTCCCTTCAAGTTTGGCAGAGAGCCGTTGT	1500
Db	1441	GCCACCCCTGTCCAGATTTATGAGCTTGTCCCTTCAAGTTTGGCAGAGAGCCGTTGT	1500
Qy	1501	TCTACATGAGCTTTATGATTTGTTGAGAGGAGAGATGAGAAACAATGTGAGTCTCCCTG	1560
Db	1501	TCTACATGAGCTTTATGATTTGTTGAGAGGAGAGATGAGAAACAATGTGAGTCTCCCTG	1560
Qy	1561	TGATTTGTTTGGGAAATGTGAGAAAGAGTGCCTTGTGCAAAATCAACTGTGCA	1620
Db	1561	TGATTTGTTTGGGAAATGTGAGAAAGAGTGCCTTGTGCAAAATCAACTGTGCA	1620
Qy	1621	AAATGCAACAAATTAATTTTCCAGCAGTCTTTTCCATGAGGATAGTAAAGTGTGCTT	1680
Db	1621	AAATGCAACAAATTAATTTTCCAGCAGTCTTTTCCATGAGGATAGTAAAGTGTGCTT	1680
Qy	1681	CAGCTGTGAGATTAATTTGTTGTTTCAACCTGATACATGATTTATTCATTCACAGA	1740
Db	1681	CAGCTGTGAGATTAATTTGTTGTTTCAACCTGATACATGATTTATTCATTCACAGA	1740
Qy	1741	GTGTGTCAAGTCTTACCTGTGTCAGAGGACAGATTTTCAATATCAATCAATTTCC	1800
Db	1741	GTGTGTCAAGTCTTACCTGTGTCAGAGGACAGATTTTCAATATCAATCAATTTCC	1800
Qy	1801	TCTCTCAGACAGCCTGGGAGAGGGGTATGTTCTCTGTCATCAGAGATCTCAG	1860
Db	1801	TCTCTCAGACAGCCTGGGAGAGGGGTATGTTCTCTGTCATCAGAGATCTCAG	1860
Qy	1861	GCTCAGAGACTGCAAGCTGTTGCCCAAGTCAACAGCTAGTGAAGACAGAGAGTTTC	1920
Db	1861	GCTCAGAGACTGCAAGCTGTTGCCCAAGTCAACAGCTAGTGAAGACAGAGAGTTTC	1920
Qy	1921	ATCTGTTGTGACTTAAAGTCAAGTCTCTTCACTACCCCAACAGCTTGTGCTCA	1980
Db	1921	ATCTGTTGTGACTTAAAGTCAAGTCTCTTCACTACCCCAACAGCTTGTGCTCA	1980
Qy	1981	CCAAAAGTGTCCCAAAAAGAGAGAAATGAGATTTTCTTGAAGGATGACATCTGGA	2040
Db	1981	CCAAAAGTGTCCCAAAAAGAGAGAAATGAGATTTTCTTGAAGGATGACATCTGGA	2040
Qy	2041	ATTAAAGTCAAACTAATTTCTCATCTCTTAAAGTAACTACTGTTAGAAACAGCAT	2100
Db	2041	ATTAAAGTCAAACTAATTTCTCATCTCTTAAAGTAACTACTGTTAGAAACAGCAT	2100
Qy	2101	GTTTCAAGTGTGGGGAGGCGCTCTTCTAATGAAGCAATGATATGACATGCTCCCT	2160
Db	2101	GTTTCAAGTGTGGGGAGGCGCTCTTCTAATGAAGCAATGATATGACATGCTCCCT	2160
Qy	2161	CTTTGGCAGTTGCAATTAATCTTTGAAAGGTATATGAAGTGAAGTGAATTTGCAAT	2220
Db	2161	CTTTGGCAGTTGCAATTAATCTTTGAAAGGTATATGAAGTGAAGTGAATTTGCAAT	2220
Qy	2221	CCTGAGAAACAGTACTTAATGATTAATTTGAGGCGAGATTTAAATTTGCAAT	2280
Db	2221	CCTGAGAAACAGTACTTAATGATTAATTTGAGGCGAGATTTAAATTTGCAAT	2280
Qy	2281	CAGTTAGACAGCACTGAGACCAATTAATCAACGCTGAGAGAAATCAACCGAGAGGCG	2340
Db	2281	CAGTTAGACAGCACTGAGACCAATTAATCAACGCTGAGAGAAATCAACCGAGAGGCG	2340
Qy	2341	TGTGTGAACATGTTGTAATATGCACTGGAACCTGAACCTTACGCCACTCCACAA	2400
Db	2341	TGTGTGAACATGTTGTAATATGCACTGGAACCTGAACCTTACGCCACTCCACAA	2400
Qy	2401	TGATGTTTCAAGTGTCAATGAGCTGTGSCACATGATTAATCAGAGTCTTAAAGTT	2460
Db	2401	TGATGTTTCAAGTGTCAATGAGCTGTGSCACATGATTAATCAGAGTCTTAAAGTT	2460
Qy	2461	TAAAGTTGACATGATTAATTAAGCATCTTTCTTGAAGTTTAAATTAATTAATCAAT	2520
Db	2461	TAAAGTTGACATGATTAATTAAGCATCTTTCTTGAAGTTTAAATTAATTAATCAAT	2520
Qy	2521	AAGTTGCACTTAAGTAATCAAGATTAATCACTTCACTGCAAGAGAGAGAGAGAGAG	2580
Db	2521	AAGTTGCACTTAAGTAATCAAGATTAATCACTTCACTGCAAGAGAGAGAGAGAGAG	2580
Qy	2581	AAAAAA 2586	
Db	2581	AAAAAA 2586	
RESULT 11			
BD093626 2660 bp DNA linear PAT 27-AUG-2002			
LOCUS BD093626			
DEFINITION Cell proliferation inhibiting proteins, polynucleotides, antisense polynucleotides to the polynucleotides, and cell			



proliferation inhibiting agents, cancer diagnostic agents, cancer therapeutic agents and compositions for gene therapy using same.

ACCESSION BD093626.1 GI:22639214

VERSION WO 0138528-A/2

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 2660)

Namba, M. and Teuji, T.

Cell proliferation inhibiting proteins, polynucleotides, antienspolynucleotides to the polynucleotides, and cell proliferation inhibiting agents, cancer diagnostic agents, cancer therapeutic agents and compositions for gene therapy using same

Patent: WO 0138528-A 2 31-MAY-2001;

HISAMITSU PHARMACEUTICAL CO INC, MASAYOSHI NAMBA, TOSHIBA TSUJI

OS Homo sapiens (human)

PN WO 0138528-A/2

PD 31-MAY-2001

PF 30-AUG-2000 WO 2000P005879

PI 19-NOV-1999 JP 99P 330604

PI MASAYOSHI NAMBA, TOSHIBA TSUJI

PC C12N15/12, C07K14/47, C12Q1/68, C12P21/02, A61K38/17, A61K31/711,

PC A61K48/00

CC

FEATURES

source

1. 2660

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

BASE COUNT 634 a 703 c 738 g 585 t

ORIGIN

Query Match 99.4%; Score 2571.4; DB 6; Length 2660;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2584; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

554 ATGTGACCGAGAAATTACAAAGTAAACAACACAGACTGACAAATGCTTTTACG 613

541 AGACGTTATCAATCTGTGGAGAGCAAGAAAGGACCAAGATGATCATCG 600

614 AGACGTTATCAATCTGTGGAGAGCAAGAAAGGACCAAGATGATCATCG 673

601 ACAGAGCTGTGGGCGCCAGATGATGACAGTTTGGCAGTTCCAGTACCTGCCAGC 660

674 ACAGAGCTGTGGGCGCCAGATGATGACAGTTTGGCAGTTCCAGTACCTGCCAGC 723

661 CATGCCGGGGCCAGAGATGCTCTGCACCCGGGACAGTATGCTGTGAGACCAAGTGT 720

734 CATGCCGGGGCCAGAGATGCTCTGCACCCGGGACAGTATGCTGTGAGACCAAGTGT 793

721 GTGCTGTGGGCTCACTGCACCAAAATGGCCACAGGGGACCAATGGGACCATGTGACA 780

794 GTGCTGTGGGCTCACTGCACCAAAATGGCCACAGGGGACCAATGGGACCATGTGACA 853

781 ACCAGAGGACTGCAAGCCGGGCTGTGCTGCTTCCAGAGAGGCTGTGCTTCCCTG 840

854 ACCAGAGGACTGCAAGCCGGGCTGTGCTGCTTCCAGAGAGGCTGTGCTTCCCTG 913

841 TGTGCAACCCCTGCGCCGTGGAGGAGGAGCTTGGCATGACCCCGACCGGCTTCTG 900

914 TGTGCAACCCCTGCGCCGTGGAGGAGGAGCTTGGCATGACCCCGACCGGCTTCTG 973

901 ACCTCATACCTTGGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 960

974 ACCTCATACCTTGGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 1033

961 GCCCTCTGCGCCAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAG 1020

1034 GCTCTCTGCGCCAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAG 1093

1021 GAAAGCCGTGACCAAGATGGGAGATCTGTGCTGCCAGAGATCTGCCAGATGATGAAG 1080

1094 GAAAGCCGTGACCAAGATGGGAGATCTGTGCTGCCAGAGATCTGCCAGATGATGAAG 1153

1081 TTGGCAGCTTCAATGAGAGATGCTGCCAGAGATCTGCCAGAGATCTGCCAGAGATCTG 1140

1154 TTGGCAGCTTCAATGAGAGATGCTGCCAGAGATCTGCCAGAGATCTGCCAGAGATCTG 1213

1141 AAGAGATGCGCTGGGGGAGCTTGCAGCTTGCAGCTTGCAGCTTGCAGCTTGCAGCTT 1200

1214 AAGAGATGCGCTGGGGGAGCTTGCAGCTTGCAGCTTGCAGCTTGCAGCTTGCAGCTT 1273

1201 TTTAGATCTGAGACCAAGCTGTGGGTGATGTGCAATGAAATAGCTAATTTATTTCCCA 1260

1274 TTTAGATCTGAGACCAAGCTGTGGGTGATGTGCAATGAAATAGCTAATTTATTTCCCA 1333

1261 GGTGTGCTTTAGAGCTGTGGGCTGACAGGCTTCTTCTTCAATCTTCCAGTAAATT 1320

1334 GGTGTGCTTTAGAGCTGTGGGCTGACAGGCTTCTTCTTCAATCTTCCAGTAAATT 1393

1321 TCCCTCTGCTTGAAGCAAGATGAGTGTGTGCAATTTGCTTCCAGCTTCCAGCTTCT 1380

1394 TCCCTCTGCTTGAAGCAAGATGAGTGTGTGCAATTTGCTTCCAGCTTCCAGCTTCT 1453

1381 CCAAGGCTTCAAGCTGTGGGCTGACAGGCTTCTTCTTCAATCTTCCAGTAAATT 1440

1454 CCAAGGCTTCAAGCTGTGGGCTGACAGGCTTCTTCTTCAATCTTCCAGTAAATT 1513

1441 GCCACCCCTGTCCAGATTAATGAGCTTGTGCTTCAACAGTTTGGAGACAGCCGTTGT 1500

1514 GCCACCCCTGTCCAGATTAATGAGCTTGTGCTTCAACAGTTTGGAGACAGCCGTTGT 1573

1501 TCTACATGCTTTGATTAATTTGTTGAGGGGAGGAGATGAGAACTAGTGAAGTCTCTC 1560

1574 TCTACATGCTTTGATTAATTTGTTGAGGGGAGGAGATGAGAACTAGTGAAGTCTCTC 1633

1561 TGATGCTTTGGGAGAAATGTGAGAAAGATGCTTGTTCATTAATCAATCAATCTTGCAA 1620

1634 TGATGCTTTGGGAGAAATGTGAGAAAGATGCTTGTTCATTAATCAATCAATCTTGCAA 1693



301 TGTTCGCGAGGTTGAGAACTGATGAGACACGACACAAATTCGAGCGGCTGG 360  
374 TGTTCGCGAGGTTGAGAACTGATGAGACACGACACAAATTCGAGCGGCTGG 433  
361 AAGAGATGAGAGCAGAAAGAGCTGCTGCTAAAGCATCATCAAGAGTGAACCTGGCAACT 420  
434 AAGAGATGAGAGCAGAAAGAGCTGCTGCTAAAGCATCATCAAGAGTGAACCTGGCAACT 493  
421 TACCTCCAGCTATCACAATGAGACCAACAGACAGCAAGAGTGGAAATATACATCC 480  
494 TACCTCCAGCTATCACAATGAGACCAACAGACAGCAAGAGTGGAAATATACATCC 553  
481 ATGTGACACGAGAAATTCACAAATTAACCAACAGACTGGAACAAATGCTTTTCAG 540  
554 ATGTGACACGAGAAATTCACAAATTAACCAACAGACTGGAACAAATGCTTTTCAG 613  
541 AGACAGTATCATCTGTGGGAGACGAAAGAGCAGAGAGCAGAGTGCATCATCG 600  
614 AGACAGTATCATCTGTGGGAGACGAAAGAGCAGAGAGCAGAGTGCATCATCG 673  
601 AGAGAGCTGTGGGAGCAGCATGTACTGCAAGTTTGCAGCTTCCAGTACCTCCAGC 660  
674 AGAGAGCTGTGGGAGCAGCATGTACTGCAAGTTTGCAGCTTCCAGTACCTCCAGC 733  
661 CATGCGGAGGAGCAGAGATGCTGTGACACCGGAGACAGTGAAGTGTGAGACAGAGCTGT 720  
734 CATGCGGAGGAGCAGAGATGCTGTGACACCGGAGACAGTGAAGTGTGAGACAGAGCTGT 793  
721 GTGTGTGGGAGTCACTGACCAAAATGAGCAACAGGAGGAGCAGAAATGAGCACTGTGAC 780  
794 GTGTGTGGGAGTCACTGACCAAAATGAGCAACAGGAGGAGCAGAAATGAGCACTGTGAC 853  
781 ACCAGAGGAGCTGCGAGCGGAGGCTGTGTGCTTCCAGAGAGGCTGTGTGCTGCTG 840  
854 ACCAGAGGAGCTGCGAGCGGAGGCTGTGTGCTTCCAGAGAGGCTGTGTGCTGCTG 913  
841 TGTGACACACCTGCGGAGGAGGCTGTGTGCTTCCAGAGAGGCTGTGTGCTGCTG 900  
914 TGTGACACACCTGCGGAGGAGGCTGTGTGCTTCCAGAGAGGCTGTGTGCTGCTG 973  
901 ACCCTATCACTCTGGAGAGTGAAGCTGATGAGAGCTTGAACGATGCTTGTGCTGCTG 960  
974 ACCCTATCACTCTGGAGAGTGAAGCTGATGAGAGCTTGAACGATGCTTGTGCTGCTG 1033  
961 GCTCTCTGCGAGCGGAGCAGACAGCAGCTGTGATGTGTGCAAGCGAGCTTCCGCTG 1020  
1034 GCTCTCTGCGAGCGGAGCAGACAGCAGCTGTGATGTGTGCAAGCGAGCTTCCGCTG 1093  
1021 GAGAGCGGTGACCAAGATGGGAGAGTCTGCTGCCAGAGAGGTCCCGATGATGAAG 1080  
1094 GAGAGCGGTGACCAAGATGGGAGAGTCTGCTGCCAGAGAGGTCCCGATGATGAAG 1153  
1081 TTGGGAGCTTCAATGAGAGAGTGGGAGGCTGAGAGCTGAGAGAGGAGCTGAGCTG 1140  
1154 TTGGGAGCTTCAATGAGAGAGTGGGAGGCTGAGAGCTGAGAGAGGAGCTGAGCTG 1213  
1141 AAGAGATGAGCGCTGGGAGAGCTGCGGCTGCGCGCTGCACTGTGTGGAGGAGAGAG 1200  
1214 AAGAGATGAGCGCTGGGAGAGCTGCGGCTGCGCGCTGCACTGTGTGGAGGAGAGAG 1273  
1201 TTATGATCTGAGACAGAGCTGTGGGATGATGATGATGATGATGATGATGATGATGATG 1260  
1274 TTATGATCTGAGACAGAGCTGTGGGATGATGATGATGATGATGATGATGATGATGATG 1333  
1261 GGTGTGTGCTTTAAGCGTGGGCTGACAGAGCTTCTTCAATCTTCTTCCAGTAAGTT 1320  
1334 GGTGTGTGCTTTAAGCGTGGGCTGACAGAGCTTCTTCAATCTTCTTCCAGTAAGTT 1393  
1321 TCCCTCTGCTGAGACAGATGAGTGTGTGATGATGATGATGATGATGATGATGATGATG 1380  
1394 TCCCTCTGCTGAGACAGATGAGTGTGTGATGATGATGATGATGATGATGATGATGATG 1453  
1381 CCAGGCTTCACTGTGTGCTTGGAGAGTCAAGGAGGTTAACTGACAGAGAGGTTT 1440

1454 CCAGGCTTCACTGTGTGCTTGGAGAGTCAAGGAGGTTAACTGACAGAGAGGTTT 1513  
1441 GCGACCCCTGTCAAGTTATGAGTGTGCTGCTTCACTGATGAGAGAGAGCTGCTG 1500  
1514 GCGACCCCTGTCAAGTTATGAGTGTGCTGCTTCACTGATGAGAGAGAGCTGCTG 1573  
1501 TCTACATGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560  
1574 TCTACATGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1633  
1561 TGAATGCTTTGGGAGAAATGAGAGAGAGTGGGAGAGAGTGGGAGAGAGTGGGAG 1620  
1634 TGAATGCTTTGGGAGAAATGAGAGAGAGTGGGAGAGAGTGGGAGAGAGTGGGAG 1693  
1621 AATGACAAATGAAATTTTCCAGAGCTTCTTCCATGAGGAGATGATGATGATGATG 1680  
1694 AATGACAAATGAAATTTTCCAGAGCTTCTTCCATGAGGAGATGATGATGATGATG 1753  
1681 CAGCTGTGAGATGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1740  
1754 CAGCTGTGAGATGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1813  
1741 GTGTGTGAGCTTCACTGAGCTTGTGAGAGAGAGATTTTCAATATCCAGATCAATCC 1800  
1814 GTGTGTGAGCTTCACTGAGCTTGTGAGAGAGAGATTTTCAATATCCAGATCAATCC 1873  
1801 TCTCTAGACACAGCTTGGGAGAGGAGTCAATGCTTCTGCTGCTGCTGCTGCTG 1860  
1874 TCTCTAGACACAGCTTGGGAGAGGAGTCAATGCTTCTGCTGCTGCTGCTGCTG 1933  
1861 GTCACAGAGCTGAGAGCTTGTGAGAGAGAGTCAACAGTATGAGAGAGAGAGAG 1920  
1934 GTCACAGAGCTGAGAGCTTGTGAGAGAGAGTCAACAGTATGAGAGAGAGAGAG 1993  
1921 ATGTGTGTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980  
1994 ATGTGTGTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2053  
1981 CCAAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2038  
2054 CCAAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2113  
2039 GAAATTAAGTCAAACTAATTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2098  
2114 GAAATTAAGTCAAACTAATTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2173  
2099 GTGTGTGAGAGTGGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2158  
2174 GTGTGTGAGAGTGGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2233  
2159 GTGTGTGAGAGTGGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2218  
2234 GTGTGTGAGAGTGGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2293  
2219 AACTGAGAGAAACAGTACTGATGATGATGATGATGATGATGATGATGATGATG 2278  
2294 AACTGAGAGAAACAGTACTGATGATGATGATGATGATGATGATGATGATGATG 2353  
2279 ATCACTTAGAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATG 2338  
2354 ATCACTTAGAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATG 2413  
2339 GCTGTGTGAAACATGTTGATGATGATGATGATGATGATGATGATGATGATGATG 2398  
2414 GCTGTGTGAAACATGTTGATGATGATGATGATGATGATGATGATGATGATGATG 2473  
2399 AATGATGTTTCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 2458  
2474 AATGATGTTTCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 2533  
2459 TTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2518



Db 1181 AGCTTATGAGAGAGTGGCCAGAGCTGAGAGACCTGAGAGAGAGCTGAGAGAG 1240  
 Qy 1146 ATGGCCCTGGGGAGAGCTGCGGCTGCGCCGCTGCACTGCTGGAGGGAGAGATTAG 1205  
 Db 1241 ATGGCCCTGGGGAGAGCTGCGGCTGCGCCGCTGCACTGCTGGAGGGAGAGATTAG 1300  
 Qy 1206 ATCTGAGCAGAGCTGGGGTAGATGTCAGTAAGTAATAGCTAATTTATTTCCCGAGTGT 1265  
 Db 1301 ATCTGAGCAGAGCTGGGGTAGATGTCAGTAAGTAATAGCTAATTTATTTCCCGAGTGT 1360  
 Qy 1266 GTGCTTTAGGCGTGGGCTGACAGAGCTTCTTCTACATCTTCTTCCAGTAGATTTCCTCC 1325  
 Db 1361 GTGCTTTAGGCGTGGGCTGACAGAGCTTCTTCTACATCTTCTTCCAGTAGATTTCCTCC 1420  
 Qy 1326 TCTGGCTTGACAGCAGATGAGTGTGTCATTTGTCAGCTCCCGCAGGCTGTTCTCCAG 1385  
 Db 1421 TCTGGCTTGACAGCAGATGAGTGTGTCATTTGTCAGCTCCCGCAGGCTGTTCTCCAG 1480  
 Qy 1386 CTTCACAGCTGCTGGCTGGGAGAGTCAAGCAGGGTTAACTGACAGAGAGAGTTGCCAC 1445  
 Db 1481 CTTCACAGCTGCTGGCTGGGAGAGTCAAGCAGGGTTAACTGACAGAGAGAGTTGCCAC 1540  
 Qy 1446 CCTGTCACAGATTAATGGCTGGCTGCTCTACAGCTGACAGAGAGAGCTGTTGTTCTAC 1505  
 Db 1541 CCTGTCACAGATTAATGGCTGGCTGCTCTACAGCTGACAGAGAGAGCTGTTGTTCTAC 1600  
 Qy 1506 ATGGCTTTGATTAATTTGAGGGAGAGAGATGAGAAACAATGAGTCTCCCTCTGATT 1565  
 Db 1601 ATGGCTTTGATTAATTTGAGGGAGAGAGATGAGAAACAATGAGTCTCCCTCTGATT 1660  
 Qy 1566 GGTGTTGGGGAAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1625  
 Db 1661 GGTGTTGGGGAAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1720  
 Qy 1626 CAACAATGAATTTTCCAGCAGAGCTTTTCCATGAGCAGATGAGTGGCTGCTCAGCT 1685  
 Db 1721 CAACAATGAATTTTCCAGCAGAGCTTTTCCATGAGCAGATGAGTGGCTGCTCAGCT 1780  
 Qy 1686 GTTGCAGATGAATTTGTTCTGTTCAACCTGATACATGATGTTATTCACAGCAGAGTGT 1745  
 Db 1781 GTTGCAGATGAATTTGTTCTGTTCAACCTGATACATGATGTTATTCACAGCAGAGTGT 1840  
 Qy 1746 GCTCAGCTCTACCTCTGTCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1805  
 Db 1841 GCTCAGCTCTACCTCTGTCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1900  
 Qy 1806 CAGCAGAGCTGGGAGAGGGGCTCATTTGTTCTCTGCTCATCAGGATCTCAGAGGCTCA 1865  
 Db 1901 CAGCAGAGCTGGGAGAGGGGCTCATTTGTTCTCTGCTCATCAGGATCTCAGAGGCTCA 1960  
 Qy 1866 GAGACTGACAGCTGCTGGCCCAAGTCAACAGCTAGTGAAGACCAAGAGAGAGTTTCACTG 1925  
 Db 1961 GAGACTGACAGCTGCTGGCCCAAGTCAACAGCTAGTGAAGACCAAGAGAGAGTTTCACTG 2020  
 Qy 1926 GTTGTGACTTAAGCTCAAGTCTGCTCTCCACATACCCCAACAGAGCTTGGTGGCAGCAAA 1985  
 Db 2021 GTTGTGACTTAAGCTCAAGTCTGCTCTCCACATACCCCAACAGAGCTTGGTGGCAGCAAA 2080  
 Qy 1986 AGTGTCTCCCAAG 2043  
 Db 2081 AGTGTCTCCCAAG 2140  
 Qy 2044 AAGGTCAACTAATTTCTCAGATCTCTTAAAGTAACTAATCTGTTAGAAACAGAGCTGTT 2103  
 Db 2141 AAGGTCAACTAATTTCTCAGATCTCTTAAAGTAACTAATCTGTTAGAAACAGAGCTGTT 2200  
 Qy 2104 CTGACAGTGGGGGAG 2163  
 Db 2201 CTGACAGTGGGGGAG 2260  
 Qy 2164 TGGCAGTTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 2223  
 Db 2261 TGGCAGTTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 2320

Qy 2224 GCAGAAACAGTACTTGAAGTATGAGGGGAGAGATTATTAATGAATTTGCAAAATCAC 2283  
 Db 2221 GCAGAAACAGTACTTGAAGTATGAGGGGAGAGATTATTAATGAATTTGCAAAATCAC 2280  
 Qy 2284 TTGACAGCAACTGAGACAACTTATCAACACAGTGGAGAGAAATCAAAACGAGCAGGCTGT 2343  
 Db 2281 TTGACAGCAACTGAGACAACTTATCAACACAGTGGAGAGAAATCAAAACGAGCAGGCTGT 2440  
 Qy 2244 GTGAAACATGTTGTAATATATGACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2403  
 Db 2441 GTGAAACATGTTGTAATATATGACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2500  
 Qy 2404 TGTGTTGAGTGTGATGAGTGTGTCACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 2463  
 Db 2501 TGTGTTGAGTGTGATGAGTGTGTCACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2560  
 Qy 2464 AGTTGACATGATGATGATTAAGCAGTGTCTTGAAGTTTAAATTAATGATTAATGAACATAG 2523  
 Db 2561 AGTTGACATGATGATGATTAAGCAGTGTCTTGAAGTTTAAATTAATGATTAATGAACATAG 2620  
 Qy 2524 TTGCATTTAGAAATCAAGCAATTAATCACTTCAACTGCAAAATTAATTAATTAATTAAT 2583  
 Db 2621 TTGCATTTAGAAATCAAGCAATTAATCACTTCAACTGCAAAATTAATTAATTAATTAAT 2680  
 Qy 2584 AAA 2586  
 Db 2681 AAA 2683

RESULT 14  
 BD093627  
 LOCUS 2632 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Cell proliferation inhibiting proteins, polynucleotides, antisensepolynucleotides to the polynucleotides, and cell proliferation inhibiting agents, cancer diagnostic agents, cancer therapeutic agents and compositions for gene therapy using same.

ACCESSION BD093627  
 VERSION 1  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2632)  
 AUTHORS Namba,M. and Tsuji,T.  
 TITLE Cell proliferation inhibiting proteins, polynucleotides, antisensepolynucleotides to the polynucleotides, and cell proliferation inhibiting agents, cancer diagnostic agents, cancer therapeutic agents and compositions for gene therapy using same

JOURNAL Patent: WO 0138528-A 3 31-May-2001;  
 HISAMITSU PHARMACEUTICAL CO INC,MASAYOSHI NAMBA,TOSHITAYA TSUJII  
 COMMENT OS Homo sapiens (human)  
 PN WO 0138528-A/3  
 PD 31-MAY-2001  
 PF 30-AUG-2000 WO 2000JP005879  
 PR 19-NOV-1999 JP 99P 330604  
 PI MASAYOSHI NAMBA,TOSHITAYA TSUJII  
 PC C12N15/12,C07K14/47,C12Q1/68,C12P21/02,A61K38/17,A61K31/711,  
 A61K48/00  
 CC

FEATURES  
 source Location/Qualifiers  
 1..2632  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 BASE COUNT 646 a 647 c 740 g 599 t  
 ORIGIN

Query Match 94.6%; Score 2446.4; DB 6; Length 2632;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 2459; Conservative 0; Mismatches 1; Indels 2; Gaps 1;



QY 126 GGGGCGGCTGCGGGCGCAGAGCGAGATGACAGCGCTTGGGGCCACCTGCTGCTCTG 185  
Db 171 GGGGCGGCTGCGGGCGCAGAGCGAGATGACAGCGCTTGGGGCCACCTGCTGCTCTG 230  
QY 186 CTGCTGGCGGGCGGGTCCCAAGGCCCCCGGCTCCGACGGGACCTGGGCTTCA 245  
Db 231 CTGCTGGCGGGCGGGTCCCAAGGCCCCCGGCTCCGACGGGACCTGGGCTTCA 290  
QY 246 GTCAAGCCCCGCGCTCTAGCTACCCGACGAGAGGACCAACCTCAATGAGATGTT 305  
Db 291 GTCAAGCCCCGCGCTCTAGCTACCCGACGAGAGGACCAACCTCAATGAGATGTT 350  
QY 306 CGCGAGTTGAGAACTGATGAGAGACACGAGACCAATTTGGCGACCGCGTGGAGAG 365  
Db 351 CGCGAGTTGAGAACTGATGAGAGACACGAGACCAATTTGGCGACCGCGTGGAGAG 410  
QY 366 ATGAGAGCAGAGAAAGTGTGCTAAAGCATCATCAGAGTGAACCTGGCAACTTACCT 425  
Db 411 ATGAGAGCAGAGAAAGTGTGCTAAAGCATCATCAGAGTGAACCTGGCAACTTACCT 470  
QY 426 CCCAGCTATCACAATGAGACCAACACAGACAGAGGTTGAAATAATACATCATGTG 485  
Db 471 CCCAGCTATCACAATGAGACCAACACAGACAGAGGTTGAAATAATACATCATGTG 530  
QY 486 CACCGAATAATTCAGAGATTAACCAACACAGCTGAGCAAAATGCTTTTCAAGACA 545  
Db 531 CACCGAATAATTCAGAGATTAACCAACACAGCTGAGCAAAATGCTTTTCAAGACA 590  
QY 546 GTATCATCATCTGTGGAG 605  
Db 591 GTATCATCATCTGTGGAG 650  
QY 606 GACTGTGGGCGCCAGCATGTACTGCGAAGTTTGCCAGCTTCCAGTACACTGCGACCATGC 665  
Db 651 GACTGTGGGCGCCAGCATGTACTGCGAAGTTTGCCAGCTTCCAGTACACTGCGACCATGC 710  
QY 666 CGGGGCGAGAGAGAGCTGTGACCCGGGACAGTGAAGTGTGGAGACAGCTGTGTGTC 725  
Db 711 CGGGGCGAGAGAGAGCTGTGACCCGGGACAGTGAAGTGTGTGGAGACAGCTGTGTGTC 770  
QY 726 TGGGGTCACTGACCAAAATGGCCACAGGGGAGCAATGAGCAATCTGTGACACAG 785  
Db 771 TGGGGTCACTGACCAAAATGGCCACAGGGGAGCAATGAGCAATCTGTGACACAG 830  
QY 786 AGGACCTGCGAGCGGGCTGTGCTGTGCTTCCAGAGAGGCGTGTTCCTCGTGTGTC 845  
Db 831 AGGACCTGCGAGCGGGCTGTGCTGTGCTTCCAGAGAGGCGTGTTCCTCGTGTGTC 890  
QY 846 ACACCCCTGCGAGCGGGCTGTGCTGTGCTTCCAGATGCCCGGACCGGCTTGTGACCTC 905  
Db 891 ACACCCCTGCGAGCGGGCTGTGCTGTGCTTCCAGATGCCCGGACCGGCTTGTGACCTC 950  
QY 906 ATCACTGGAGAGCTAGAGACCTGATGAGACCTTGAACCAATGCTTGTGCAAGTGTGTC 965  
Db 951 ATCACTGGAGAGAGCTAGAGACCTGATGAGACCTTGTGCAAGTGTGTC 1010  
QY 966 CTCTGCGAGCCCAAGCCAGCCAGCTGTGTATGTGTGCAAGCCGACCTTGTGGGGAGC 1025  
Db 1011 CTCTGCGAGCCCAAGCCAGCCAGCTGTGTATGTGTGCAAGCCGACCTTGTGGGGAGC 1070  
QY 1026 CGTGAACAAAGATGGGAGATCTGTGTGCGCAGAGAGTCCCGATGATGTAAGTTGGC 1085  
Db 1071 CGTGAACAAAGATGGGAGATCTGTGTGCGCAGAGAGTCCCGATGATGTAAGTTGGC 1130  
QY 1086 AGCTTCATGAGAGAGTGCAGAGAGCTGAGAGAGCTGAGAGAGAGAGAGAGAGAG 1145  
Db 1131 AGCTTCATGAGAGAGTGCAGAGAGCTGAGAGAGCTGAGAGAGAGAGAGAGAGAG 1190  
QY 1146 ATGGGCTGGGGAGAGCTGTGGGCTGTGGCTGTGGCTGTGGAGGGAGAGAGATTAG 1205  
Db 1191 ATGGGCTGGGGAGAGCTGTGGGCTGTGGCTGTGGCTGTGGAGGGAGAGAGATTAG 1250

QY 1206 ATCTGAGCCAGGCTGTGGTATGATGTGCAATGAAATAGCTAATTTATTTCCAGGTGT 1265  
Db 1251 ATCTGAGCCAGGCTGTGGTATGATGTGCAATGAAATAGCTAATTTATTTCCAGGAGGT 1310  
QY 1266 GTGCTTTAGGGGTGGGCTGACCAAGCTTCTCTACATCTTCTTCCAGTAAGTTTCCC 1325  
Db 1311 GTGCTTTAGGGGTGGGCTGACCAAGCTTCTCTACATCTTCTTCCAGTAAGTTTCCC 1370  
QY 1326 TCTGGCTTGAAGACATGAGAGTGTGTGATTTGTTCAGCTCCCGAGGCTGTCTCCAG 1385  
Db 1371 TCTGGCTTGAAGACATGAGAGTGTGTGATTTGTTCAGCTCCCGAGGCTGTCTCCAG 1430  
QY 1386 CTTCACAGTGTGAGCTTGGAGAGAGTCAAGAGGTTTAACTGAGAGAGAGAGTGGCAC 1445  
Db 1431 CTTCACAGTGTGAGCTTGGAGAGAGTCAAGAGGTTTAACTGAGAGAGAGAGTGGCAC 1490  
QY 1446 CCCTGTCCAGATTATTTGCTGCTGCTTACAGATTGGCAGACAGCGTTTGTCTAC 1505  
Db 1491 CCCTGTCCAGATTATTTGCTGCTGCTTACAGATTGGCAGACAGCGTTTGTCTAC 1550  
QY 1506 ATGGCTTGTATATTTGTGAGGGAGAGAGATGAAACAAATGGAGTCTGCTGAT 1565  
Db 1551 ATGGCTTGTATATTTGTGAGGGAGAGAGATGAAACAAATGGAGTCTGCTGAT 1610  
QY 1566 GGTTTGGGAAATGTGAGAAAGTGCCTGCTTGGCAATCAACTGAGCAAAATG 1625  
Db 1611 GGTTTGGGAAATGTGAGAAAGTGCCTGCTTGGCAATCAACTGAGCAAAATG 1670  
QY 1626 CAACAATGAATTTTCCAGAGCTTCTTCAATGGGCAATGATAGCTGTGCTGACT 1685  
Db 1671 CAACAATGAATTTTCCAGAGCTTCTTCAATGGGCAATGATAGCTGTGCTGACT 1730  
QY 1686 GTTGAGATGAATGTGCTGCTTCACTGATATGATGTTATTTATTCAGAGAGTGT 1745  
Db 1731 GTTGAGATGAATGTGCTGCTTCACTGATATGATGTTATTTATTCAGAGAGTGT 1790  
QY 1746 GCTCAGCTCTACCTGTGTGCGAGGAGCATTTTCAATCCAGATCAATTCCTGCT 1805  
Db 1791 GCTCAGCTCTACCTGTGTGCGAGGAGCATTTTCAATCCAGATCAATTCCTGCT 1850  
QY 1806 CAGCAGCTGGGAGAGGGGCTGATTTCTGCTGCTGATCAGAGAGCTCAGAGGCTCA 1865  
Db 1851 CAGCAGCTGGGAGAGGGGCTGATTTCTGCTGCTGATCAGAGAGCTCAGAGGCTCA 1910  
QY 1866 GAGACTGCAAGCTGTGCTGCGCAAGTCAACAGCTAGTGAAGCCAGAGAGTTCATGT 1925  
Db 1911 GAGACTGCAAGCTGTGCGCAAGTCAACAGCTAGTGAAGCCAGAGAGTTCATGT 1970  
QY 1926 GTTGTGACTTAACTCACTGCTCTCTCACTACCCCAACAGGCTGTGGGCCCAAA 1985  
Db 1971 GTTGTGACTTAACTCACTGCTCTCTCACTACCCCAACAGGCTGTGGGCCCAAA 2030  
QY 1986 AGTGTCTCCCAAAAGAGAGAGATGGATTTTCTTTTGAAGCATGACATCTGAAAT 2043  
Db 2031 AGTGTCTCCCAAAAGAGAGAGATGGATTTTCTTTTGAAGCATGACATCTGAAAT 2090  
QY 2044 AAGGTCAAACTAATCTCACTCCCTTAAAGTAACTAAGTAAAGAGAGAGTGT 2103  
Db 2091 AAGGTCAAACTAATCTCACTCCCTTAAAGTAACTAAGTAAAGAGAGAGTGT 2150  
QY 2104 CTCAAGTGTGGGAGAGCGGCTTCTAATGAAGCAATGATATGACATGCTCCCTCT 2163  
Db 2151 CTCAAGTGTGGGAGAGCGGCTTCTAATGAAGCAATGATATGACATGCTCCCTCT 2210  
QY 2164 TGGCAGTTGCAATTAATCTTGAAGGATATGACTGAGGCTGACATACAGTTTAACT 2223  
Db 2211 TGGCAGTTGCAATTAATCTTGAAGGATATGACTGAGGCTGACATACAGTTTAACT 2270  
QY 2224 GCGAAGACAGTACTAAGTAAATTTGAGGCGAGGATTAATGAATTTGCAAAATCAC 2283  
Db 2271 GCGAAGACAGTACTAAGTAAATTTGAGGCGAGGATTAATGAATTTGCAAAATCAC 2330  
QY 2284 TTAGCAGCAACTGAAGACATTAATCAACAGTGAAGAAATCAACGAGCAGGCTGT 2343

Db	2331	TTAGCACAACCTGAAGACCAATTATTCACCAAGTGAAGAAATTCAAACCGACACAGGGCTGT	2390
QY	2344	GTGAACATGGTTGTAAATATGCGACTGGGAACATGAACTGTAGCGCACTGCACAAATGA	2403
Db	2391	GTGAACATGGTTGTAAATATGCGACTGGGAACATGAACTTACGCCACTGCCAATAATGA	2450
QY	2404	TGTTTTCAAGTGTCAATGACTGTGGCCACCATGATATCATCTCAAGTCTTAAAGTTAA	2463
Db	2451	TGTTTTCAGTGTCATGACTGTGGCCACCATGATATCATCAAGTCTTAAAGTTAA	2510
QY	2464	AGTTGCACATGATGTATPAAGCATGCTTCTTGAAGTTTAAATATGTATPAACATPAAG	2523
Db	2511	AGTTGCACATATGTATPAAGCATGCTTCTTGAAGTTTAAATATGTATPAACATPAAG	2570
QY	2524	TTGCATTAGAAATCAAGCATPAATCACTTCACTCAACAAAAA	2583
Db	2571	TTGCATTAGAAATCAAGCATPAATCACTTCACTCAACAAAAA	2630
QY	2584	AA 2585	
Db	2631	AA 2632	

RESULT 15	AX235333	LOCUS	AX235333	2479 bp	DNA	linear	PAT 11-SEP-2001
		DEFINITION	Sequence 1 from Patent WO0163295.				
		ACCESSION	AX235333				
		VERSION	AX235333.1	GI:15593878			

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
ORGANISM	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Heath, H.M., Parekh, R.B., Rohlf, C. and Patel, T.P.
TITLE	Dpi-6, a therapeutic biomarker in neurological disorders
JOURNAL	Patent: WO 0163285-A 1 30-AUG-2001;
JOURNAL	Oxford Glycosciences (UK) Limited (GB)

```

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
38. .1090
CDS
note="Unnamed protein product"

```

BASE COUNT	625 a	618 c	668 g	567 t	1 others
ORIGIN	625 a	618 c	668 g	567 t	1 others

Query Match	Similarity	94.6%	Score 2445.2	DB 6	Length 2479
Best Local	Similarity	99.8%	Prod. No. 0		
Matches 2459	Conservative		Mismatches 4	Indels 2	Gaps 1
QY	124	GGGGGGGGGCTGCGGGCGCAAGCGGAGATGACAGCGCTTGGGGCCACCCTGCTGTGCC	183		
Db	9	GGGGGGGGGCTGCGGGCGCAAGCGGAGATGACAGCGCTTGGGGCCACCCTGCTGTGCC	68		
QY	184	TGCTGCTGAGCGGGCGGCTGCCACAGGCCCGCCCGCTTCGACGGGAGACTTGGGCTC	243		
Db	69	TGCTGCTGAGCGGGCGGCTGCCACAGGCCCGCCCGCTTCGACGGGAGACTTGGGCTC	128		
QY	244	CAGTCAGACCGCGCCCGGCTCTACACTACCGCAGAGAGGCCACCCTCAATAGATGCT	303		

Db	129	CAGTCAAGCCCGGCCGCTCTCAGCTACCCGACGAGGAGGCGCACCTCTCAATGAGATGT	188
QY	304	TCCGCGAGGTTTGAAGAACTGATGGAAGACACGACGACAAATTGGCGAGCGGTGGAA	363
Db	189	TCCGCGAGGTTTGAAGAACTGATGGAAGACACGACGACAAATTGGCGAGCGGTGGAA	248
QY	364	AGATGAGAGCGAAGAAAGCTGCTGTAAACATCATCAGAAGTGAACCTGGCAAACTTAC	423
Db	249	AGATGAGAGCGAAGAAAGCTGCTGTAAACATCATCAGAAGTGAACCTGGCAAACTTAC	308
QY	424	CTCCCACTTATCAATATGAGACCAACACACAGAAAGTTGGAAATATATACATCCATG	483
Db	309	CTCCCACTTATCAATATGAGACCAACACACAGAAAGTTGGAAATATATACATCCATG	368
QY	484	TGCACCGAGAAATTCACAAATTAACCAACAACAGACTGAGCAAAATGGTCTTTTACAGA	543
Db	369	TGCACCGAGAAATTCACAAATTAACCAACAACAGACTGAGCAAAATGGTCTTTTACAGA	426
QY	544	CAGTTATCACTCTGTGGAGACGAAAGAGGCGAAGAGAGCCACGAGTGCATATCGACG	603
Db	429	CAGTTATCACTCTGTGGAGACGAAAGAGGCGAAGAGAGCCACGAGTGCATATCGACG	488
QY	604	AGGACTGTGGGCCCCAGATGTATCTGCGCAGTTTGGCACTTCCAGTACACCTGCCAGCAT	663
Db	489	AGGACTGTGGGCCCCAGATGTATCTGCGCAGTTTGGCACTTCCAGTACACCTGCCAGCAT	548
QY	664	GCCGAGGAGCAGAGGATGCTTGCAACCCGGGACAGTGAAGTCTGTGAGACCAAGCTGTGT	723
Db	549	GCCGAGGAGCAGAGGATGCTTGCAACCCGGGACAGTGAAGTCTGTGAGACCAAGCTGTGT	608
QY	724	TCTGGGGTCACTGACCAAAATGGCCACACAGGGGACAAATGGGACCATCTGTATCAAC	783
Db	609	TCTGGGGTCACTGACCAAAATGGCCACACAGGGGACAAATGGGACCATCTGTATCAAC	668
QY	784	AGAGGAGCTGCAAGCCGAGGCTGTGCTGTGCTTCCAGAGAGGCTGTTCCCTGTGT	843
Db	669	AGAGGAGCTGCAAGCCGAGGCTGTGCTGTGCTTCCAGAGAGGCTGTTCCCTGTGT	728
QY	844	GCAACACCCCTTGCTGTGAGAGGGGCGACCTTTGCCATACCCCGCCAGCCGGTTTGGAC	903
Db	729	GCAACACCCCTTGCTGTGAGAGGGGCGACCTTTGCCATACCCCGCCAGCCGGTTTGGAC	788
QY	904	TCAATCACCTGGGAGCTTGAAGCTTGAAGGCTTGAACCGATGCTTGTGTGCAAGTGGC	963
Db	789	TCAATCACCTGGGAGCTTGAAGGCTTGAAGGCTTGAACCGATGCTTGTGTGCAAGTGGC	848
QY	964	TGCTTGTGCAAGCCCCACAGCCACAGCTTGATGTGTGTGCAAGCCGACTTGTGGGGA	1023
Db	849	TGCTTGTGCAAGCCCCACAGCCACAGCTTGATGTGTGTGCAAGCCGACTTGTGGGGA	908
QY	1024	GCGGTGACCAAGATGGGGAAGTCCGTGTGCCACAGAGGTTCCCGCATGAGTATGAAGTTG	1083
Db	909	GCGGTGACCAAGATGGGGAAGTCCGTGTGCCACAGAGGTTCCCGCATGAGTATGAAGTTG	968
QY	1084	GCACTTCATGAGAGAGGTGCGCCAGAGAGCTGAGGACCTGAGAGAGAGCTTGACTGAAG	1143
Db	969	GCACTTCATGAGAGAGGTGCGCCAGAGAGCTGAGGAGCTGAGAGAGAGCTTGACTGAAG	1028
QY	1144	AGATGGGCTTGGGGGAAGCTTGGGCTGCCGCTTGCATCTGTGGAGGGGAAGAAGATT	1203
Db	1029	AGATGGGCTTGGGGGAAGCTTGGGCTGCCGCTTGCATCTGTGGAGGGGAAGAAGATT	1088
QY	1204	AGATCTGGACACAGGCTGTGGGTATATGTGAATGAATAATAGCTAATTTATTTCCCAAGT	1263
Db	1089	AGATCTGGACACAGGCTGTGGGTATATGTGAATGAATAATAGCTAATTTATTTCCCAAGT	1148
QY	1264	GTTGTGCTTTAAGCGCTGGGCTGAACAGGCTTTCTTCACTATTTCTTCCAGTAAGTTTCC	1323
Db	1149	GTTGTGCTTTAAGCGCTGGGCTGAACAGGCTTTCTTCACTATTTCTTCCAGTAAGTTTCC	1208
QY	1324	CCTGTGGCTTGAAGCATGAGGTTTGTGATTTGTTCAGGCTCCCAAGGCTGTCTTCCA	1383

Db 1209 CCTGTGCTTGACGACATGAGTGTGTGCAATTTGTCAGCTCCGCCAGGCTGTCTCCA 1268  
 QY 1384 GGCTTCACAGTCTGTGCTTGGGAGAGTCAAGCAGGGTTAACTGACGAGCAAGTTGCC 1443  
 Db 1269 GGCTTCACAGTCTGTGCTTGGGAGAGTCAAGCAGGGTTAACTGACGAGCAAGTTGCC 1328  
 QY 1444 ACCCTCTCCAGATTAATTTGGCTGTGCTTGGCTCAAGTTGGCAGACAGCGTTGGTCT 1503  
 Db 1329 ACCCTCTCCAGATTAATTTGGCTGTGCTTGGCTCAAGTTGGCAGACAGCGTTGGTCT 1388  
 QY 1504 ACATGCTTTGATTAATTTGGCTGTGCTTGGCTCAAGTTGGCAGACAGCGTTGGTCT 1563  
 Db 1389 ACATGCTTTGATTAATTTGGCTGTGCTTGGCTCAAGTTGGCAGACAGCGTTGGTCT 1448  
 QY 1564 TTGGTTTGGGGAATGTGGAGAGAGTGCCTGCTTGGCAACATCAACTGCGCAAAA 1623  
 Db 1449 TTGGTTTGGGGAATGTGGAGAGAGTGCCTGCTTGGCAACATCAACTGCGCAAAA 1508  
 QY 1624 TGCAACAATGAATTTTCCAGCAGTTCTTCCATGGGCAATAGTAAGTGTGCTTCAG 1683  
 Db 1509 TGCAACAATGAATTTTCCAGCAGTTCTTCCATGGGCAATAGTAAGTGTGCTTCAG 1568  
 QY 1684 CTGTTCAGATGAATATTTCTGTTCACCTTCGATTAATGTGTTTATTCATCCAGCAGT 1743  
 Db 1569 CTGTTCAGATGAATATTTCTGTTCACCTTCGATTAATGTGTTTATTCATCCAGCAGT 1628  
 QY 1744 TTGCTCAGCTCCTACCTCTGTGCGAGGGCAGCATTTTCATATCCAAAGATCAATCCCTCT 1803  
 Db 1629 TTGCTCAGCTCCTACCTCTGTGCGAGGGCAGCATTTTCATATCCAAAGATCAATCCCTCT 1688  
 QY 1804 CTCGACACAGCTTGGGAGGGGGTCAATTTCTCTCTCCATCAGGATCTCAGAGCT 1863  
 Db 1689 CTCGACACAGCTTGGGAGGGGGTCAATTTCTCTCTCCATCAGGATTTTCAAGGCT 1748  
 QY 1864 CAGAGACGCAAGCTGTGCTGCGCAAGTCAACAGCTAGTGAAGACGAGCAGTTTCATC 1923  
 Db 1749 CAGAGACGCAAGCTGTGCTGCGCAAGTCAACAGCTAGTGAAGACGAGCAGTTTCATC 1808  
 QY 1924 TGATTTGACTCTAAGCTCAAGTGTCTCTCCATACCCCAACAGCCTTGTGCGCA 1983  
 Db 1809 TGATTTGACTCTAAGCTCAAGTGTCTCTCCATACCCCAACAGCCTTGTGCGCA 1868  
 QY 1984 AAATGCTCCCCCAAGAGAGAGAAATGGGATTTTC- -TTGAGGCAATGCAATCTGGA 2041  
 Db 1869 AAATGCTCCCCCAAGAGAGAGAAATGGGATTTTC- -TTGAGGCAATGCAATCTGGA 1928  
 QY 2042 TTAAGTCAAACTAATCTCAATCCCTCTAAAGTAACCTAGTTAGAACAGCAGT 2101  
 Db 1929 TTAAGTCAAACTAATCTCAATCCCTCTAAAGTAACCTAGTTAGAACAGCAGT 1988  
 QY 2102 TTCTCAAGTGTGGGCGAGCGCTCTCTAATGAAGCAATGATTTGACATGTCCTC 2161  
 Db 1989 TTCTCAAGTGTGGGCGAGCGCTCTCTAATGAAGCAATGATTTGACATGTCCTC 2048  
 QY 2162 TTGCGAGTTGCTAATTAATTTGAAGGATATGACTGAGCTAGCATACAGTTAAC 2221  
 Db 2049 TTGCGAGTTGCTAATTAATTTGAAGGATATGACTGAGCTAGCATACAGTTAAC 2108  
 QY 2222 CTGAGAAAACGTAATTAATTTGAGGCGAGATTAATAATGAATTTGCAAAATC 2281  
 Db 2109 CTGAGAAAACGTAATTAATTTGAGGCGAGATTAATAATGAATTTGCAAAATC 2168  
 QY 2282 ACTTAGCAGCACTGAGAGCAATTAATCAACAGTGGAGAAATCAAAACGAGAGGCT 2341  
 Db 2169 ACTTAGCAGCACTGAGAGCAATTAATCAACAGTGGAGAAATCAAAACGAGAGGCT 2228  
 QY 2342 GTGTGAAAACATGTTGTAATGCGACTGCGAACACTGAATCTAGCCCACTCCAAAT 2401  
 Db 2229 GTGTGAAAACATGTTGTAATGCGACTGCGAACACTGAATCTAGCCCACTCCAAAT 2288  
 QY 2402 GATGTTTCAAGTGTCAAGAGCTGTGCGCACTGTAATTCACAGAGTTCTTAAAGTT 2461  
 Db 2289 GATGTTTCAAGTGTCAAGAGCTGTGCGCACTGTAATTCACAGAGTTCTTAAAGTT 2348

QY 2462 AAAGTTGCAATGATTTGTAATGAAGCATGCTTTCTTTGAGTTTAAATTAATTAACAATA 2521  
 Db 2349 AAAGTTGCAATGATTTGTAATGAAGCATGCTTTCTTTGAGTTTAAATTAATTAACAATA 2408  
 QY 2522 AGTTGCAATTTGAATTAAGCATTAATCACTTCAACTGCAAAAAA 2581  
 Db 2409 AGTTGCAATTTGAATTAAGCATTAATCACTTCAACTGCTAAAAA 2468  
 QY 2582 AAAAA 2586  
 Db 2469 AAAAA 2473

Search completed: February 19, 2004, 21:18:11  
 Job time : 9417 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: February 20, 2004, 14:56:18 ; Search time 24 Seconds  
(without alignments)  
685,806 Million cell updates/sec

Title: US-10-063-671-8  
Perfect score: 1880

Sequence: 1 MQRGLATLCLLAAAVPTA.....EMALGPAAAAALLGGEEL 350

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1880	100.0	350	1 DKK3_HUMAN	Q94944 homo sapien
2	1589	94.5	349	1 DKK3_MOUSE	Q94944 homo musc
3	1017	54.1	350	1 DKK3_CHICK	Q94944 gallus gall
4	214.5	11.4	224	1 DKK4_HUMAN	Q94944 homo sapien
5	174.5	9.3	266	1 DKK1_HUMAN	Q94907 homo sapien
6	165.5	8.8	272	1 DKK1_MOUSE	Q94908 mus musc
7	162	8.6	259	1 DKK2_HUMAN	Q94942 homo sapien
8	154	8.2	259	1 DKK2_MOUSE	Q94948 mus musc
9	145	7.7	242	1 SGY1_HUMAN	Q94985 homo sapien
10	138	7.3	577	1 TRB6_CAVPO	P18725 cavia porce
11	131.5	7.0	676	1 TRB5_HUMAN	P18564 homo sapien
12	126	6.7	788	1 TRB6_HUMAN	P18564 homo sapien
13	126	6.7	1394	1 TRB5_HUMAN	P22064 homo sapien
14	126	6.7	1595	1 TRB1_HUMAN	Q14766 homo sapien
15	125.5	6.7	230	1 SGY1_MOUSE	Q94942 mus musc
16	123.5	6.6	787	1 TRB6_MOUSE	Q94982 mus musc
17	119	6.3	2318	1 NTC3_MOUSE	Q00174 dtrosophila
18	117	6.2	3172	1 LMA_DROME	Q13751 homo sapien
19	116	6.2	1172	1 LMB3_HUMAN	P10040 dtrosophila
20	116	6.2	2139	1 CRB_DROME	Q10040 dtrosophila
21	115	6.1	1807	1 TRB4_RAT	Q94944 rat
22	113	6.0	618	1 DL3_HUMAN	Q94944 homo sapien
23	113	6.0	3562	1 PGCV_CHICK	Q94944 gallus gall
24	112	6.0	1389	1 TRB5_MOUSE	Q94944 mus musc
25	112	6.0	1713	1 TRB1_MOUSE	Q94944 mus musc
26	110.5	5.9	864	1 LDBR_MOUSE	P33551 mus musc
27	110.5	5.9	2214	1 NORL_HUMAN	Q94944 h. sapien
28	110	5.9	2524	1 SORL_XENTLA	P21783 xenopus lae
29	109.5	5.8	655	1 TRB5_PAPCY	Q00741 papio cynoc
30	109.5	5.8	1712	1 TRB1_RAT	Q00918 rat
31	109.5	5.8	1822	1 TRB4_HUMAN	P16144 homo sapien
32	109	5.8	1168	1 LMB3_MOUSE	Q61087 mus musc
33	109	5.8	2319	1 NTC3_RAT	Q94172 rat

34	108.5	5.8	757	1 COMP_HUMAN	P49747 homo sapien
35	108.5	5.8	852	1 SRCH_RABIT	P16230 coryctolagus
36	108	5.7	1170	1 TRB1_HUMAN	P07996 homo sapien
37	107.5	5.7	799	1 TRB5_HUMAN	P18084 homo sapien
38	107	5.7	589	1 DL3_RAT	O88671 rat
39	107	5.7	755	1 COMP_RAT	P35444 rat
40	107	5.7	1693	1 SAS_DROME	Q04164 dtrosophila
41	106.5	5.7	3695	1 LMA5_HUMAN	O15230 homo sapien
42	106	5.6	227	1 AGT_OYSA	P11219 coryctolagus
43	106	5.6	1221	1 FBL2_MOUSE	P37889 mus musc
44	106	5.6	2471	1 NTC2_HUMAN	Q04721 homo sapien
45	105.5	5.6	96	1 BVA_BOMVA	Q94944 bombyx mori

## ALIGNMENTS

RESULT 1	ID	DKK3_HUMAN	STANDARD;	PRT;	350 AA.
AC	Q94944	Q94944			
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DE	Dickkopf related protein-3 precursor (Dkk-3) (Dkk-3)				
GN	DKK3 OR REIC				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TRISUE-Fetal brain;				
RX	MEDLINE=20035735; PubMed=10570958;				
RA	Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W.,				
RA	Amara V.L., Brown D.E., Guyot D., Mays G., Leiby K., Chang B.,				
RA	Drong T., Goodenart A.D.J., Gearing D.P., Sokol S.Y., McCarthy S.A.,				
RT	"Functional and structural diversity of the human Dickkopf gene				
RT	family.";				
RL	Gene 238:301-313(1999).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Tanaka S., Sugimachi K.,				
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20119095; PubMed=10652205;				
RA	Tsuji T., Miyazaki M., Sakaguchi M., Inoue Y., Namba M.,				
RA	"A REIC gene shows down-regulation in human immortalized cells and				
RT	human tumor-derived cell lines.";				
RT	Biochem. Biophys. Res. Commun. 268:20-24(2000).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	Rate G., Mitsuya T.,				
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21673998; PubMed=11814687;				
RA	Kobayashi K., Ouchida M., Tsuji T., Hanafusa H., Miyazaki M.,				
RA	Namba M., Shimizu N., Shimizu K.,				
RT	"Reduced expression of the REIC/Dkk-3 gene by promoter-				
RT	hypermethylation in human tumor cells.";				
RL	Gene 282:151-158(2002).				
RN	[6]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Kidney;				
RX	MEDLINE=22388257; PubMed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Steinmetz G.M., Schuler G.D.,				
RA	Altschuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Shat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton W., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,				

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mallya S.J., Rosak S.A., McKernan K.J., Malek J.A., Gunartene P.H., Richey S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallat D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).

CC -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY (POTENTIAL).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN HEART, BRAIN, AND SPINAL CORD.

CC -1- PTM: N-GLYCOSYLATED.

CC -1- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.

CC -----

CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

DR EMBL: AF177396; AAF02676.1; -

DR EMBL: AB033421; BAA85488.1; -

DR EMBL: AB034203; BAA90548.1; -

DR EMBL: AB035182; BAA87044.2; -

DR EMBL: AB045205; BAA87044.2; JOINED.

DR EMBL: AB045206; BAA87044.2; JOINED.

DR EMBL: AB045207; BAA87044.2; JOINED.

DR EMBL: AB045208; BAA87044.2; JOINED.

DR EMBL: AB045209; BAA87044.2; JOINED.

DR EMBL: AB045210; BAA87044.2; JOINED.

DR EMBL: AB057591; BAA84360.1; -

DR EMBL: AB057804; BAA84361.1; -

DR EMBL: BC007660; BAA87044.2; -

DR EMBL: HGNC:2893; DKX3.

DR MIM: 605416; -

DR GO: GO:0005615; C:extracellular space; TAS.

DR GO: GO:0007345; P:embryogenesis and morphogenesis; TAS.

DR InterPro: IPR006796; dickkopf\_N.

DR Pfam: PF04706; dickkopf\_N\_1.

DR Developmental: protein; Signal; Wnt signaling pathway; Glycoprotein.

KW SIGNAL

FT SIGNAL 1 16 POTENTIAL.

FT CHAIN 17 350 DICKKOPF RELATED PROTEIN-3.

FT DOMAIN 147 195 DKK-TYPE CYS-1.

FT DOMAIN 208 284 DKK-TYPE CYS-2.

FT DOMAIN 338 343 POLY-ALA.

FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 335 335 G -> R (IN REF. 4).

FT SEQUENCE 350 AA; 38291 MW; 72F504122B40AF8E CRC64;

Query Match 100.0%; Score 1880; DB 1; Length 350; Best Local Similarity 100.0%; Fred. No. 3.6e-128; Indels 0; Gaps 0; Matches 350; Conservative 0; Mismatches 0;

QY 1 MORGATLCLLLAAVPTAPAPATSAVPKGPALSPVSEBALTINEMFREVEELMED 60

DB 1 MORGATLCLLLAAVPTAPAPATSAVPKGPALSPVSEBALTINEMFREVEELMED 60

QY 61 TQHLRSAAVEMEBEAAAARSSSEVNLANLPSPSHNETNTDTKKNNTTIVHEIKHTN 120

DB 61 TQHLRSAAVEMEBEAAAARSSSEVNLANLPSPSHNETNTDTKKNNTTIVHEIKHTN 120

QY 121 NOTSQWFESEVITVSVDDEGRSHSECTIDEDCGPSMYCQFASFOYTQPCRCQRMCTR 180

DB 121 NOTSQWFESEVITVSVDDEGRSHSECTIDEDCGPSMYCQFASFOYTQPCRCQRMCTR 180

QY 181 DSECCGQLCVMWGCTKATRGSGNGTICDNORDQPELCAFORGLTFPCTPLPVAGEL 240

DB 181 DSECCGQLCVMWGCTKATRGSGNGTICDNORDQPELCAFORGLTFPCTPLPVAGEL 240

QY 241 CHDPASRLDLITWLEPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQGEILL 300

DB 241 CHDPASRLDLITWLEPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQGEILL 300

QY 301 PREVPDEYVGSFMEYVROELEDLERSTEMALGE2AAALALGEEI 350

DB 301 PREVPDEYVGSFMEYVROELEDLERSTEMALGE2AAALALGEEI 350

RESULT 2

ID DKK3 MOUSE STANDARD; PRT: 349 AA.

AC Q9OUN9;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 15-SEP-2003 (Rel. 42, Last annotation update)

DE Dickkopf related protein-3 precursor (Dkk-3) (Dkkopf-3) (mdk-3).

GN DKK3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI\_TaxId=10090;

RP SEQUENCE FROM N.A.

RX MEDLINE=99425169; PubMed=10495270;

RA Monaghan P.A., Kioschis P., Wu W., Zuniga A., Bock D., Poustka A., Dellus H., Niehus C.,

RT "Dickkopf genes are co-ordinately expressed in mesodermal lineages." Mech. Dev. 87:45-56(1999).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=20035735; PubMed=10570958;

RA Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W., Amaravadi L., Brown D.E., Guyot D., Mays G., Ieib K., Chang B., Duong T., Goodheart A.D.C., Gearing D.P., Sokol S., McCarthy S.A.,

RT "Functional and structural diversity of the human Dickkopf gene family." Gene 238:301-313(1999).

RL [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Liver.

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I., Saito T., Okazaki H., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T., Fleischnann W., Gaasterland T., Gissi C., King B., Kochwa H., Kuenl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P., Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L., Wyszah-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontsuki S., Hayashizaki Y.,

RT "Functional annotation of a full-length mouse cDNA collection." Nature 409:685-690(2001).

RL Nature 409:685-690(2001).

CC -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY (POTENTIAL).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN, EYE, AND HEART.

```

CC TISSUE=Lens fibers;
RX MEDLINE=96437509; PubMed=8840185;
RA Sawada K., Agata K., Eguchi G.,
RT "Characterization of terminally differentiated cell state by
RT categorizing cDNA clones derived from chicken lens fibers.";
RL Int. J. Dev. Biol. 40:531-535(1996).
CC -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN EYE LENS.
CC -1- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
-----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; D26311; BAA05373.1; -.
DR HSSP; P26687; 1IMT.
DR InterPro; IPR006796; dickkopf_N.
DR Pfam; PF04706; dickkopf_N.1
KM Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 350 DICKKOPF RELATED PROTEIN-3.
FT DOMAIN 139 187 DKK-TYPE CYS-1.
FT DOMAIN 200 277 DKK-TYPE CYS-2.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 350 AA; 39208 MW; 57BE7ED850089DAE CRC64;

Query Match 54.1%; Score 1017; DB 1; Length 350;
Best Local Similarity 54.4%; Pred. No. 4e-66;
Matches 193; Conservative 49; Mismatches 83; Indels 30; Gaps 4;

QY 8 L L C L L I A A A V P T A P A P A P T A S P A V K G P A L S Y P Q E A T L N E M F R E V E L I M E D T O K L R S 67
Db 14 L L L A V A L A L C C A A G S G G R R A - - - - - A S I G E M L R E V E A L M E D T O K L R N 59

QY 68 A V E M E M E E A A A S S P V N L A N L P P S Y N H E T M T D K Y G N T I N H A R E I K T I N N O T G M V 127
Db 60 A V E M E M E E E G A K K L S E V N P E N L P P T Y N H S N S Y E T R I G N T V O T H E I D K T D R I T S T I 119

QY 128 F S E T V I T S V D E G R S R S H E C I I D E D C P S Y M Y C O F A S F O Y T C O P C R G O R M L C T R D S E C G D 187
Db 120 F S E I I I S I N G E N K N H E C I I D E D C T G Y C Q F S T E Y V C O P K T Q H T C S R V E C G D 179

QY 188 Q L C W M G H C T M A R G S N G T I C D N O R D C O P E L C A F O R G L L F P V T P L P V E G L C H D P A S R 247
Db 180 Q L C W M G C R A T S G E N G I T C E N O H D N P O T C A F O K E L L F P V C T P L P E G E P C H D P S N R 239

QY 248 L L D I T I E L P P D G L D R C P C A S G L C O P H - S H S I V Y C K E T F V G S R D O D G E - - - - - 297
Db 240 L L N D I T E L P P D V L E R C P C A S G L I C Q P O S H S T S Y C E L S N E T R K N E K E D P L I N D E M P 299

QY 298 - - I L P R E V D E Y F V G S F M E E V R O E L D E R S L T E M A L G E P A A A A A L L G E E I 350
Db 300 F I S I L P R D I I S D Y E E S S V I O E V R K E L S L E - - - - D O A G V S E H D P A D L F L G D E I 350

RESULT 4
DCK4 HUMAN STANDARD; PRT; 224 AA.
AC Q9UBT3; Q9Y4C3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dickkopf related protein-4 precursor (Dkk-4) (Dickkopf-4) (hDkk-4) .
DN DKK4.

```

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.  
 CX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-28 AND 134-144.  
 RX MEDLINE=20035735; PubMed=10570958;  
 RA Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W.,  
 Amaravadi L., Brown D.E., Guyot C., Mays G., Leiby K., Chang B.,  
 Duong T., Goodheart A.D.J., Gearing D.P., Sokol S.Y., McCarthy S.A.,  
 RT "Functional and structural diversity of the human Dickkopf gene  
 family.";  
 RL Gene 238:301-313 (1999).  
 RP SEQUENCE FROM N.A.  
 RA Tate G., Mitsuya T.,  
 RT "Human Dickkopf as well as DAN family members, Cerberus and Gremlin,  
 are preferentially expressed in the epithelial malignant cell lines,";  
 RL J. Biochem. Mol. Biol. Biophys. 3:239-242 (1999).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RA Tate G., Suzuki T., Mitsuya T.,  
 RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN CEREBELLUM, T-CELLS, ESOPHAGUS,  
 AND LUNG.  
 CC -1- PTM: APPARS NOT TO BE GLYCOSYLATED.  
 CC -1- PTM: CAN ALSO BE PROTEOLYTICALLY PROCESSED BY A FURIN-LIKE  
 PROTEASE.  
 CC -1- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.  
 CC  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>  
 or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC  
 CC EMBL; AF177397; AAF02677.1; -  
 DR EMBL; AB018005; BAA33475.1; -  
 DR EMBL; AB018003; BAA33475.1; JOINED.  
 DR EMBL; AB018004; BAA33475.1; JOINED.  
 DR EMBL; AB017788; BAA33438.1; -  
 DR HSSP; P25687; 11MT.  
 DR GeneW; HGNC:2894; DKX4.  
 DR MIM; 605417; -  
 DR GO; GO:0030178; P:negative regulation of wnt receptor signal. .; NAS.  
 DR InterPro; IPR006796; dickkopf\_N.  
 DR Pfam; PF04706; dickkopf\_N; 1.  
 KM Developmental protein; Signal; Wnt signaling pathway.  
 FT SIGNAL 1 18  
 FT CHAIN 19 224 DICKKOPF RELATED PROTEIN-4.  
 FT CHAIN 134 224 DICKKOPF RELATED PROTEIN-4 SHORT FORM.  
 FT DOMAIN 41 90 DKX-TYPE CYS-1.  
 FT DOMAIN 145 218 DKX-TYPE CYS-2.  
 FT CONFLICT 93 93 M -> L (IN REF. 3).  
 SQ SEQUENCE 224 AA; 24875 MW; 45F8BEC476961357 CRC64;  
 Query Match 11.4%; Score 214.5; DB 1; Length 224;  
 Best Local Similarity 26.5%; Pred. No. 1.2e-08;  
 Matches 57; Conservative 21; Mismatches 72; Indels 65; Gaps 7;  
 QY 124 GQMVSEVITVSGDEEG-RRSHECTIDECGSPMYC-QFASFOYTCQPCRGOMLCTRD 181  
 DB 17 GALTVDNNIRASADLHGARKSGCGLSPDQNTKFCQCPDDEKPFATCGLRRCORD 76  
 QY 132 SECCGDLCTWGHCTKM-----A 199  
 DB 77 AMCCGGTLCVNDVCTTMDANFILERQLDEODGTHAETGHPVOENQPKKPSIKSGG 136  
 QY 200 TGGNGTICNDQDQPGICAFORGLLFPVCTPLPVEGELC---HDPASRLDLITWE 255

DB 137 RKGGEGECCLTFDGPGLCA--RHFWTKCKEVLLGGYCSRGHDTAQAEI----- 190  
 QY 256 LEPDGLRCPGASGLLCP-----HSHSLVYVCK 285  
 DB 191 -----FQRCDCGPGLLCRSQLTSNRQHLRLVQO 219  
 RESULT 5  
 ID DKX1 HUMAN STANDARD; PRT; 266 AA.  
 AC 094907;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Dickkopf related protein-1 precursor (DKK-1) (Dickkopf-1) (DDK-1)  
 DE (SK).  
 GN DKX1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.  
 CX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leiomyosarcoma;  
 RX MEDLINE=99313900; PubMed=10383463;  
 RA Fedi P., Ballico A., Nieto Sorla A.,  
 RA Bottaro D.P., Kraus M.H., Aaronson S.A.,  
 RT "Isolation and biochemical characterization of the human DKK-1  
 homologue, a novel inhibitor of mammalian Wnt signaling,";  
 RL J. Biol. Chem. 274:19465-19472 (1999).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Renal kidney;  
 RX MEDLINE=20035735; PubMed=10570958;  
 RA Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W.,  
 Amaravadi L., Brown D.E., Guyot C., Mays G., Leiby K., Chang B.,  
 Duong T., Goodheart A.D.J., Gearing D.P., Sokol S.Y., McCarthy S.A.,  
 RT "Functional and structural diversity of the human Dickkopf gene  
 family,";  
 RL Gene 238:301-313 (1999).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RA Tate G., Suzuki T., Mitsuya T.,  
 RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20422487; PubMed=10965128;  
 RA Roessler E., Du Y., Glinika A., Dutra A., Niehrs C., Muenke M.,  
 RT "The genomic structure, chromosome location, and analysis of the human  
 DKK1 head inducer gene as a candidate for holoprosencephaly,";  
 RL Cytogenet. Cell Genet. 89:220-224 (2000).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22386257; PubMed=12477932;  
 RA Strausberg R.L., Fellgoid E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein W.J., Utsdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bork S.A., McEwan P.J., McKernan K.J., Malek J.A., Gudarath P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smallegange D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Warr M.A.,

```

RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences."
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PLACENTA.
CC -1- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: AF127563; AAD21087.1; -.
DR EMBL: AF177394; AAF02674.1; -.
DR EMBL: AB020315; BAA34651.1; -.
DR EMBL: AB020314; BAA34651.1; JOINED.
DR EMBL: AF261158; AAG15544.1; -.
DR EMBL: AF261157; AAG15544.1; JOINED.
DR EMBL: BC001539; AAO10359.1; -.
DR Genew; HGNC:2891; DKK1.
DR MIM; 605189; -.
DR GO; GO:0008083; F: growth factor activity; TAS.
DR GO; GO:0004871; F: signal transducer activity; TAS.
DR InterPro; IPR006796; dickkopf_N.
DR Pfam; PF04706; dickkopf_N.1.
DR Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 266 DICKKOPF RELATED PROTEIN-1.
FT DOMAIN 85 138 DKK-TYPE CYS-1.
FT DOMAIN 189 263 DKK-TYPE CYS-2.
FT CARBOHYD 256 256 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 266 AA; 28671 MW; 5E878B2CCE42365A CRC64;

Query Match 9.3%; Score 174.5; DB 1; Length 266;
Best Local Similarity 25.6%; Pred. No. 1;e-05;
Matches 50; Conservative 18; Mismatches 60; Indels 67; Gaps 8;

QY 145 HECITDEDGCGSMYCOF-----SFQYTCQPCGQRMCLTRDSECCGQDLCVWGHG--- 195
DB 83 YPCAEDCECGIDRYCASTRGAGVQ-ICLACKRRKRCRHAHMCPPGVYCKNGICVSS 141
QY 196 -----TKY-ATRGSNGTICDNQDCCPELCC 220
DB 142 DQNHFRGEIETITESFGNDHSTLDGYSRPTTLSSKMYHTKGQGGSVCLRSSPCASGLCC 201
QY 221 AFOGGLLPVCTPLPYVEGELC---HDPASRLDLITWLEPFGALDRCPASGLCC--- 273
DB 202 A--RHFWSKICKPVLEKEGVCTKRRKSHGLEI-----FQRCYCGEGLSCKIQK 249
QY 274 ---QPHSHSLVYVCK 285
DB 250 DHQASNSRLHTCQ 264

RESULT 6
ID DKK1 MOUSE STANDARD; PRT; 272 AA.
AC 054908;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dickkopf related protein-1 precursor (Dkk-1) (Dkkopf-1) (mdk-1).
GN DKK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RX MEDLINE=98111224; PubMed=9450748;
RA Glinka A, Mu W, Delling H, Monaghan A.P., Blumenstock C, Niehrs C.;
RT "Dickkopf-1 is a member of a new family of secreted proteins and
RT functions in head induction."
RL Nature 391:357-362(1998).
CC -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: AF030433; AAC02426.1; -.
DR HSSP; P25687; 1MT.
DR MGD; MGI:1329040; DKK1.
DR InterPro; IPR006796; dickkopf_N.
DR Pfam; PF04706; dickkopf_N.1.
DR Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 272 DICKKOPF RELATED PROTEIN-1.
FT DOMAIN 86 141 DKK-TYPE CYS-1.
FT DOMAIN 195 269 DKK-TYPE CYS-2.
FT CARBOHYD 262 262 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 272 AA; 29268 MW; AB9FA35DPA57D3EE CRC64;

Query Match 8.8%; Score 165.5; DB 1; Length 272;
Best Local Similarity 22.3%; Pred. No. 4.9e-05;
Matches 59; Conservative 27; Mismatches 98; Indels 81; Gaps 9;

QY 87 LANLPSPYHNETNTQYKGNNTIHYHREIHKITNNQTSQMYFSETVITSYGDDEGR--- 143
DB 21 LCLSLPLGASATLVNLVNSAI---KNLPPLGAGAGQPSGAVSAGVLYEGGNKYQT 77
QY 144 -----SHEITDEDGCGSMYCOFAS-----FYTCQPCGQRMCLTRDSECCGQDLCV 191
DB 78 LDNYQPYPCAEDCEGSDPEYCSPPSRGAGVGVQICLACKRRRRCMTHAACCPGNKYC 137
QY 192 WGHG-----TKMA-----TRGSNTICDN 210
DB 138 NGICMPDSHSHFPRGEIESITENLGNHNAAAGDYPRTTLTSKIYHTKGQEGSVCLR 197
QY 211 QRDCCPGILCAFORGLLPVCTPLPYVEGELC---HDPASRLDLITWLEPFGALDRCP 267
DB 198 SSDCAAGLCCA--RHFWSKICKPVLEKEGVCTKRRKSHGLEI-----FQRCYC 245
QY 268 ASGLLC-----QPHSHSLVYVCK 285
DB 246 GEGLACRIQKHQASNSRLHTCQ 270

RESULT 7
ID DKK2 HUMAN STANDARD; PRT; 259 AA.
AC 09UNH2; Q9UHU3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dickkopf related protein-2 precursor (Dkk-2) (dickkopf-2) (mdk-2).
GN DKK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=Fetal lung;
RX MEDLINE=20035735; PubMed=10570958;
RA Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W.,

```

RA Amaravadi L., Brown D.E., Guyot D., Mays G., Leiby K., Chang B.,  
 RA Duong T., Goodearl A.D.U., Gearing D.P., Sokol S.I., McCarthy S.A.,  
 RT "Functional and structural diversity of the human Dickkopf gene  
 RL family.";  
 RL Gene 238:301-313(1999) ..  
 RP SEQUENCE FROM N.A.  
 RA Tanaka S., Sugimachi K., Sugimachi K.;  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [1]  
 RP SEQUENCE OF 75-259 FROM N.A.  
 RA Tate G., Suzuki T., Mitsuura T.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SKELETAL MUSCLE AND  
 CC LUNG.  
 CC -1- PTM: MAY BE PROTEOLYTICALLY PROCESSED BY A FUZIN-LIKE PROTEASE.  
 CC -1- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC DR EMBL; AF177395; AAF0675.1; -;  
 DR EMBL; AB033308; BAA8545.1; -;  
 DR EMBL; AB035181; BAA87056.1; -;  
 DR EMBL; AB035180; BAA87056.1; JOINED.  
 DR Genew; HGNC:2892; DK2.  
 DR MIM; 605415; -;  
 DR GO; GO:0005645; C:extracellular space; TAS.  
 DR InterPro; IPR006796; dickkopf\_N.  
 DR Pfam; PF04706; dickkopf\_N.1.  
 KM Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.  
 FT SIGNAL 1 33 POTENTIAL.  
 FT CHAIN 34 259 DICKKOPF RELATED PROTEIN-2.  
 FT DOMAIN 78 127 DKR-TYPE CYS-1.  
 FT DOMAIN 183 256 DKR-TYPE CYS-2.  
 FT CARBOHYD 52 52 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT SEQUENCE 259 AA; 28447 MW; 39DDA3FA8975EB87F CRC64;  
 SQ  
 Query Match 8.6%; Score 162; DB 1; Length 259;  
 Best Local Similarity 24.0%; Pred. No. 8.3e-05;  
 Matches 50; Conservative 24; Mismatches 60; Indels 74; Gaps 9;  
 QY 137 GDEGR--RSHECIIDEDGSPMYC---QFASFOYTCQPCRGOMLCTRDSECCGDDQ 189  
 Db 65 GSKKXKSLGQAYPCSSDKEGVRGYSHPQSS--ACWVCRKKRCHRDGMCCEGTR 121  
 QY 190 CVMGHC-----TKMA-TRGSNGT 206  
 Db 122 CNGGICIPVTESILTPHLPALDGRHRDRNHHGNSHDLGWNIGRPHMKPHIKGHEG 181  
 QY 207 ICDNQRDCQPGLCAPFGRLFPVCTPLPYVEGELC--HDPASRLDLITWELPDDGALD 263  
 Db 182 PCLRSSDIDIFGCCA--RHFWTKICKPVLHGEVCTQKRKKGSHGLEI-----FQ 229  
 QY 264 RCPGASGLICOP-----HSHSLVYVCK 285  
 Db 230 RCDCAKGLSCRWKDATYSSKARLHVQ 257  
 RESULT 8  
 ID DK2 MOUSE STANDARD; PRT; 259 AA.  
 AC Q9QY28;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Dickkopf related protein-2 precursor (Dkk-2) (Dkkopf-2) (mdk-2).  
 GN DK2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=99425169; PubMed=10495270;  
 RA Monaghan P.A., Kioschis P., Wu W., Zuniga A., Bock D., Pousetka A.,  
 RA Delius H., Niens C.;  
 RT "Dickkopf genes are co-ordinately expressed in mesodermal lineages".  
 RL Mech. Dev. 87:45-56(1999).  
 CC -1- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: MAY BE PROTEOLYTICALLY PROCESSED BY A FUZIN-LIKE PROTEASE.  
 CC -1- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC DR EMBL; AJ243963; CAB60110.1; -;  
 DR MGD; MGI:1890663; Dkk2.  
 DR InterPro; IPR006796; dickkopf\_N.  
 DR Pfam; PF04706; dickkopf\_N.1.  
 KM Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.  
 FT SIGNAL 1 33 POTENTIAL.  
 FT CHAIN 34 259 DICKKOPF RELATED PROTEIN-2.  
 FT DOMAIN 78 127 DKR-TYPE CYS-1.  
 FT DOMAIN 183 256 DKR-TYPE CYS-2.  
 FT CARBOHYD 52 52 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT SEQUENCE 259 AA; 28416 MW; EAAB76F2D2C9780D CRC64;  
 SQ  
 Query Match 8.2%; Score 154; DB 1; Length 259;  
 Best Local Similarity 23.6%; Pred. No. 0.00031;  
 Matches 49; Conservative 24; Mismatches 61; Indels 74; Gaps 9;  
 QY 137 GDEGR--RSHECIIDEDGSPMYC---QFASFOYTCQPCRGOMLCTRDSECCGDDQ 189  
 Db 65 GSKKXKSLGQAYPCSSDKEGVRGYSHPQSS--ACWVCRKKRCHRDGMCCEGTR 121  
 QY 190 CVMGHC-----TKMA-TRGSNGT 206  
 Db 122 CNGGICIPVTESILTPHLPALDGRHRDRNHHGNSHDLGWNIGRPHMKPHIKGHEG 181  
 QY 207 ICDNQRDCQPGLCAPFGRLFPVCTPLPYVEGELC--HDPASRLDLITWELPDDGALD 263  
 Db 182 PCLRSSDIDIFGCCA--RHFWTKICKPVLHGEVCTQKRKKGSHGLEI-----FQ 229  
 QY 264 RCPGASGLICOP-----HSHSLVYVCK 285  
 Db 230 RCDCAKGLSCRWKDATYSSKARLHVQ 257  
 RESULT 9  
 SG1 HUMAN  
 ID SG1 HUMAN STANDARD; PRT; 242 AA.  
 AC Q9UK85;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Scggy-1 protein precursor (SGY-1).  
 GN SGY1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]





FT DISULFID 253 BY SIMILARITY.  
 FT DISULFID 265 529 BY SIMILARITY.  
 FT DISULFID 311 315 BY SIMILARITY.  
 FT DISULFID 326 338 BY SIMILARITY.  
 FT DISULFID 335 370 BY SIMILARITY.  
 FT DISULFID 349 349 BY SIMILARITY.  
 FT DISULFID 351 361 BY SIMILARITY.  
 FT DISULFID 376 381 BY SIMILARITY.  
 FT DISULFID 378 411 BY SIMILARITY.  
 FT DISULFID 383 396 BY SIMILARITY.  
 FT DISULFID 398 403 BY SIMILARITY.  
 FT DISULFID 417 422 BY SIMILARITY.  
 FT DISULFID 419 450 BY SIMILARITY.  
 FT DISULFID 424 433 BY SIMILARITY.  
 FT DISULFID 435 442 BY SIMILARITY.  
 FT DISULFID 456 461 BY SIMILARITY.  
 FT DISULFID 458 504 BY SIMILARITY.  
 FT DISULFID 463 473 BY SIMILARITY.  
 FT DISULFID 476 479 BY SIMILARITY.  
 FT DISULFID 483 492 BY SIMILARITY.  
 FT DISULFID 489 561 BY SIMILARITY.  
 FT DISULFID 508 537 BY SIMILARITY.  
 FT CARBOHYD 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 555 555 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NON\_TIR 577 577  
 SQ SEQUENCE 577 AA; 62298 MW; B83B469C83EDCC9 CRC64;  
 Query Match 7.3%; Score 138; DB 1; Length 577;  
 Best Local Similarity 26.4%; Pred. No. 0.011;  
 Matches 46; Conservative 22; Mismatches 66; Indels 40; Gaps 10;

QY 154 GPSNYCPFAFQYTCPCRCQRMCTDSEC-CGDOQCWVG-----HCYKATR--GSN 204  
 DB 393 GP-VCCQDNF--SC--VRHNGILGSGNGDCECECVCRSGWTGECYCNCTSTDTICISBD 446  
 QY 205 GTICDNCRDCCPGPLGCAFCRGLLEPVCTPLPVEGELCHDPASRLDLITWELSPDG---- 260  
 DB 447 GTLCGSGGDCVCGKCVCTNPGASGPTCEPCPT-----CSDPCNKRSCIECHLSADQPEP 502  
 QY 261 -ALDRCPQ-----SGLTQPSHSLVYCKFTFVGSRPDQSEILL 300  
 DB 503 ECVDKCKLAGVTTISKADFSKDSVSCSLQGEN---ECLITFLISTDNEGKTI 553

RESULT 11  
 PRIS HUMAN STANDARD; PRT; 676 AA.  
 AC P07225; Q15518;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Vitamin K-dependent protein S precursor.  
 GN PROS1 OR PROS.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87092407; PubMed=3467362;  
 RA Hoskins J., Norman D.K., Beckmann R.J., Long G.L.;  
 RT "Cloning and characterization of human liver cDNA encoding a protein  
 S precursor";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:349-353(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=88005138; PubMed=2820795;  
 RA Ploos van Amstel H.K., van der Zanden A.L., Reitsma P.H.,  
 RA Bertina R.M.;  
 RT "Human protein S cDNA encodes Phe-16 and Tyr 222 in consensus  
 sequences for the post-translational processing.";  
 RL FEBS Lett. 222:186-190(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91084444; PubMed=2148110;  
 RA Schmidl D.K., Tatro A.V., Phelps L.G., Tomczak J.A., Long G.L.;  
 RT "Organization of the human protein S genes";  
 RL Biochemistry 29:7845-7852(1990).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Liver;  
 RX MEDLINE=91084445; PubMed=2148111;  
 RA Ploos van Amstel H.K., Reitsma P.H., der Logt C.P., Bertina R.M.;  
 RT "Intron-exon organization of the active human protein S gene PS alpha  
 and its pseudogene PS beta: duplication and silencing during primate  
 evolution.";  
 RL Biochemistry 29:7853-7861(1990).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Uterus;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausberg R.U., Reingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shermen C.W., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshitoki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamarate P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.W., Matra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RP SEQUENCE OF 27-676 FROM N.A.  
 RX MEDLINE=86313649; PubMed=254413;  
 RA Lundwall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,  
 RA Stenflo J., Wydo R.;  
 RT "Isolation and sequence of the cDNA for human protein S, a regulator  
 of blood coagulation.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).  
 RN [7]  
 RP VARIANT HEBERLEN PRO-501.  
 RX MEDLINE=90335440; PubMed=2143091;  
 RA Bertina R.M., Ploos van Amstel H.K., van Wijngaarden A.,  
 RA Coenen J., Leemhuis M.P., Deutz-Terlouw P.P., van der Linden I.K.,  
 RA Reitsma P.H.;  
 RT "Heerlen polymorphism of protein S, an immunologic polymorphism due  
 to dimorphism of residue 460.";  
 RL Blood 76:538-548(1990).  
 RN [8]  
 RP VARIANT PROS DEFICIENCY SER-258.  
 RA Cooper D.N.;  
 RL Unpublished observations (SEP-1993).  
 RN [9]  
 RP VARIANT TOKUSHIMA GLUT-196.  
 RX MEDLINE=94129009; PubMed=8298131;  
 RA Haysashi T., Nishiooka J., Shigeakiyo T., Saito S., Suzuki K.;  
 RT "Protein S Tokushima: abnormal molecule with a substitution of Glu  
 for Lys-155 in the second epidermal growth factor-like domain of  
 protein S.";



BL00d 83:683-690(1994).  
 (10)  
 VARIANTS PROS DEFICIENCY CYS-482; CYS-485 AND GLY-561, AND VARIANTS  
 RP PRO-501 AND MET-559.  
 RX MEDLINE=99374922; PubMed=10447256;  
 RA Espinosa-Parilla Y., Morell M., Souto J.C., Tirado I.,  
 Fontcuberta J., Estivill X., Sala N.;  
 RT "Protein S gene analysis reveals the presence of a cosegregating  
 mutation in most pedigrees with type I but not type III PS  
 deficiency.";  
 RL Hum. Mutat. 14:30-39(1999).  
 CC -1- FUNCTION: ANTICOAGULANT PLASMA PROTEIN. IT IS A COFACTOR TO  
 CC ACTIVATED PROTEIN C IN THE DEGRADATION OF COAGULATION FACTORS VA  
 CC AND VIIIA. IT HELPS TO PREVENT COAGULATION AND STIMULATING  
 CC FIBRINOLYSIS.  
 CC -1- SUBCELLULAR LOCATION: Extracellular.  
 CC -1- TISSUE SPECIFICITY: Plasma.  
 CC -1- DISEASE DEFECTS IN PROS1 ARE ASSOCIATED WITH AN INCREASED RISK TO  
 CC DEVELOP THROMBOTIC DISEASE (THROMBOPHILIA).  
 CC -1- SIMILARITY: Contains 2 laminin G-like domains.  
 CC -1- SIMILARITY: Contains 4 EGF-like domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M15036; AAA36479.1; -;  
 DR EMBL; Y00692; CAA68687.1; -;  
 DR EMBL; Y00692; CAA68688.1; ALT\_SEQ.  
 DR EMBL; M57853; AAA60357.1; -;  
 DR EMBL; M57840; AAA60357.1; JOINED.  
 DR EMBL; M57841; AAA60357.1; JOINED.  
 DR EMBL; M57842; AAA60357.1; JOINED.  
 DR EMBL; M57843; AAA60357.1; JOINED.  
 DR EMBL; M57844; AAA60357.1; JOINED.  
 DR EMBL; M57845; AAA60357.1; JOINED.  
 DR EMBL; M57846; AAA60357.1; JOINED.  
 DR EMBL; M57847; AAA60357.1; JOINED.  
 DR EMBL; M57848; AAA60357.1; JOINED.  
 DR EMBL; M57849; AAA60357.1; JOINED.  
 DR EMBL; M57850; AAA60357.1; JOINED.  
 DR EMBL; M57851; AAA60357.1; JOINED.  
 DR EMBL; M57852; AAA60357.1; JOINED.  
 DR EMBL; M36564; AAA60180.1; -;  
 DR EMBL; M36551; AAA60180.1; JOINED.  
 DR EMBL; M36552; AAA60180.1; JOINED.  
 DR EMBL; M36553; AAA60180.1; JOINED.  
 DR EMBL; M36554; AAA60180.1; JOINED.  
 DR EMBL; M36555; AAA60180.1; JOINED.  
 DR EMBL; M36556; AAA60180.1; JOINED.  
 DR EMBL; M36557; AAA60180.1; JOINED.  
 DR EMBL; M36558; AAA60180.1; JOINED.  
 DR EMBL; M36559; AAA60180.1; JOINED.  
 DR EMBL; M36560; AAA60180.1; JOINED.  
 DR EMBL; M36561; AAA60180.1; JOINED.  
 DR EMBL; M36563; AAA60180.1; JOINED.  
 DR EMBL; BC015801; AAA15801.1; -;  
 DR PIR; A35610; KKHUS.  
 DR HSP; P00740; ICFH.  
 DR HSP; HANC; 9456; PROS1.  
 DR MIM; 176880; -;  
 DR GO; GO:0004866; F:endorpeptidase inhibitor activity; TAS.  
 DR GO; GO:0007596; P:blood coagulation; TAS.  
 DR InterPro; IPR000152; Asx hydroxyl.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_Like.  
 DR InterPro; IPR001791; Laminin\_G.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 4.  
 DR Pfam; PF00594; gla; 1.

DR Pfam; PF00054; Laminin\_G; 1.  
 DR SMART; SMO0179; EGF\_CA; 3.  
 DR SMART; SMO069; GLA; 1.  
 DR SMART; SMO0282; LamG; 2.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 4.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_CA; 3.  
 DR PROSITE; PS00011; GLUT\_CARBOXYLATION; 1.  
 DR PROSITE; PS50025; LAM\_G\_DOMAIN; 2.  
 KM Plasma; Gamma-carboxyglutamic acid; Calcium; Vitamin K; Zymogen;  
 KM blood coagulation; Hydroxylation; Glycoprotein; Signal; Repeat;  
 KM EGF-like domain; Polymorphism; Disease mutation; Thrombophilia.  
 FT SIGNAL 1 24  
 FT PROPEP 25 41  
 FT CHAIN 42 676  
 FT DOMAIN 42 86  
 FT DOMAIN 87 116  
 FT DOMAIN 117 155  
 FT DOMAIN 157 200  
 FT DOMAIN 201 242  
 FT DOMAIN 243 283  
 FT DOMAIN 299 475  
 FT DOMAIN 484 666  
 FT MOD\_RES 47 47  
 FT MOD\_RES 48 48  
 FT MOD\_RES 55 55  
 FT MOD\_RES 57 57  
 FT MOD\_RES 60 60  
 FT MOD\_RES 61 61  
 FT MOD\_RES 66 66  
 FT MOD\_RES 67 67  
 FT MOD\_RES 70 70  
 FT MOD\_RES 73 73  
 Query Match 7.0%; Score 131.5; DB 1; Length 676;  
 Best Local Similarity 24.0%; Pred. No. 0.039;  
 Matches 83; Conservative 43; Mismatches 129; Indels 91; Gaps 21;  
 QY 3 RIGATLTLCLLAAAPVTPAPAPATSAFVKRGPALSTPOEATLNMREVEELMEDTQ 62  
 DB 7 RCGALLACLLV-----LVSANFLSKQASQVLRK-RRANSLLEETK 50  
 QY 63 --HKLRAVEEMAEBAKASSSEVNLALPPSYHNETTDTKVGNTIHHREIHKTN 120  
 DB 51 QGNLRECEBELONKEAREV-----FENDPETD-----YFYKVLVCLAS 91  
 QY 121 NOTGMVFSEYVITSVGEDEGRSHCEITDEDCP-----SMYQC--FAFQYTCQP- 170  
 DB 92 FQTGLFTAROSTNAYPD--LRSCVNALPDCSPPLPCNEDGYMCKGKASFTCTCKPG 148  
 QY 171 CRGQRMCTRDSECCGDLCTVNGHCTKMA--TRGS-----NG-TICDNQDRC----- 214  
 DB 149 WQGRK--CEFDINECDKPNINGGSCQICDNTPGSHCSCKGFWLMSKXCKXVDECS 206  
 QY 215 -QPLCCAFQRLGFLPVCTPLFVBGSLCHDPASRLDLITWLEPDGALDRP---CASG 270  
 DB 207 LKPSICGT-----AVCKNIPGDFE-CECPGKYRNKSKSCED---IDCSNNYCAQ- 254  
 QY 271 LIGQPHSHSLVYVC--KPTFVGSRPDDG---EILLPREVPREYEV 310  
 DB 255 -LCVNYPGYTCYCDGKGFKAQDKSCSEVSVCLPLNLDTKYEL 299  
 RESULT 12  
 ID ITB6\_HUMAN STANDARD; PRT; 788 AA.  
 AC P18564; O16500;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Integrin beta-6 precursor.  
 GN ITGB6.

OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TTSUB=Pancras;  
 RX MEDLINE=90307653; PubMed=2365683;  
 RA Sheppard D., Rozzo C., Starr L., Quaranta V., Eble D.J., Pytela R.;  
 RT "Complete amino acid sequence of a novel integrin beta subunit (beta  
 6) identified in epithelial cells using the polymerase chain  
 reaction.";  
 RT J. Biol. Chem. 265:11502-11507 (1990).  
 RP [2]  
 RP REVISIONS TO 18-24; 158; 642 AND 719.  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 116-197 FROM N.A.  
 RX MEDLINE=93002753; PubMed=1382574;  
 RA Jiang W.M., Jenkins D., Yuan Q., Leung E., Choo K.H., Watson J.D.,  
 RA Kristensen G.W.;  
 RT "The gene organization of the human beta 7 subunit, the common beta  
 RT subunit of the leukocyte integrins HML-1 and LPAW-1.";  
 RL Int. Immunol. 4:1031-1040 (1992).  
 CC -1 FUNCTION: INTEGRIN ALPHA-V/BETA-6 IS A RECEPTOR FOR FIBRONECTIN  
 CC AND CYTOACTIN. IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGANDS.  
 CC -1 SUBUNIT: HEMEROPIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-6  
 CC ASSOCIATES WITH ALPHA-V.  
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1 SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.  
 CC -1 SIMILARITY: Contains 2 WMPA-like domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

FT REPEAT 544 582 III.  
 FT REPEAT 583 619 IV.  
 FT DISULFID 23 454 BY SIMILARITY.  
 FT DISULFID 31 41 BY SIMILARITY.  
 FT DISULFID 34 70 BY SIMILARITY.  
 FT DISULFID 44 59 BY SIMILARITY.  
 FT DISULFID 197 204 BY SIMILARITY.  
 FT DISULFID 252 293 BY SIMILARITY.  
 FT DISULFID 394 406 BY SIMILARITY.  
 FT DISULFID 426 670 BY SIMILARITY.  
 FT DISULFID 452 456 BY SIMILARITY.  
 FT DISULFID 467 479 BY SIMILARITY.  
 FT DISULFID 476 511 BY SIMILARITY.  
 FT DISULFID 481 490 BY SIMILARITY.  
 FT DISULFID 492 502 BY SIMILARITY.  
 FT DISULFID 517 522 BY SIMILARITY.  
 FT DISULFID 519 552 BY SIMILARITY.  
 FT DISULFID 524 537 BY SIMILARITY.  
 FT DISULFID 539 544 BY SIMILARITY.  
 FT DISULFID 538 563 BY SIMILARITY.  
 FT DISULFID 560 591 BY SIMILARITY.  
 FT DISULFID 565 574 BY SIMILARITY.  
 FT DISULFID 576 583 BY SIMILARITY.  
 FT DISULFID 597 602 BY SIMILARITY.  
 FT DISULFID 599 645 BY SIMILARITY.  
 FT DISULFID 604 614 BY SIMILARITY.  
 FT DISULFID 617 620 BY SIMILARITY.  
 FT DISULFID 624 633 BY SIMILARITY.  
 FT DISULFID 630 702 BY SIMILARITY.  
 FT DISULFID 649 678 BY SIMILARITY.  
 FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 541 541 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 575 575 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 788 AA; 85935 MW; EDB7D533BE4C6C4D CRC64;  
 Query Match 6.7%; Score 126; DB 1; Length 788;  
 Best Local Similarity 20.5%; Pred. No. 0.12;  
 Matches 76; Conservative 45; Mismatches 130; Indels 120; Gaps 18;  
 QY 42 QERATINEMFRE-----VEEIMEDTQHKLR--SAVEEMBAE-EAAKASSE-VNLA-- 88  
 DB 332 QERVHLYENYAKLIPGATVGLQKDSGNTLLQILSAVEHRSVELVYGDTEGINTLST 391  
 QY 89 ----NLPSEYHNETITDLYGN-----NTIHYREIHKITNNQTG---QNVFS-- 129  
 DB 392 ALCNNGTLPFOHKCKSHMKVGDPAFVTVNIIPHCERRRHIIIPVYGDALELVSP 451  
 QY 130 -----EYVITSVGBEERBSHECTIDE-----DQPSM----- 157  
 DB 452 CNDCQKEVEVNSKCHHNGSFQCGVCAHPGHNRPCECGEDMLSTDSCKEAPDHSC 511  
 QY 158 -----YCOFASFQYTCPCRCGQMLCTRDSQC-CGDQLCYW 192  
 DB 512 SGNGDCVCGCICHLSPYGNITGVYCCDNF--SC--VNHKGLCGSNGDCGCEVCVS 567  
 QY 193 G-----HCTKATR--GSGNTICNQRCCQGLCAFPGRGLLPVCTGLPBGELCHP 244  
 DB 568 GWTGEYCNCTTSDSCVSDGVLCGSRGCVCGKCTNPASGPTCEKCP-----CGP 623  
 QY 245 ASRLDLITWLELPDQ-----ALDRCPASGLICQPHSHSL-----VYVCKPTV 289  
 DB 624 CNKRSGICIBCHLSAQAQAECEVDKCKLAGATISEEDRSXDSVSGSLQGENECILITL 683  
 QY 290 GSRDQDGEILL 300  
 DB 684 ITTDNEKTI 694



FT DISULFID 1144 1155 BY SIMILARITY.  
 FT DISULFID 1150 1164 BY SIMILARITY.  
 FT DISULFID 1166 1179 BY SIMILARITY.  
 FT DISULFID 1298 1309 BY SIMILARITY.  
 FT DISULFID 1304 1318 BY SIMILARITY.  
 FT DISULFID 1320 1333 BY SIMILARITY.  
 FT DISULFID 1339 1354 BY SIMILARITY.  
 FT DISULFID 1349 1363 BY SIMILARITY.  
 FT DISULFID 1365 1378 BY SIMILARITY.  
 FT MOD\_RES 647 647 HYDROXYLATION.  
 FT CARBOHYD 810 810 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 870 870 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 923 923 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1039 1039 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 365 365 /FTID=CAR\_000184.  
 FT CONFLICT 504 504 Y -> H (IN REF. 2).  
 FT CONFLICT 1334 1334 A -> T (IN REF. 2).  
 FT CONFLICT 1394 1394 F -> V (IN REF. 2).  
 SQ SEQUENCE 1394 AA; 152791 MM; DEFGA81A40B2CTD1 CRC64;

Query Match Best Local Similarity 22.5%; Score 126; DB 1; Length 1394;  
 Matches 90; Conservative 37; Mismatches 133; Indels 140; Gaps 25;

QY 25 PRATSAVPKPGALSYPOEATINREVEHEIMEDTOHKLNSAVEEMKAPAAKASSE 84  
 DB 437 PVAKSTHPPPLPAKEP-----VEALTPSRHGAASA-----EPVATAPPEKE 480  
 QY 85 VMLANLPSYHNETNTDTRV-----GNNTIHYR-----EIHKTIN 120  
 DB 481 I-----PSIDQE-----KTKLEPQPOLSPGISALHHPQPVVIEKTSPPVVEVAPEAS 531  
 QY 121 NONGCVNFBETVTSVDEBGRSHCEIIDED-CGPNWCOPASQYTOQPRG-----Q 174  
 DB 532 TSASAVIAPTOYTEI-----NCTVNPDIICGAG-HCINLPRVYTICIEGTRFSEQ 582  
 QY 175 RMLCTRDSECCGDO-LCVWGHCTKATKRS-----NCTICNORDC-OPGLC 219  
 DB 583 QRCVVIDECTYQVHCSCQRCEN--TEGSFLCICPAGFMASBEGINCIDVDECELRPDVC 640  
 QY 220 -----CAF-----ORGLLPPV---CTPLPVGEIC-HDPASRLIDLIT- 253  
 DB 641 GEGHCVNTVGAFCRCYCDSGYRMTORGCEDEICNPFCTPDEQCNSPFSYQCVPTB 700  
 QY 254 ---WE---LEPDGALDRCPGASG-----LLCOPHSHSLVYVCKPTFGSRD---Q 294  
 DB 701 GFRGWMGQCLDVDECELEPNVCANGDCSNLEGSYMGSCCHKG---YTRTPDHKCRDIDECQ 757  
 QY 295 DGEILLPREVPDEYEVGSF-----MEVROGEIDLE 325  
 DB 758 QGNLCVNGQCKN--TEGSFRCTCGGYQLSAARDQEDID 795

RESULT 14  
 ID LABEL HUMAN STANDARD; PRT; 1595 AA.  
 AC Q14766;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Latent transforming growth factor beta binding protein, isoform 1L  
 DE precursor (LTBP-1) (Transforming growth factor beta-1 binding protein  
 1) (TGF-beta1-BP-1).  
 GN LTBP1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_Taxid=9606;  
 RN [1]

RP SEQUENCE OF 1-346 FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=96125117; PubMed=8537398;  
 RA Olofsson A., Ichijo H., Wren A., ten Dijke P., Miyazono K.,  
 RA Heldin C.-H.;  
 RT "Efficient association of an amino-terminally extended form of human  
 RT latent transforming growth factor-beta binding protein with the  
 RT extracellular matrix";  
 RL J. Biol. Chem. 270:31294-31297(1995).  
 RX [2].  
 RP SEQUENCE OF 347-1595 FROM N.A.  
 RC TISSUE=Fibroblast, and Platelet;  
 RX MEDLINE=90275601; PubMed=2350783;  
 RA Kanazaki T., Olofsson A., Mores A., Wernstedt C., Hellman U.,  
 RA Miyazono K., Claesson-Welsh L., Heldin C.-H.;  
 RT "TGF-beta 1 binding protein: a component of the large latent complex  
 RT of TGF-beta 1 with multiple repeat sequences";  
 RL Cell 61:1051-1061(1990).  
 RN [3].  
 RP INTERACTION WITH FIBRILLIN.  
 RX PubMed=1429738;  
 RA Isogai Z., Ono R.N., Ushiro S., Keene D.R., Chen Y., Mazzieri R.,  
 RA Charbonneau N.L., Reinhardt D.P., Rifkin D.B., Sakai L.Y.;  
 RT "Latent transforming growth factor beta-binding protein 1 interacts  
 RT with fibrillin and is a microfibril-associated protein";  
 RL J. Biol. Chem. 278:2750-2757(2003).  
 CC -1 SUBUNIT: The large latent complex of TGF-beta1 from platelets is  
 CC composed of the TGF-beta1 molecule noncovalently associated with a  
 CC disulfide-bonded complex of a dimer of the N-terminal propeptide  
 CC of the TGF-beta1 precursor and a third component denoted TGF-  
 CC beta1-BP. TGF-beta1-BP does not bind directly to active TGF-BETA1.  
 CC Binds to fibrillin.  
 CC -1 SUBCELLULAR LOCATION: Secreted.  
 CC -1 ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=long;  
 CC IsoId=Q14766-1; Sequence=Displayed;  
 CC Name=short;  
 CC IsoId=P22064-1; Sequence=External;  
 CC -1 TISSUE SPECIFICITY: The long isoform is found in fibroblasts.  
 CC -1 PFM: CONTAINS HYDROXYLATED ASPARAGINE RESIDUES (BY SIMILARITY).  
 CC -1 SIMILARITY: Contains 16 EGF-like domains.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See [http://www.ebi.ac.uk/announcements/](http://www.ebi.ac.uk/announcements)  
 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC DR EMBL; LA8925; AAA96327.1; -;  
 CC DR EMBL; M34057; AAA61160.1; ALT\_INIT.  
 CC DR HSSP; P08709; IBP9.  
 CC DR MIM; 150380; -;  
 CC GO; GO:000578; C:extracellular matrix; NAS.  
 CC GO; GO:0005024; F:transforming growth factor-beta receptor ac. .; NAS.  
 CC DR InterPro; IPR000152; Asx\_hydroxyl.  
 CC DR InterPro; IPR001881; EGF\_Ca.  
 CC DR InterPro; IPR006209; EGF\_like.  
 CC DR InterPro; IPR002212; Fibril-assoc.  
 CC Pfam; PF00068; EGF; 15.  
 CC Pfam; PF00683; TB; 4.  
 CC SMART; SM00119; EGF\_CA; 13.  
 CC PROSITE; PS001010; ASX\_HYDROXYL; 13.  
 CC PROSITE; PS00022; EGF\_1; 2.  
 CC PROSITE; PS01186; EGF\_2; 1.  
 CC PROSITE; PS01187; EGF\_CA; 15.  
 CC Growth factor binding; Repeat; EGF-like domain; Hydroxylation; Signal;  
 CC Glycoprotein; Alternative splicing.  
 CC SIGNAL 23 POTENTIAL.  
 CC CHAIN 1 LATENT TRANSFORMING GROWTH FACTOR BETA  
 CC BINDING PROTEIN, ISOFORM 1L.

```

FT DOMAIN 501 541 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT REPEAT 549 613 REPEAT A.
FT DOMAIN 747 788 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 789 830 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 831 871 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 872 911 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 912 952 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 953 993 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1034 1075 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1076 1117 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1118 1159 EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1160 1202 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
FT REPEAT 1218 1285 EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
FT REPEAT 1298 1340 EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).
FT REPEAT 1391 1463 EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1495 1535 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1536 1580 EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
FT SITE 1048 1050 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 505 516 BY SIMILARITY.
FT DISULFID 511 525 BY SIMILARITY.
FT DISULFID 527 540 BY SIMILARITY.
FT DISULFID 751 763 BY SIMILARITY.
FT DISULFID 774 787 BY SIMILARITY.
FT DISULFID 793 805 BY SIMILARITY.
FT DISULFID 800 814 BY SIMILARITY.
FT DISULFID 816 829 BY SIMILARITY.
FT DISULFID 835 846 BY SIMILARITY.
FT DISULFID 841 855 BY SIMILARITY.
FT DISULFID 858 870 BY SIMILARITY.
FT DISULFID 876 887 BY SIMILARITY.
FT DISULFID 882 896 BY SIMILARITY.
FT DISULFID 899 910 BY SIMILARITY.
FT DISULFID 916 927 BY SIMILARITY.
FT DISULFID 922 936 BY SIMILARITY.
FT DISULFID 938 951 BY SIMILARITY.
FT DISULFID 957 968 BY SIMILARITY.
FT DISULFID 963 977 BY SIMILARITY.
FT DISULFID 979 992 BY SIMILARITY.
FT DISULFID 998 1009 BY SIMILARITY.
FT DISULFID 1004 1018 BY SIMILARITY.
FT DISULFID 1020 1033 BY SIMILARITY.
FT DISULFID 1039 1051 BY SIMILARITY.
FT DISULFID 1046 1060 BY SIMILARITY.
FT DISULFID 1062 1074 BY SIMILARITY.
FT DISULFID 1080 1092 BY SIMILARITY.
FT DISULFID 1086 1101 BY SIMILARITY.
FT DISULFID 1103 1116 BY SIMILARITY.
FT DISULFID 1122 1134 BY SIMILARITY.
FT DISULFID 1128 1143 BY SIMILARITY.
FT DISULFID 1145 1158 BY SIMILARITY.
FT DISULFID 1164 1176 BY SIMILARITY.
FT DISULFID 1171 1185 BY SIMILARITY.
FT DISULFID 1187 1201 BY SIMILARITY.
FT DISULFID 1302 1315 BY SIMILARITY.
FT DISULFID 1310 1324 BY SIMILARITY.
FT DISULFID 1326 1339 BY SIMILARITY.
FT DISULFID 1345 1356 BY SIMILARITY.
FT DISULFID 1351 1365 BY SIMILARITY.
FT DISULFID 1367 1380 BY SIMILARITY.
FT DISULFID 1499 1510 BY SIMILARITY.
FT DISULFID 1505 1519 BY SIMILARITY.
FT DISULFID 1521 1534 BY SIMILARITY.
FT DISULFID 1540 1555 BY SIMILARITY.
FT DISULFID 1550 1564 BY SIMILARITY.
FT DISULFID 1566 1579 BY SIMILARITY.
FT MOD_RSS 848 848 HYDROXYLATION (BY SIMILARITY).
FT MOD_RSS 1011 1011 HYDROXYLATION (BY SIMILARITY).
FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1071 1071 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1124 1124 N-LINKED (GLCNAC. . .) (POTENTIAL).

```

```

FT CARBOHYD 1240 1240 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1595 AA; 173229 MW; 6A091EBA8556D85 CRC64;
Query Match 6.7%; Score 126; DB 1; Length 1595;
Best Local Similarity 22.5%; Pred. No. 0.26; Indels 140; Gaps 25;
Matches 90; Conservative 37; Mismatches 133;
25 PRATAPVAPKPGALSYPOEATLNMFRVEELMEDIOHKLSAVEEMAEAAKASSE 84
638 PVAKSTHPPPLPAKEP-----VVALFPSEHGARS-EPVATAPPEKE 681
85 VVALPSPSYNENMTDTRV-----GNTTHVR-----EIHKTN 120
682 I-----PSLDOE---KRLLEPGQPQLSPGISALHLHPQFVVIKTPSPYVVEVAPAS 732
121 NOTGQMFSEVITVSGDEGRSHCEIIBD-CGSPWYCOFASFOYTCPCRG-----Q 174
733 TSSAQVLAIPQVTEI-----NECTVNPDIQAG-HCLNLPVRYNCICYEGYRFEQ 783
175 RMLCTRDECCGSDQ-LCYWGHCTKMATRG-----NGTICDNQDC-QPGLC 219
784 QKRCVDIDECTQVQHTLCSQGRGEN--TEGSFLICICPAGFMASERGTNCIDVDECLRPDVC 841
220 -----CAF-----ORGLFPV---CTPLPYEGELC-HDPASRLDLIT- 253
842 GEGHCVTNVGAFRCYCDGSRMTGRGCEIDDECLNPSTCPDEOCVNSPSSYQCVPT 901
254 ---WE---LEPDGALDRCPQASG-----LTCQPHSHLVYVCKPTFGVSRD---Q 294
902 GFRGNQGOCLDDECLFPNVCAANGDCSNLEGSYMCSCRG---YTRTPDHGHCRIDECQ 958
295 DEILLPREVDEYEVGSF-----MEVRQELPDE 325
959 QGNLCVNGQCKN--TEGSFRCTCGGYQLSAKQDCEDID 996
RESULT 15
ID_SGV1_MOUSE STANDARD; PRT; 230 AA.
AC QGQZL9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Soggy-1 protein precursor (SGY-1).
GN SGY1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20035735; PubMed=10570958;
RA Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W.,
RA Amaravadi L., Brown D.B., Guyot D., Mays G., Leiby K., Chang B.,
RA Duong T., Goodheart A.D.J., Gearing D.P., Sokol S.I., McCreary S.A.;
RT "Functional and structural diversity of the human Dickopf gene
RT family."
RL Gene 238:301-313(1999).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed in testis.
CC -|- SIMILARITY: TO THE N-TERMINAL SECTION OF DKX-3.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; AF177399; AA02679.1; -
CC DR EMBL; MG1:1354963; SGY1.
CC KW Signal; Glycoprotein.

```

FT	SIGNAL	1	20	POTENTIAL.
FT	CHAIN	21	230	SOGV-1 PROTEIN
FT	CARBOHYD	31	31	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	102	102	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	230 AA;	26663 MW;	E3C95330935DDDBA CRC64;

Query Match  
 Best Local Similarity 26.6%;  
 Matches 38; Conservative 25; Mismatches 53; Indels 27; Gaps 2;

QY	1	MORLGATLILCLIA---AAVPTAPAPATSAFYKGGPALSYPOEATLNEMFRVEE	56
DB	1	MCRLRYTLILLPLAFVSSALPIHDVDSQONTSGFLGLQRLQSFSRLPLKNDLRLDLDN	60
QY	57	LMEDTQHKLSAVEEWEAEBAAKASSEVYLANLPSSYHNENTNTDTKVGNNTIHYHREIH	116
DB	61	FF-----SSPMDFRDLPRNFHQENQEHKMGKNTLSSHLQID	97
QY	117	KITNNQGMVFSEVITSVGE	139
DB	98	KVTNQGEVHISEKYEASIEPE	120

Search completed: February 20, 2004, 18:49:40  
 Job time : 29 secs





17-SEP-1997; 97US-0059121.  
PR 17-SEP-1997; 97US-0059122.  
PR 17-SEP-1997; 97US-0059184.  
PR 18-SEP-1997; 97US-0059263.  
PR 18-SEP-1997; 97US-0059266.  
PR 15-OCT-1997; 97US-0062125.  
PR 17-OCT-1997; 97US-0062285.  
PR 17-OCT-1997; 97US-0062287.  
PR 21-OCT-1997; 97US-0063486.  
PR 24-OCT-1997; 97US-0062814.  
PR 24-OCT-1997; 97US-0062816.  
PR 24-OCT-1997; 97US-0063045.  
PR 24-OCT-1997; 97US-0063120.  
PR 24-OCT-1997; 97US-0063121.  
PR 24-OCT-1997; 97US-0063127.  
PR 24-OCT-1997; 97US-0063128.  
PR 27-OCT-1997; 97US-0063329.  
PR 27-OCT-1997; 97US-0063327.  
PR 28-OCT-1997; 97US-0063541.  
PR 28-OCT-1997; 97US-0063542.  
PR 28-OCT-1997; 97US-0063544.  
PR 28-OCT-1997; 97US-0063549.  
PR 28-OCT-1997; 97US-0063550.  
PR 28-OCT-1997; 97US-0063564.  
PR 29-OCT-1997; 97US-0063435.  
PR 29-OCT-1997; 97US-0063704.  
PR 29-OCT-1997; 97US-0063732.  
PR 29-OCT-1997; 97US-0063738.  
PR 29-OCT-1997; 97US-0063734.  
PR 29-OCT-1997; 97US-0064215.  
PR 29-OCT-1997; 97US-0063735.  
PR 31-OCT-1997; 97US-0063870.  
PR 31-OCT-1997; 97US-0064103.  
PR 03-NOV-1997; 97US-0064248.  
PR 07-NOV-1997; 97US-0064809.  
PR 12-NOV-1997; 97US-0065186.  
PR 17-NOV-1997; 97US-0065846.  
PR 18-NOV-1997; 97US-0065893.  
PR 21-NOV-1997; 97US-0066120.  
PR 21-NOV-1997; 97US-0066364.  
PR 24-NOV-1997; 97US-0066772.  
PR 24-NOV-1997; 97US-0066466.  
PR 24-NOV-1997; 97US-0066770.  
PR 24-NOV-1997; 97US-0066511.  
PR 24-NOV-1997; 97US-0066453.  
XX (GETH ) GENENTECH INC.  
PA  
PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;  
XX WPI; 1999-229533/19.  
DR P-PSDB; AAY13384.  
XX  
PT New isolated human genes and polypeptides used in, e.g. treatment of  
XX gastrointestinal ulceration  
PS  
PS Claim 2; Fig 83; 320p; English.  
XX  
XX AAX5213-74 encode secreted and transmembrane human proteins, and are  
CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,  
CC fetal brain, fetal liver and fetal retina. The encoded polypeptides,  
CC have specific uses based on their homology to known polypeptides,  
CC e.g. PRO211 and PRO217 can be used for disorders associated with the  
CC preservation and maintenance of gastrointestinal mucosa and the repair  
CC of acute and chronic mucosal lesions (e.g. enterocolitis,  
CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital  
CC microvillus atrophy), skin diseases associated with abnormal  
CC keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as  
CC lung squamous cell carcinoma of the vulva and gliomas), potent effects on  
CC cell growth and development, diseases related to growth or survival of  
CC nerve cells including Parkinson's disease, Alzheimer's disease, ALS,  
CC neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for  
CC reducing dermal scarring. PRO264 can be used as a target for anti-tumor

CC drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia  
CC areata; PRO269 can be used as an anti-thrombotic agent; PRO287  
CC polypeptides and portions may have therapeutic applications in wound  
CC healing and tissue repair; PRO317 can be used for treating problems of  
CC the kidney, uterus, endometrium, blood vessels, or related tissue, e.g.  
CC in the heart of genital tract.  
XX  
SQ Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;  
Query Match 100.0%; Score 2586; DB 20; Length 2586;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGCCGGGCTCCCGACACCCCGGGCCCGCCACCGCGCGCTCCCGCATCTCCACCCGAGC 60  
DB 1 CGCCGGGCTCCCGACACCCCGGGCCCGCCACCGCGCGCTCCCGCATCTCCACCCGAGC 60  
QY 61 CCGGCGGCTCCCGGCGGAGCGAGATCCAGTCGCGCCGCGCAGCGCAACTCGTCCA 120  
DB 61 CCGGCGGCTCCCGGCGGAGCGAGATCCAGTCGCGCCGCGCAGCGCAACTCGTCCA 120  
QY 121 GTCGGGGCGGCGGTGCGGGCGCGAGCGGAGATGCAAGCGGCTTTGGGACCTGCTGT 180  
DB 121 GTCGGGGCGGCGGTGCGGGCGCGAGCGGAGATGCAAGCGGCTTTGGGACCTGCTGT 180  
QY 181 GCGTGTGTGCGGCGGCGGCGGATCCCGACCGCCCGCGCGCTCCGACCGGACCTCGG 240  
DB 181 GCGTGTGTGCGGCGGCGGCGGATCCCGACCGCCCGCGCGCTCCGACCGGACCTCGG 240  
QY 241 CTCGAGTCAAGCCCGCGCGCTCTTCACTTACCCGAGAGAGGCCACTCTCATATGAGA 300  
DB 241 CTCGAGTCAAGCCCGCGCGCTCTTCACTTACCCGAGAGAGGCCACTCTCATATGAGA 300  
QY 301 TGTTCGCGAGGTTGAGAACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
DB 301 TGTTCGCGAGGTTGAGAACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
QY 361 AAGAGATGAG 420  
DB 361 AAGAGATGAG 420  
QY 421 TACCTCCAGCTATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
DB 421 TACCTCCAGCTATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
QY 481 ATGTGACCGAGAAATTCACAGATTAACAACAACAGACTGAGCAAAATGCTTTTCAG 540  
DB 481 ATGTGACCGAGAAATTCACAGATTAACAACAACAGACTGAGCAAAATGCTTTTCAG 540  
QY 541 AGACAGTTATCACTCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
DB 541 AGACAGTTATCACTCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
QY 601 ACGAGAGCTGTGGGCGGAGATGATGCTGCACTTGGCACTTCACTTCAGCTGCAGC 660  
DB 601 ACGAGAGCTGTGGGCGGAGATGATGCTGCACTTGGCACTTCACTTCAGCTGCAGC 660  
QY 661 CATGCCGGGCGCAGAGATGCTCTGCAACCGGAGACGTGATGATGATGATGATGATG 720  
DB 661 CATGCCGGGCGCAGAGATGCTCTGCAACCGGAGACGTGATGATGATGATGATGATG 720  
QY 721 GTGTCTGGGCTCACTGACCAAAATGCGACAGGGGCACAATATGGAACCATCTGTGACA 780  
DB 721 GTGTCTGGGCTCACTGACCAAAATGCGACAGGGGCACAATATGGAACCATCTGTGACA 780  
QY 781 ACGAGAGAGCTGTGACCGGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
DB 781 ACGAGAGAGCTGTGACCGGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
QY 841 TGTTCACACCCCTGCGCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
DB 841 TGTTCACACCCCTGCGCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900

QY 901 ACCTCATACCTGAGAGCTAGAGCCTGATGAGCCTTGACCGATCCCTTGCCAGTG 960  
DB 901 ACCTCATACCTGAGAGCTAGAGCCTGATGAGCCTTGACCGATCCCTTGCCAGTG 960  
QY 961 GGCCTCCCTGAG 1020  
DB 961 GGCCTCCCTGAG 1020  
QY 1021 GAG 1080  
DB 1021 GAG 1080  
QY 1081 TTGGCAGCTTCAATGAG 1140  
DB 1081 TTGGCAGCTTCAATGAG 1140  
QY 1141 AAGAGATGAG 1200  
DB 1141 AAGAGATGAG 1200  
QY 1201 TTATGATCTGAG 1260  
DB 1201 TTATGATCTGAG 1260  
QY 1261 GGTGTGTGCTTTAG 1320  
DB 1261 GGTGTGTGCTTTAG 1320  
QY 1321 TCCCTCTGAGCTTGAAG 1380  
DB 1321 TCCCTCTGAGCTTGAAG 1380  
QY 1381 CCAAGCTTCAAG 1440  
DB 1381 CCAAGCTTCAAG 1440  
QY 1441 GCAAGCTTCAAG 1500  
DB 1441 GCAAGCTTCAAG 1500  
QY 1501 TCTACATGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
DB 1501 TCTACATGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
QY 1561 TGAATGCTTGGGAG 1620  
DB 1561 TGAATGCTTGGGAG 1620  
QY 1621 AAATGCAAAATGAAATTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680  
DB 1621 AAATGCAAAATGAAATTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680  
QY 1681 CAGCTGTGAG 1740  
DB 1681 CAGCTGTGAG 1740  
QY 1741 GTGTGTGCTGAGCTTCACTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
DB 1741 GTGTGTGCTGAGCTTCACTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
QY 1801 TCTCTCAG 1860  
DB 1801 TCTCTCAG 1860  
QY 1861 GCTCAG 1920  
DB 1861 GCTCAG 1920  
QY 1921 ATCTGTGTGAG 1980  
DB 1921 ATCTGTGTGAG 1980  
QY 1981 CCAAAAGTGTCCCAAAAG 2040

DB 1981 CCAAAAGTGTCCCAAAAG 2040  
QY 2041 ATTAAGGTCAAACTTAATTTCTACATCCCTCTTAAAGTAATTAATTAATTAATTAAT 2100  
DB 2041 ATTAAGGTCAAACTTAATTTCTACATCCCTCTTAAAGTAATTAATTAATTAATTAAT 2100  
QY 2101 GTTCTCAG 2160  
DB 2101 GTTCTCAG 2160  
QY 2161 CTTTGAG 2220  
DB 2161 CTTTGAG 2220  
QY 2221 CTTTGAG 2280  
DB 2221 CTTTGAG 2280  
QY 2281 CACTTACAG 2340  
DB 2281 CACTTACAG 2340  
QY 2341 TGTGTGAAG 2400  
DB 2341 TGTGTGAAG 2400  
QY 2401 TGAATGCTTGGGAG 2460  
DB 2401 TGAATGCTTGGGAG 2460  
QY 2461 TAAAGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
DB 2461 TAAAGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
QY 2521 AAGTGTCAATTAAG 2580  
DB 2521 AAGTGTCAATTAAG 2580  
QY 2581 AAAAAA 2586  
DB 2581 AAAAAA 2586  
  
RESULT 2  
AAF92061  
ID AAF92061 standard; cDNA; 2586 BP.  
XX  
AC AAF92061;  
XX  
DT 15-MAY-2001 (first entry)  
XX  
DE Human PRO295 cDNA.  
XX  
KW Human; PRO protein; mapping; ss.  
XX  
OS Homo sapiens.  
XX  
PN M0200116318-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 24-AUG-2000; 2000MO-US23328.  
XX  
PR 01-SEP-1999; 99MO-US20111.  
PR 15-SEP-1999; 99MO-US21090.  
PR 07-DEC-1999; 99US-0169495.  
PR 09-DEC-1999; 99US-0170262.  
PR 11-JAN-2000; 2000MO-US04341.  
PR 18-FEB-2000; 2000MO-US04342.  
PR 22-FEB-2000; 2000MO-US04414.  
PR 01-MAR-2000; 2000MO-US05601.





QY 61 CCGGCGGCTCCCGGCGGAGCGAGATCCAGTCCGGCCCGGCAAGCCGAATTCGGTCCA 120  
DB 61 CCGGCGGCTCCCGGCGGAGCGAGATCCAGTCCGGCCCGGCAAGCCGAATTCGGTCCA 120  
QY 121 GTGCGGCGCGCGCTCGCGGCGCGAGAGCGAGATGCGAGCTGGGGCCACCTGCTGT 180  
DB 121 GTGCGGCGCGCGCTCGCGGCGCGAGAGCGAGATGCGAGCTGGGGCCACCTGCTGT 180  
QY 181 GCTGCTGCTGCGGCGGCGGCTGCTCCAGCGGCCCGCGCGCTGCGAGCGGAGCTCGG 240  
DB 181 GCTGCTGCTGCGGCGGCGGCTGCTCCAGCGGCCCGCGCGCTGCGAGCGGAGCTCGG 240  
QY 241 CTCGAGTCAAGCCCGGCTCTGAGCTACCGGAGGAGGAGCCCTCAATGAGA 300  
DB 241 CTCGAGTCAAGCCCGGCTCTGAGCTACCGGAGGAGGAGCCCTCAATGAGA 300  
QY 301 TGTTCGCGGAGTTGAGAACTGATGAGAGCAGCAGCAAAATTGCGAGCGGCTGG 360  
DB 301 TGTTCGCGGAGTTGAGAACTGATGAGAGCAGCAGCAAAATTGCGAGCGGCTGG 360  
QY 361 AAGAGATGAGGAGAGAGAGTGTCTAAGCATCATCAGAGTGAAGCTGGCAACT 420  
DB 361 AAGAGATGAGGAGAGAGAGTGTCTAAGCATCATCAGAGTGAAGCTGGCAACT 420  
QY 421 TACCTCCAGCTATCAATGAGACCAAGCAGAGCGAAGGTTGAAATTAACATCC 480  
DB 421 TACCTCCAGCTATCAATGAGACCAAGCAGAGCGAAGGTTGAAATTAACATCC 480  
QY 481 ATGTGACCGAGAAATTCAGAAATTAACCAACCAAGAGCTGGAGCAAAATGCTTTTCA 540  
DB 481 ATGTGACCGAGAAATTCAGAAATTAACCAACCAAGAGCTGGAGCAAAATGCTTTTCA 540  
QY 541 AGACAGTTATCACATCTGTGGAGAGCAAGAGAGGAGAGGAGCCAGAGTGCATCTG 600  
DB 541 AGACAGTTATCACATCTGTGGAGAGCAAGAGAGGAGAGGAGCCAGAGTGCATCTG 600  
QY 601 ACAGAGATGTGGGCGGCGAGATGCTGCAAGTTGCGAGCTTCCAGTCCAGCTGCAGC 660  
DB 601 ACAGAGATGTGGGCGGCGAGATGCTGCAAGTTGCGAGCTTCCAGTCCAGCTGCAGC 660  
QY 661 CATGCGGCGCGAGAGATGCTGCAAGTTGCGAGCTTCCAGTCCAGCTGCAGCTGT 720  
DB 661 CATGCGGCGCGAGAGATGCTGCAAGTTGCGAGCTTCCAGTCCAGCTGCAGCTGT 720  
QY 721 GTGTCTGGGCTCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 780  
DB 721 GTGTCTGGGCTCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 780  
QY 781 ACCAGAGGAGCTGCAAGCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
DB 781 ACCAGAGGAGCTGCAAGCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
QY 841 TGTGCAACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
DB 841 TGTGCAACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
QY 901 ACCTCATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
DB 901 ACCTCATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
QY 961 GCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
DB 961 GCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
QY 1021 GGAAGCGTGAAG 1080  
DB 1021 GGAAGCGTGAAG 1080  
QY 1081 TTGGCAGCTTCATGAG 1140  
DB 1081 TTGGCAGCTTCATGAG 1140

QY 1141 AAGAGATGAG 1200  
DB 1141 AAGAGATGAG 1200  
QY 1201 TTTAGATCTGAGACAGGCTGTGGGTAGATGTGCAATGAAATAGCTAATTTATTTCCCA 1260  
DB 1201 TTTAGATCTGAGACAGGCTGTGGGTAGATGTGCAATGAAATAGCTAATTTATTTCCCA 1260  
QY 1261 GGTGTGCTTTAGGCGGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320  
DB 1261 GGTGTGCTTTAGGCGGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320  
QY 1321 TCCCTCTGCTGCTGAGCAGATGAGGTGTGATGATTTGATCACTTCCAGCTGCTGCT 1380  
DB 1321 TCCCTCTGCTGCTGAGCAGATGAGGTGTGATGATTTGATCACTTCCAGCTGCTGCT 1380  
QY 1381 CCAGGCTTCACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
DB 1381 CCAGGCTTCACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
QY 1441 GGCACCCCTGTCAGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
DB 1441 GGCACCCCTGTCAGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
QY 1501 TCTACATGCTTTGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
DB 1501 TCTACATGCTTTGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
QY 1561 TGATTGCTTTGGGAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620  
DB 1561 TGATTGCTTTGGGAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620  
QY 1621 AAATGCAACAAATGATTTTCCAGCAGCTTTTCCATGAGGCAATGAGTGTGCTT 1680  
DB 1621 AAATGCAACAAATGATTTTCCAGCAGCTTTTCCATGAGGCAATGAGTGTGCTT 1680  
QY 1681 CAGCTGTTGAGAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
DB 1681 CAGCTGTTGAGAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
QY 1741 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800  
DB 1741 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800  
QY 1801 TCTCTGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860  
DB 1801 TCTCTGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860  
QY 1861 GCTCAGAGAGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920  
DB 1861 GCTCAGAGAGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920  
QY 1921 ATCTGTTGTTGATCTTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980  
DB 1921 ATCTGTTGTTGATCTTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980  
QY 1981 CCAAAAGTGTCCCAAAAG 2040  
DB 1981 CCAAAAGTGTCCCAAAAG 2040  
QY 2041 ATTAAGTCAAACTAATTTTCACTCCCTTAAAGATTAATCTAGTAAAGACAGAGT 2100  
DB 2041 ATTAAGTCAAACTAATTTTCACTCCCTTAAAGATTAATCTAGTAAAGACAGAGT 2100  
QY 2101 GTTCTCACAGTGTGGGAGCGGCTCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160  
DB 2101 GTTCTCACAGTGTGGGAGCGGCTCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160  
QY 2161 CTTTGGCAGTTGCTTATGTAATTTGAAAGATATATGAGAGAGAGAGAGAGAGAGAG 2220  
DB 2161 CTTTGGCAGTTGCTTATGTAATTTGAAAGATATATGAGAGAGAGAGAGAGAGAGAG 2220  
QY 2221 CTTGCGAG 2280  
DB 2221 CTTGCGAG 2280



```

Db      2221 CCTGAGAAACAGTACTAGTAATTTGAGGCGAGATTATTAATGAATTTGCAAAAT 2280
OY      2281 CACTTAGAGCACTGAGAGCAATTTATCAACCACTGGAGAAAATCAACCGACAGGGC 2340
Db      2281 CACTTAGAGCACTGAGAGCAATTTATCAACCACTGGAGAAAATCAACCGACAGGGC 2340
OY      2341 TGTGTGAAACATGGTTGTAATATGAGCACTGGCAACACTGAACTTACGCCACTCCACAA 2400
Db      2341 TGTGTGAAACATGGTTGTAATATGAGCACTGGCAACACTGAACTTACGCCACTCCACAA 2400
OY      2401 TGATGTTTTCAGGTGTCATGAGCTGTTGCCACCATGATTCATCCAGAGTCTTTAAAGTT 2460
Db      2401 TGATGTTTTCAGGTGTCATGAGCTGTTGCCACCATGATTCATCCAGAGTCTTTAAAGTT 2460
OY      2461 TAAAGTTCACATATGTTGTAATGAGCACTGTTCTTTGAGTTTAAATGATGTAATCAAT 2520
Db      2461 TAAAGTTCACATATGTTGTAATGAGCACTGTTCTTTGAGTTTAAATGATGTAATCAAT 2520
OY      2521 AAGTTGATTTGGAATCAAGCATTAATCACTTCACTGCAAAAAA 2580
Db      2521 AAGTTGATTTGGAATCAAGCATTAATCACTTCACTGCAAAAAA 2580
OY      2581 AAAAAA 2586
Db      2581 AAAAAA 2586

```

## RESULT 4

ABST74381 ID ABST74381 standard; cDNA, 2586 BP.

ABST74381; 10-DEC-2002 (first entry)

Human cDNA encoding secreted/transmembrane protein PRO295.

Human, ss; gene, secreted protein; transmembrane protein; anti-rheumatic;

antiarthritic; osteopathic; sports-related joint problem;

articular cartilage defect; osteoarthritis; rheumatoid arthritis.

Homo sapiens.

US2002119130-A1.

23-AUG-2002.

06-DEC-2001; 2001US-0006867.

```

XX      29-OCT-1997; 97US-063435P.
PR      29-OCT-1997; 97US-064215P.
PR      22-APR-1998; 98US-082797P.
PR      22-APR-1998; 98US-083495P.
PR      15-MAY-1998; 98US-085797P.
PR      10-JUN-1998; 98US-088811P.
PR      10-JUN-1998; 98US-088824P.
PR      10-JUN-1998; 98US-088825P.
PR      11-JUN-1998; 98US-088863P.
PR      12-JUN-1998; 98US-089105P.
PR      16-JUN-1998; 98US-089514P.
PR      16-SEP-1998; 98WO-US01930.
PR      08-MAR-1999; 98WO-US05028.
PR      14-MAY-1999; 98WO-US10733.
PR      02-JUN-1999; 98WO-US12252.
PR      01-SEP-1999; 98WO-US20111.
PR      15-SEP-1999; 98WO-US21190.
PR      15-SEP-1999; 98WO-US21194.
PR      22-DEC-1999; 99WO-US30720.
PR      18-FEB-2000; 2000WO-US04341.
PR      18-FEB-2000; 2000WO-US04342.
PR      30-MAR-2000; 2000WO-US08439.
PR      22-MAY-2000; 2000WO-US14042.

```

```

PR      02-JUN-2000; 2000WO-US15264.
PR      23-AUG-2000; 2000WO-US23522.
PR      24-AUG-2000; 2000WO-US23328.
PR      10-NOV-2000; 2000WO-US30873.
PR      01-DEC-2000; 2000WO-US32378.
PR      20-DEC-2000; 2000WO-US34956.
PR      28-FEB-2001; 2001WO-US06520.
PR      20-JUN-2001; 2001WO-US19692.
PR      29-JUN-2001; 2001WO-US21066.
PR      09-JUL-2001; 2001WO-US21735.

```

(GENT) GENENTECH INC.

Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

Grimaldi JC, Gurney AL, Watanabe CK, Wood WJ;

WPI; 2002-731348/79.

P-PSDB; ABG95854.

New isolated secreted and transmembrane PRO polypeptide useful for

modulating biological activity of a cell, or for treating

sports-related joint problems, osteoarthritis or rheumatoid arthritis

Claim 2; Fig 7; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO polypeptide having 80 or sequence identity to a sequence appearing as ABG95851-ABG95934 or their associated signal peptide, or a sequence of an extracellular domain of the proteins with their associated signal peptide or lacking its associated signal peptide. Also included are the nucleic acids encoding the proteins, vectors, host cells, fusion proteins and antibodies which specifically bind to the proteins. The proteins are useful for detecting a polypeptide designated as A, B, C or D in a sample suspected of containing an A, B, C or D polypeptide, by contacting the sample with a polypeptide designated as E, F, G, H or I (or vice versa) and determining the formation of an A/E, B/F, B/G, C/H or D/I polypeptide conjugate in the sample, where the formation of the conjugate is indicative of the presence of an A, B, C or D polypeptide in the sample, where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises a cell suspected of expressing the A, B, C or D polypeptide. The A, B, F, G, H or I polypeptide is labeled with a detectable label or is attached to a solid support. The proteins are useful for linking a bioactive molecule to a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies against them are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I. The cell is killed. The proteins are useful for identifying agonists or antagonists, for the preparation of a medicament useful in the treatment of a condition which is responsive to the proteins, as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. Nucleic acids encoding the proteins are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, for the preparation of the proteins, to generate transgenic or knockout animals which are useful in the development and screening of therapeutic useful reagents, for chromosome identification, and in gene therapy. The antibody is useful as a therapeutic agent, in a diagnostic assay and for affinity purification of the protein from recombinant cell culture natural sources. The present sequence encodes a novel secreted or transmembrane protein of the invention.

Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;

Query Match 100.0%; Score 2586; DB 24; Length 2586;

Best Local Similarity 100.0%; Pred. No. 0; Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGGCTCCCGACCCGCGGCGCCGACCGGCGCTCCCGCATCTGACCCGCGAGC 60  
 Db 1 CCGCGGCTCCCGACCCGCGGCGCCGACCGGCGCTCCCGCATCTGACCCGCGAGC 60  
 QY 61 CCGGCGGCTCCCGGCGGAGCGAGCAGATCCAGTCCGCGCCGCGACGCAATCGGTCCA 120  
 Db 61 CCGGCGGCTCCCGGCGGAGCGAGCAGATCCAGTCCGCGCCGCGACGCAATCGGTCCA 120  
 QY 121 GTGCGGCGCGCGCTGCGGCGCGAGCGGAGATGAGCGGCTTGGGCGACCCGTGCT 180  
 Db 121 GTGCGGCGCGCGCTGCGGCGCGAGCGGAGATGAGCGGCTTGGGCGACCCGTGCT 180  
 QY 181 GCGTGTGTGCGCGCGCGGCTCCGACGCGCGCCGCGCGCTCCGACGCGGAGCTCGG 240  
 Db 181 GCGTGTGTGCGCGCGCGGCTCCGACGCGCGCCGCGCGCTCCGACGCGGAGCTCGG 240  
 QY 241 CTCGAGTCAAGCCCGGCGCGCTCTCACTACCCGAGAGAGAGCCACCTTCATAGGA 300  
 Db 241 CTCGAGTCAAGCCCGGCGCGCTCTCACTACCCGAGAGAGAGCCACCTTCATAGGA 300  
 QY 301 TGTTCGCGAGTTGAGGAATGATGAGAGACAGCAGCAGCAAAATTGCGACGCGGTGG 360  
 Db 301 TGTTCGCGAGTTGAGGAATGATGAGAGACAGCAGCAGCAAAATTGCGACGCGGTGG 360  
 QY 361 AAGAGATGAGAGCAGAAAGCTGCTTAAAGCATCATCAGAAAGTGAACCTGGCAACT 420  
 Db 361 AAGAGATGAGAGCAGAAAGCTGCTTAAAGCATCATCAGAAAGTGAACCTGGCAACT 420  
 QY 421 TACCTCCGAGTTCACAAATGAGACCAACAGACAGAGGTGGAATTAATACCATCC 480  
 Db 421 TACCTCCGAGTTCACAAATGAGACCAACAGACAGAGGTGGAATTAATACCATCC 480  
 QY 481 ATGTGCACTGAGAAATTCACAAATTAACCAACAGACAGTGAATGTGCTTTTCA 540  
 Db 481 ATGTGCACTGAGAAATTCACAAATTAACCAACAGACAGTGAATGTGCTTTTCA 540  
 QY 541 AGACAGTATCACTCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
 Db 541 AGACAGTATCACTCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
 QY 541 AGACAGTATCACTCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
 Db 541 AGACAGTATCACTCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
 QY 601 ACGAGAGCTGTGGGCGCGAGATGTGACCGGAGCAAGTTCAGACTTCAGTCCAGC 660  
 Db 601 ACGAGAGCTGTGGGCGCGAGATGTGACCGGAGCAAGTTCAGACTTCAGTCCAGC 660  
 QY 661 CATCCCGGCGCGAGAGATGTGACCGGAGCAAGTTCAGACTTCAGTTCAGTTCAG 720  
 Db 661 CATCCCGGCGCGAGAGATGTGACCGGAGCAAGTTCAGACTTCAGTTCAGTTCAG 720  
 QY 721 GTGTCTGGGCTCACTGACCAAAATGAGCAGAGGCGAGCAATGGGACCATCTGTGACA 780  
 Db 721 GTGTCTGGGCTCACTGACCAAAATGAGCAGAGGCGAGCAATGGGACCATCTGTGACA 780  
 QY 781 ACCAGAGGAGTGTGACGCGGCGCTGTGTGTGCTTCAGAGAGGCTGTGTGCTGCTG 840  
 Db 781 ACCAGAGGAGTGTGACGCGGCGCTGTGTGTGCTTCAGAGAGGCTGTGTGCTGCTG 840  
 QY 841 TGTGACACCCCTGCGGTGAGGCGAGCTTGTGACACCCGCGAGCGGCTTGTG 900  
 Db 841 TGTGACACCCCTGCGGTGAGGCGAGCTTGTGACACCCGCGAGCGGCTTGTG 900  
 QY 901 ACCTCATCACTGAGAGTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 960  
 Db 901 ACCTCATCACTGAGAGTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 960  
 QY 961 GCGTCTGTGACGCGCGAGCGAGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020  
 Db 961 GCGTCTGTGACGCGCGAGCGAGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020  
 QY 1021 GAGGCGGTGACCAAGATGAGGAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080  
 Db 1021 GAGGCGGTGACCAAGATGAGGAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080  
 QY 1081 TTGGAGCTTCAATGAGAGAGTGTGCGCAGAGAGCTGAGAGAGCTGAGAGAGCTGAG 1140

Db 1081 TTGGAGCTTCAATGAGAGAGTGTGCGCAGAGAGCTGAGAGAGCTGAGAGAGCTGAG 1140  
 QY 1141 AAGAGATGAGGCTGTGGGAGAGCTGTGGGAGAGCTGTGGGAGAGCTGTGGGAGAGAG 1200  
 Db 1141 AAGAGATGAGGCTGTGGGAGAGCTGTGGGAGAGCTGTGGGAGAGCTGTGGGAGAGAG 1200  
 QY 1201 TTATGATCTGAGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260  
 Db 1201 TTATGATCTGAGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260  
 QY 1261 GGT 1320  
 Db 1261 GGT 1320  
 QY 1321 TCCCTGTGCTTGAACAGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380  
 Db 1321 TCCCTGTGCTTGAACAGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380  
 QY 1381 CAGGCTTCAAGCTGT 1440  
 Db 1381 CAGGCTTCAAGCTGT 1440  
 QY 1441 GCGACCCCTGTCCAGATTTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500  
 Db 1441 GCGACCCCTGTCCAGATTTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500  
 QY 1501 TCTCATGCTTTGATTAATGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560  
 Db 1501 TCTCATGCTTTGATTAATGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560  
 QY 1561 TGAATGCTTTTGT 1620  
 Db 1561 TGAATGCTTTTGT 1620  
 QY 1621 AAATGCAAAATGAAATTTTCCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680  
 Db 1621 AAATGCAAAATGAAATTTTCCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680  
 QY 1681 CAGGCTTGAAGATGAAATGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740  
 Db 1681 CAGGCTTGAAGATGAAATGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740  
 QY 1741 GT 1800  
 Db 1741 GT 1800  
 QY 1801 TGTCTCAGACAGCTGTGGGAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860  
 Db 1801 TGTCTCAGACAGCTGTGGGAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860  
 QY 1861 GCTCAGAGAGTGAAGT 1920  
 Db 1861 GCTCAGAGAGTGAAGT 1920  
 QY 1921 ATCTGT 1980  
 Db 1921 ATCTGT 1980  
 QY 1981 CCAAAAGT 2040  
 Db 1981 CCAAAAGT 2040  
 QY 2041 ATTTAGTCAAACTTAATTTCTCAATCCCTCTTAAAGTAACTAGTGTAGAGAGAGAG 2100  
 Db 2041 ATTTAGTCAAACTTAATTTCTCAATCCCTCTTAAAGTAACTAGTGTAGAGAGAGAG 2100  
 QY 2101 GTTCTCAGAGTGTGGGAGCGGCTTCTTATGAGAGCAATGATATTGACACTGTCTCT 2160  
 Db 2101 GTTCTCAGAGTGTGGGAGCGGCTTCTTATGAGAGCAATGATATTGACACTGTCTCT 2160  
 QY 2161 CTTTGGAGCTTCAATTTGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2220

```

Db      2161 CTTGGCAGTGCATTAGTACTTGAAGGTATATGACTGAGCGTACAGTTAA 2220
QY      2221 CCTGCAAAAACAGTACTTAGTATATGAGGCGAGGATTAATAATGAAATTTGCAAAAT 2280
Db      2221 CCTGCAAAAACAGTACTTAGTATATGAGGCGAGGATTAATAATGAAATTTGCAAAAT 2280
QY      2281 CACTTGACACCACTGAGAGCACTTATCAACGAGTGAAGAAATCAACCCGAGCAGGCG 2340
Db      2281 CACTTGACACCACTGAGAGCACTTATCAACGAGTGAAGAAATCAACCCGAGCAGGCG 2340
QY      2341 TGTGTGAACATGGTTGTATATATGCGACTGCGAAGCTGAACTCTACGCACTCCACAAA 2400
Db      2341 TGTGTGAACATGGTTGTATATATGCGACTGCGAAGCTGAACTCTACGCACTCCACAAA 2400
QY      2401 TGATGTTTTCAGGCTGATGAGCTGTTGCCACCATGATATCAACCGAGTCTTAAGTT 2460
Db      2401 TGATGTTTTCAGGCTGATGAGCTGTTGCCACCATGATATCAACCGAGTCTTAAGTT 2460
QY      2461 TAAAGTGCACATGATGTATTAAGCATGCTTCTTTGAGTTTAATTAATTAACAT 2520
Db      2461 TAAAGTGCACATGATGTATTAAGCATGCTTCTTTGAGTTTAATTAATTAACAT 2520
QY      2521 AAGTTGATTGAGAAATCAAGCATTAATCACTTCACTGCAAAAAA 2580
Db      2521 AAGTTGATTGAGAAATCAAGCATTAATCACTTCACTGCAAAAAA 2580
QY      2581 AAAAAA 2586
Db      2581 AAAAAA 2586

```

RESULT 5  
ABL95585  
ID ABL95585 standard; cDNA; 2586 BP.

```

XX      19-JUL-2002 (first entry)
XX      Human angiogenesis related cDNA PRO295 SEQ ID NO: 49.
XX      Human: angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
XX      atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
XX      cardiatic; cytosolic; antiangiogenic; hypotensive; vulnerary;
XX      antiarteriosclerotic; gene; ss.
XX      Homo sapiens.
XX      OS
XX      WO200208284-A2.
XX      31-JAN-2002.
XX      09-JUL-2001; 2001WO-US21735.
XX      20-JUL-2000; 2000US-219556P.
XX      25-JUL-2000; 2000US-220624P.
XX      25-JUL-2000; 2000US-220664P.
XX      28-JUL-2000; 2000WO-US20710.
XX      02-AUG-2000; 2000US-222695P.
XX      17-AUG-2000; 2000US-0643657.
XX      23-AUG-2000; 2000WO-US23238.
XX      07-SEP-2000; 2000US-230978P.
XX      15-SEP-2000; 2000US-000000P.
XX      18-SEP-2000; 2000US-0664610.
XX      18-SEP-2000; 2000US-0665350.
XX      24-OCT-2000; 2000US-042922P.
XX      08-NOV-2000; 2000US-0709238.
XX      08-NOV-2000; 2000WO-US30952.
XX      10-NOV-2000; 2000WO-US30953.
XX      01-DEC-2000; 2000WO-US32678.
XX      20-DEC-2000; 2000US-0747259.
XX      20-DEC-2000; 2000WO-US34956.

```

```

PR      22-JAN-2001; 2001US-0767609.
PR      28-FEB-2001; 2001US-0796498.
PR      28-FEB-2001; 2001WO-US06520.
PR      01-MAR-2001; 2001WO-US06668.
PR      09-MAR-2001; 2001US-0802706.
PR      14-MAR-2001; 2001US-0806889.
PR      22-MAR-2001; 2001US-0816744.
PR      05-APR-2001; 2001US-0828366.
PR      10-MAY-2001; 2001US-0854208.
PR      10-MAY-2001; 2001US-0854280.
PR      25-MAY-2001; 2001US-0866028.
PR      25-MAY-2001; 2001US-0866034.
PR      25-MAY-2001; 2001WO-US17092.
PR      30-MAY-2001; 2001US-0870574.
PR      30-MAY-2001; 2001WO-US17443.
PR      01-JUN-2001; 2001WO-US17800.
PR      20-JUN-2001; 2001WO-US19692.
PR      28-JUN-2001; 2001WO-US00000.

```

```

XX      (GETH ) GENENTECH INC.
PA      (BAKE/) BAKER K P.
PA      (FERB/) FERRARA N.
PA      (GERB/) GERBER H.
PA      (GERB/) GERRITSEN M E.
PA      (GODO/) GODDARD A.
PA      (GODO/) GODOWSKI P J.
PA      (GURN/) GURNEY A L.
PA      (HILL/) HILLAN K J.
PA      (MARS/) MASTERS S A.
PA      (PANJ/) PAN J.
PA      (PAON/) PAONTI N F.
PA      (STEP/) STEPHAN J F.
PA      (WATA/) WATANABE C K.
PA      (WILD/) WILLIAMS P M.
PA      (WOOD/) WOOD W I.

```

```

XX      Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI      Godowski PJ, Gurney AL, Hillan KJ, Masters SA, Pan J, Paoni NF,
PI      Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
XX      WPI; 2002-171999/22.
DR      P-PSDB; ABB95447.

```

```

XX      One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX      useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX      infarction), endothelial or angiogenic disorders in a mammal -
XX      Claim 1; Fig 49; 567bp; English.

```

```

XX      The present invention provides the protein and coding sequences of human
XX      PRO proteins. These are useful for treating or diagnosing a
XX      cardiovascular, endothelial or angiogenic disorder, including cardiac
XX      hypertrophy, trauma, cancer, age-related macular degeneration,
XX      atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
XX      CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
XX      angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX      healing. The present sequence is a coding sequence of the invention.

```

SO Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;

Query Match 100.0%; Score 2586; DB 24; Length 2586;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2586; Conservative 0;

```

QY      1 CGCGCGCTCCCGACCCGCGCGCCGCGCGCTCCCGATCTGCAACCCGACG 60
Db      1 CGCGCGCTCCCGACCCGCGCGCCGCGCGCTCCCGATCTGCAACCCGACG 60
QY      61 CGCGCGCTCCCGCGGAGGAGCAATCCAGTCCGCGCGCGCGCAAGTCCGATCA 120
Db      61 CGCGCGCTCCCGCGGAGGAGCAATCCAGTCCGCGCGCGCGCAAGTCCGATCA 120
QY      121 GTCGGGCGGCGGCTGCGGCGGCGAGGCGAGATGACGAGCGCTTGCGCTGT 180

```

```
Db 121 |GTCGGGCGCGCGCTGCGGCGCAGACGAGATGAGCGCTGCGGCGCACCCGCTGT 180
Qy 181 |GCGTGTGCTGGGCGGCGGCGTCCCGACGAGCGCGCGCGCGCTCGGACGCGACCTCG 240
Db 181 |GCGTGTGCTGGGCGGCGGCGTCCCGACGAGCGCGCGCGCGCTCGGACGCGACCTCG 240
Qy 241 |CTCCAGTCAAGCCCGCGCGCTCTGAGCTACCCGAGAGAGCGCACCTTCAATGAGA 300
Db 241 |CTCCAGTCAAGCCCGCGCGCTCTGAGCTACCCGAGAGAGCGCACCTTCAATGAGA 300
Qy 301 |TGTTCCGCGAGTTGAGAACTGATGAGGACGCGAGCAAAATTTGGCAGCGGCTG 360
Db 301 |TGTTCCGCGAGTTGAGAACTGATGAGGACGCGAGCAAAATTTGGCAGCGGCTG 360
Qy 361 |AAGAGATGAGGAGAGAGAGTGTCTGTAAGCATCATGAGATGAACTTGCAACT 420
Db 361 |AAGAGATGAGGAGAGAGAGTGTCTGTAAGCATCATGAGATGAACTTGCAACT 420
Qy 421 |TACCTCCAGCTATCAGATGAGACCAACAGACGAAAGTTGAAATTAATCATCC 480
Db 421 |TACCTCCAGCTATCAGATGAGACCAACAGACGAAAGTTGAAATTAATCATCC 480
Qy 481 |ATGTGACACGAGAAATTCAGATTAACAAACAGACTGAGCAATGTCTTTTCA 540
Db 481 |ATGTGACACGAGAAATTCAGATTAACAAACAGACTGAGCAATGTCTTTTCA 540
Qy 541 |AGACAGTTATCATCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 541 |AGACAGTTATCATCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Qy 601 |ACGAGACTGTGGGCGCAGAGATGATCTGACAGTTTTCAGCTTCCAGTACCTG 660
Db 601 |ACGAGACTGTGGGCGCAGAGATGATCTGACAGTTTTCAGCTTCCAGTACCTG 660
Qy 661 |CATGCCGCGGCGCAGAGAGATCTGTGACACCGGAGACGTGAGTCTGTGAGAC 720
Db 661 |CATGCCGCGGCGCAGAGAGATCTGTGACACCGGAGACGTGAGTCTGTGAGAC 720
Qy 721 |GTGTCTGGGCTGCTGACCAAAATGGCCACAGGGGAGCAATGGAGCAATGTGAGA 780
Db 721 |GTGTCTGGGCTGCTGACCAAAATGGCCACAGGGGAGCAATGGAGCAATGTGAGA 780
Qy 781 |ACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 781 |ACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Qy 841 |TGTCGACACCCCTGCGTGGAGGCGAGCTTTGGCAGTACCCCGCAGCGGCTTCT 900
Db 841 |TGTCGACACCCCTGCGTGGAGGCGAGCTTTGGCAGTACCCCGCAGCGGCTTCT 900
Qy 901 |ACCTCATCACCTGGAGAGCTAGAGCTGTGAGAGCTTGAACCGATGCCCTTGTG 960
Db 901 |ACCTCATCACCTGGAGAGCTAGAGCTGTGAGAGCTTGAACCGATGCCCTTGTG 960
Qy 961 |GCTCTCTCTGCGACCCCGCAGCGACGCTGTGTATGTGTGACAGCGACCTTGT 1020
Db 961 |GCTCTCTCTGCGACCCCGCAGCGACGCTGTGTATGTGTGACAGCGACCTTGT 1020
Qy 1021 |GAGACCGTGAACAGATGAGGAGATCTGTGCTGCCAGAGAGTCCCGAGATGAGA 1080
Db 1021 |GAGACCGTGAACAGATGAGGAGATCTGTGCTGCCAGAGAGTCCCGAGATGAGA 1080
Qy 1081 |TTGGCAGCTTTCATGAGAGAGTGGCCAGAGAGCTGAGAGACCTGAGAGAGCT 1140
Db 1081 |TTGGCAGCTTTCATGAGAGAGTGGCCAGAGAGCTGAGAGACCTGAGAGAGCT 1140
Qy 1141 |AAGAGATGAGGAGAGAGAGCTGCGGCTGCGCGCTGCACTGTGAGAGAGAGAG 1200
Db 1141 |AAGAGATGAGGAGAGAGAGCTGCGGCTGCGCGCTGCACTGTGAGAGAGAGAG 1200
Qy 1201 |TTTAGATCTGAGCAGAGCTGTGGTAGATGTGCAATGAAATAGCTAATTTATTC 1260
Db 1201 |TTTAGATCTGAGCAGAGCTGTGGTAGATGTGCAATGAAATAGCTAATTTATTC 1260

Db 1201 |TTTAGATCTGAGCAGAGCTGTGGTAGATGTGCAATGAAATAGCTAATTTATTC 1260
Qy 1261 |GATGTGTCTTAAAGCGTGGAGCTGACAGAGCTTCTTCAATCTTCTTCCAGTA 1320
Db 1261 |GATGTGTCTTAAAGCGTGGAGCTGACAGAGCTTCTTCAATCTTCTTCCAGTA 1320
Qy 1321 |TCCCTCTGCTGACAGAGATGAGAGTGTGTGATTTGATTTGATTTGATTTGAT 1380
Db 1321 |TCCCTCTGCTGACAGAGATGAGAGTGTGTGATTTGATTTGATTTGATTTGAT 1380
Qy 1381 |CCAGCTTCAAGCTGTGCTGTGGAGAGTCAAGAGAGTAACTGACAGAGAGT 1440
Db 1381 |CCAGCTTCAAGCTGTGCTGTGGAGAGTCAAGAGAGTAACTGACAGAGAGT 1440
Qy 1441 |GCAACCCCTGTCAGATTAATTTGCTGCTTTCCTTCAAGAGTGGCAGAGAG 1500
Db 1441 |GCAACCCCTGTCAGATTAATTTGCTGCTTTCCTTCAAGAGTGGCAGAGAG 1500
Qy 1501 |TCTACATGCTTATTAATTTGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 |TCTACATGCTTATTAATTTGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Qy 1561 |TGATTTGTTTGGGAAATGTGAGAAAGTGTGCTGCTTTCAGATTAATTTGAT 1620
Db 1561 |TGATTTGTTTGGGAAATGTGAGAAAGTGTGCTGCTTTCAGATTAATTTGAT 1620
Qy 1621 |AAATGCAACAAATTAATTTTCAAGAGTCTTTCAGATTAATTTGATTTGAT 1680
Db 1621 |AAATGCAACAAATTAATTTTCAAGAGTCTTTCAGATTAATTTGATTTGAT 1680
Qy 1681 |CAGCTGTGAGATGAAATGTGCTTTCAGCTGATTAATTTGATTTGATTTGAT 1740
Db 1681 |CAGCTGTGAGATGAAATGTGCTTTCAGCTGATTAATTTGATTTGATTTGAT 1740
Qy 1741 |GTGTGCTGCTGCTTCACTTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Db 1741 |GTGTGCTGCTGCTTCACTTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Qy 1801 |TCTCTCAGCAGAGCTGGGAGAGAGAGTGTCTTCTCTGCTCAGATTAATTTG 1860
Db 1801 |TCTCTCAGCAGAGCTGGGAGAGAGAGTGTCTTCTCTGCTCAGATTAATTTG 1860
Qy 1861 |GCTCAGAGAGCTGCAAGCTGTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Db 1861 |GCTCAGAGAGCTGCAAGCTGTGCGCAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Qy 1921 |ATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Db 1921 |ATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Qy 1981 |CCAAAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
Db 1981 |CCAAAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
Qy 2041 |ATTAGGCTCAAACTAATTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
Db 2041 |ATTAGGCTCAAACTAATTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
Qy 2101 |GTTCTCAGAGTGTGGGAGCGTCTTCTTCAATGAAGCAATGATTTGACATGCT 2160
Db 2101 |GTTCTCAGAGTGTGGGAGCGTCTTCTTCAATGAAGCAATGATTTGACATGCT 2160
Qy 2161 |CTTTGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
Db 2161 |CTTTGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
Qy 2221 |CTTGAGAGAAAGTAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
Db 2221 |CTTGAGAGAAAGTAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
Qy 2281 |CACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
Db 2281 |CACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
Qy 2340 |CACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
Db 2340 |CACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
```

XX	(GETH ) GENENTECH INC.
PA	
XX	Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A;
PI	Godowski PJ, Gurney AL, Hillan KJ, Martens SA, Pan J, Paoni NF;
PI	Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX	
DR	WPI; 2002-090516/12.
XX	P-PSDB; ABB#4841.
PT	One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT	useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT	infarction), endothelial or angiogenic disorders in a mammal -
XX	
PS	Claim 2; Fig 49; 565pp; English.
XX	
CC	ABL88072 to ABL88258 encode the PRO proteins given in ABB#4817 to
CC	ABB#5003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC	antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC	activities, and can be used in gene therapy. The PRO polynucleotides,
CC	proteins, agonists and antagonists are useful for treating or diagnosing
CC	a cardiovascular hypertrophy, trauma, cancer, age-related macular
CC	e.g. cardiac hypertrophy, hypertension, arterial restenosis,
CC	degenerative atherosclerosis, hyperextension, thrombophlebitis,
CC	rheumatoid arthritis, angina, myocardial infarctions, lymphoblastic,
CC	lymphangitis, tumor angiogenesis (such as breast carcinoma and liver
CC	carcinoma) and wound healing. The PRO polynucleotides have applications
CC	in molecular biology, including use as hybridisation probes, and in
CC	chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC	probes used in the exemplification of the present invention.
XX	
SQ	Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;
Query Match	100.0%; Score 2586; DB 24; Length 2586;
Best local similarity	.100.0%; Pred. No. 0;
Matches 2586;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CGCGCGCTCCCGCAACCGCGGGCCGCCACCAGCGCGCTCCGCATTTGACCCGGCAGC 60
DB	1 CGCGCGCTCCCGCAACCGCGGGCCGCCACCAGCGCGCTCCGCATTTGACCCGGCAGC 60
QY	61 CGCGCGGCGCTCCCGCGGGAAGAGAGATCCAGTCCGCGCCCGCACCGCAACTCGGTCCA 120
DB	61 CGCGCGGCGCTCCCGCGGGAAGAGATCCAGTCCGCGCGCCCGCACCGCAACTCGGTCCA 120
QY	121 GTCGGAGCGCGGCTCGCGGCGGAGAAGGAGATGACAAGCGGCTTGAGGGCCACCCGTGCT 180
DB	121 GTCGGAGCGGCGGCTCGCGGCGGAGAAGGAGATGACAAGCGGCTTGAGGGCCACCCGTGCT 180
QY	181 GCCTGCTCTGAGCGGCGGCGGTTCCTCCACGAGCCCCCGCGCTTCGACGCGGACCTCGG 240
DB	181 GCCTGCTCTGAGCGGCGGCGGTTCCTCCACGAGCCCCCGCGCTTCGACGCGGACCTCGG 240
QY	241 CTCACGTCAAAGCCCGGCGCGGCTCTCACTAACCGCAAGAGAGCCACCCCTCAATTGAGA 300
DB	241 CTCACGTAAAGCCCGGCGCGGCTCTCACTAACCGCAAGAGAGCCACCCCTCAATTGAGA 300
QY	301 TGTTCCGAGAGTTGAGAGACTGATGAGAGACACGACACCAAAATTGGCGACGCGGTGG 360
DB	301 TGTTCCGAGAGTTGAGAGACTGATGAGAGACACGACACCAAAATTGGCGACGCGGTGG 360
QY	361 AAGAGATGAGAGCAGAAAGAGTGCTGTAAGCATCATCAAGATGAACTCGGCAACT 420

```

361 AAGAGATGAGGACAGAAAGCTGCTGCTAAAGCATCATCAGAAAGTGAACCTGCAAACT 420
421 TACCTCCAGCTATCACAATGAGACCAACAGACAGAAAGTTGAAAATAATACATCC 480
421 TACCTCCAGCTATCACAATGAGACCAACAGACAGAAAGTTGAAAATAATACATCC 480
481 ATGTCCACCGAAGAAATTCACAAAGATACCAACACAGACTGACCAAAATGCTTTTCAG 540
481 ATGTCCACCGAAGAAATTCACAAAGATACCAACACAGACTGACCAAAATGCTTTTCAG 540
541 AGACAGTTATCATCTGTGGGAGCAGAAAGAGGAGAGGACAGAGTGCATCATCG 600
541 AGACAGTTATCATCTGTGGGAGCAGAAAGAGGAGAGGACAGAGTGCATCATCG 600
601 ACAGAGACTGTGGGAGCCAGCATGTACTGCAAGTTTTCAGCTTCAGATCACTGCCAGC 660
601 ACAGAGACTGTGGGAGCCAGCATGTACTGCAAGTTTTCAGCTTCAGATCACTGCCAGC 660
661 CATGCCGGGGCCAGAGAGTGTCTGCAACCCGGGACAGTGAAGTGTGGAGACAGAGCTGT 720
661 CATGCCGGGGCCAGAGAGTGTCTGCAACCCGGGACAGTGAAGTGTGGAGACAGAGCTGT 720
721 GTGTCTGGGATCTGCAACCAAAATGACCAACAGGGGACAGAAATGGACATCTGTGACA 780
721 GTGTCTGGGATCTGCAACCAAAATGACCAACAGGGGACAGAAATGGACATCTGTGACA 780
781 ACCAAGAGGACTGCGACAGCCGGGGCTGTGTCTGCTTCAGAGAGGCTGTGTTCCTTG 840
781 ACCAAGAGGACTGCGACAGCCGGGGCTGTGTCTGCTTCAGAGAGGCTGTGTTCCTTG 840
841 ACCAAGAGGACTGCGACAGCCGGGGCTGTGTCTGCTTCAGAGAGGCTGTGTTCCTTG 840
841 ACCAAGAGGACTGCGACAGCCGGGGCTGTGTCTGCTTCAGAGAGGCTGTGTTCCTTG 840
841 TGTGACACCCCTGCGCGGTGAGGGGCGAGCTTTGCAAGACCCCGCAGCGGCTTCGCG 900
841 TGTGACACCCCTGCGCGGTGAGGGGCGAGCTTTGCAAGACCCCGCAGCGGCTTCGCG 900
901 ACCTCATCATCTGTGGAGCTGAGCTGATGAGAGCTTTGACCGATGCTTGTGCGACGTG 960
901 ACCTCATCATCTGTGGAGCTGAGCTGATGAGAGCTTTGACCGATGCTTGTGCGACGTG 960
961 ACCTCATCATCTGTGGAGCTGAGCTGATGAGAGCTTTGACCGATGCTTGTGCGACGTG 960
961 ACCTCATCATCTGTGGAGCTGAGCTGATGAGAGCTTTGACCGATGCTTGTGCGACGTG 960
961 GCTCTCTGCGAGGAGCCCAAGCCAGCCAGCTGTATGTGTGACAGCCGACCTTCGTTG 1020
961 GCTCTCTGCGAGGAGCCCAAGCCAGCCAGCTGTATGTGTGACAGCCGACCTTCGTTG 1020
1021 GAGAGCGGTGACCAAGATGGGAGATCTGTGCTGCCAGAGAGCTTCCGATGATGATGAG 1080
1021 GAGAGCGGTGACCAAGATGGGAGATCTGTGCTGCCAGAGAGCTTCCGATGATGATGAG 1080
1081 TTGGCAGCTTCAATGAGAGAGGTGCGCCAGAGAGCTGGAAGACCTGGAGAGAGCTGACTG 1140
1081 TTGGCAGCTTCAATGAGAGAGGTGCGCCAGAGAGCTGGAAGACCTGGAGAGAGCTGACTG 1140
1141 AAGAGATGGCGGTGGGAGACCTGTGCGGCTGCGCGCTGCACTGTGGAGGGGAGAGAG 1200
1141 AAGAGATGGCGGTGGGAGACCTGTGCGGCTGCGCGCTGCACTGTGGAGGGGAGAGAG 1200
1201 TTGAATCTGGAACAGGCTGTGGGATGAGATGAGCAATGAAATAGCTAATTTATTTCCCA 1260
1201 TTGAATCTGGAACAGGCTGTGGGATGAGATGAGCAATGAAATAGCTAATTTATTTCCCA 1260
1261 GGTGTGTGCTTGAAGCGTGGGCTGACAGAGGCTTCTTCATCTTCTTCCAGAAAGTT 1320
1261 GGTGTGTGCTTGAAGCGTGGGCTGACAGAGGCTTCTTCATCTTCTTCCAGAAAGTT 1320
1321 TCCCTCTGCGCTTGAACAGATGAGATGAGTGTGCAATTTGTCAAGCTCCCGCAGGCTGTT 1380
1321 TCCCTCTGCGCTTGAACAGATGAGATGAGTGTGCAATTTGTCAAGCTCCCGCAGGCTGTT 1380
1381 CCAGGCTTCAAGTGTGTGCTTGGAGAGTGCAGGACAGGCTTAACTCAGAGACAGTTT 1440
1381 CCAGGCTTCAAGTGTGTGCTTGGAGAGTGCAGGACAGGCTTAACTCAGAGACAGTTT 1440
1441 GCCACCCCTGTCCAAATTTATGCTGTGCTTGTCTTACAGTTGGCAGACAGCGTTTGT 1500
1441 GCCACCCCTGTCCAAATTTATGCTGTGCTTGTCTTACAGTTGGCAGACAGCGTTTGT 1500

1441 GCCACCCCTGTCCAAATTTATGCTGTGCTTGTCTTACAGTTGGCAGACAGCGTTTGT 1500
1501 TCTACATGCTTTGATTAATTTGTTGAGGGAGAGATGAAAACAATGTGAGTCTTCCCTC 1560
1501 TCTACATGCTTTGATTAATTTGTTGAGGGAGAGATGAAAACAATGTGAGTCTTCCCTC 1560
1561 TGATTTGTTGGGAGAAATGTGAGAAAGTGTGCTGCTTTGCAACATCAACTGCGCA 1620
1561 TGATTTGTTGGGAGAAATGTGAGAAAGTGTGCTGCTTTGCAACATCAACTGCGCA 1620
1621 AATGCAAGAAATGAAATTTTCCAGCAGTCTTTCATGCGATAGTAAAGTGTGCTT 1680
1621 AATGCAAGAAATGAAATTTTCCAGCAGTCTTTCATGCGATAGTAAAGTGTGCTT 1680
1681 CAGCTGTGCAAGTGAATGTTCTGTTCACCTGCAATTCATGCTTTATTCATCAGAG 1740
1681 CAGCTGTGCAAGTGAATGTTCTGTTCACCTGCAATTCATGCTTTATTCATCAGAG 1740
1741 GGTGTGCTGAGCTCCTACCTGTGTGCAAGGAGAGATTTTCATTCAGAAATTCCTCC 1800
1741 GGTGTGCTGAGCTCCTACCTGTGTGCAAGGAGAGATTTTCATTCAGAAATTCCTCC 1800
1801 TCTTCAGACAGCTGTGGGAGGGGATGTTGTTCTCTGTTCATCAGGATTCACAGAG 1860
1801 TCTTCAGACAGCTGTGGGAGGGGATGTTGTTCTCTGTTCATCAGGATTCACAGAG 1860
1861 GCTCAGAGCTGCAAGCTGCTTCCCAAGTGCACAGAGTGAAGAGACAGAGAGTTTC 1920
1861 GCTCAGAGCTGCAAGCTGCTTCCCAAGTGCACAGAGTGAAGAGACAGAGAGTTTC 1920
1921 ATCTGTGTGATCTTAAGCTGAGTCTCTCTCACTACCAACCAACAGCTTGTGCTCA 1980
1921 ATCTGTGTGATCTTAAGCTGAGTCTCTCTCACTACCAACCAACAGCTTGTGCTCA 1980
1981 CCAAAAGTCTCCCAAAAGAGAGAGAAATGGATTTTCTTGAAGCATGCACTGTGA 2040
1981 CCAAAAGTCTCCCAAAAGAGAGAGAAATGGATTTTCTTGAAGCATGCACTGTGA 2040
2041 ATTAAGCTCAAACTAATTTCTACATCTCTTAAGTAATTAAGTGTGAAACAGAGCT 2100
2041 ATTAAGCTCAAACTAATTTCTACATCTCTTAAGTAATTAAGTGTGAAACAGAGCT 2100
2101 GTTCTCAGAGTGTGGGAGCGGCTCTTCTATGAAAGCAATGATGACATGCTGCTCCT 2160
2101 GTTCTCAGAGTGTGGGAGCGGCTCTTCTATGAAAGCAATGATGACATGCTGCTCCT 2160
2161 CTTTGGCAGTTGATTAAGTAACTTGAAGAGTATGACTGAGCGTGAACAAGTTAA 2220
2161 CTTTGGCAGTTGATTAAGTAACTTGAAGAGTATGACTGAGCGTGAACAAGTTAA 2220
2221 CCTGCAAGAAACAGTATTAGTAAATTTGTTGAGGCGAGGATTAATTAATTTGCAAAAT 2280
2221 CCTGCAAGAAACAGTATTAGTAAATTTGTTGAGGCGAGGATTAATTAATTTGCAAAAT 2280
2281 CACTGAGAGCAATGAAAGCAATTAATCAACAGGAGGAGAAATCAAAACGAGAGGCG 2340
2281 CACTGAGAGCAATGAAAGCAATTAATCAACAGGAGGAGAAATCAAAACGAGAGGCG 2340
2341 TGTGTGAAACATGTTGTAATATGCACTGCGAACACTGAATCTTACGCACTCCCAAA 2400
2341 TGTGTGAAACATGTTGTAATATGCACTGCGAACACTGAATCTTACGCACTCCCAAA 2400
2401 TGAATTTTCAGGTGCAATGAGTGTGCAACCAATGATTAATTCAGAGTCTTAAAGTT 2460
2401 TGAATTTTCAGGTGCAATGAGTGTGCAACCAATGATTAATTCAGAGTCTTAAAGTT 2460
2461 TAAAGTTGCAATGATTTGTAATGCAATGCTTTGTTGAGTTTAAATTAATTAACAT 2520
2461 TAAAGTTGCAATGATTTGTAATGCAATGCTTTGTTGAGTTTAAATTAATTAACAT 2520
2521 AAGTTGATTTAGAAATCAAGCAATTAATCACTTCAACTGCAAAAAAATTAATTAATTA 2580
2521 AAGTTGATTTAGAAATCAAGCAATTAATCACTTCAACTGCAAAAAAATTAATTAATTA 2580
```



QY	2581	AAAAAA	2586
Db	2581	AAAAAA	2586

RESULT 7  
ACA55002

XX 05-JUN-2003 (first entry)  
DT

# Novel human secreted and transmembrane protein PRO295 cDNA

Human; secreted and transmembrane protein; gene therapy; psoriasis;  
keratocyst; gastroenteritis ulceration; skin disease;  
keratinocyte differentiation; epithelial cancer; Alzheimer's disease;  
squamous cell carcinoma; Parkinson's disease; inflammatory disease;  
amylotrophic lateral sclerosis; rheumatoid arthritis; asthma;  
multiple sclerosis; organ failure; atherosclerosis; cardiac injury;  
infertility; birth defect; premature aging; AIDS; cancer;  
diabetic complication; wound repair; tissue re-growth; gene; ss.

OS Homo sapiens.

PN US2003017463-A1

PD 23-JAN-2003 .  
XX

PF 11-JUL-2001; 2001US-0903640.  
XX

PR	10-SEP-1996	98MO-UT518824
PR	14-SEP-1996	98MO-UT519177
PR	16-SEP-1996	98MO-UT519330
PR	17-SEP-1996	98MO-UT519437
PR	01-DEC-1996	98MO-UT515108
PR	08-SEP-1999	99MO-UT520594
PR	13-SEP-1999	99MO-UT520944
PR	15-SEP-1999	99MO-UT521090
PR	15-SEP-1999	99MO-UT521409
PR	05-OCT-1999	99MO-UT523069
PR	29-NOV-1999	99MO-UT528214
PR	30-NOV-1999	99MO-UT528313
PR	01-DEC-1999	99MO-UT528301
PR	02-DEC-1999	99MO-UT528554
PR	02-DEC-1999	99MO-UT528655
PR	16-DEC-1999	99MO-UT530051
PR	20-DEC-1999	99MO-UT530911
PR	05-JAN-2000	99MO-UT530219
PR	05-JAN-2000	99MO-UT530299
PR	11-FEB-2000	99MO-UT533565
PR	12-FEB-2000	99MO-UT544141
PR	24-FEB-2000	99MO-UT505064
PR	02-MAR-2000	99MO-UT505611
PR	20-MAR-2000	99MO-UT507317
PR	30-MAR-2000	99MO-UT508649
PR	22-MAY-2000	99MO-UT514042
PR	02-JUN-2000	99MO-UT515264
PR	28-JUL-2000	99MO-UT520701
PR	24-AUG-2000	99MO-UT533268
PR	17-SEP-1997	97MO-UT551139
PR	17-SEP-1997	97MO-UT551169
PR	17-SEP-1997	97MO-UT551197
PR	17-SEP-1997	97MO-UT551199
PR	17-SEP-1997	97MO-UT551212
PR	17-SEP-1997	97MO-UT551266
PR	17-SEP-1997	97MO-UT552669
PR	18-SEP-1997	97MO-UT552669
PR	15-OCT-1997	97MO-UT562126
PR	17-OCT-1997	97MO-UT562126

PR	17-OCT-1997	97US-0632287P
PR	21-OCT-1997	97US-063486P
PR	24-OCT-1997	97US-062814P
PR	24-OCT-1997	97US-062816P
PR	24-OCT-1997	97US-063110P
PR	24-OCT-1997	97US-063111P
PR	24-OCT-1997	97US-063112P
PR	24-OCT-1997	97US-063128P
PR	27-OCT-1997	97US-063329P
PR	28-OCT-1997	97US-063511P
PR	28-OCT-1997	97US-063542P
PR	28-OCT-1997	97US-063544P
PR	28-OCT-1997	97US-063549P
PR	28-OCT-1997	97US-063550P
PR	28-OCT-1997	97US-063564P
PR	28-OCT-1997	97US-063415P
PR	28-OCT-1997	97US-063704P
PR	29-OCT-1997	97US-063732P
PR	29-OCT-1997	97US-063734P
PR	29-OCT-1997	97US-063735P
PR	29-OCT-1997	97US-063738P
PR	29-OCT-1997	97US-063821P
PR	31-OCT-1997	97US-063870P
PR	31-OCT-1997	97US-064103P
PR	03-NOV-1997	97US-064288P
PR	07-NOV-1997	97US-064809P
PR	12-NOV-1997	97US-065166P
PR	11-NOV-1997	97US-065846P
PR	18-NOV-1997	97US-065613P
PR	21-NOV-1997	97US-066120P
PR	21-NOV-1997	97US-066343P
PR	21-NOV-1997	97US-066432P
PR	24-NOV-1997	97US-066466P
PR	24-NOV-1997	97US-066571P
PR	24-NOV-1997	97US-066710P
PR	24-NOV-1997	97US-066772P
PR	25-NOV-1997	97US-066840P
PR	25-NOV-1997	97US-068045P
PR	12-DEC-1997	98US-069026P
PR	04-JUN-1998	98US-039803P
PR	10-SEP-1998	98US-100262P
PR	14-SEP-1998	98US-100858P
PR	17-SEP-1998	98US-104040P
PR	13-OCT-1998	98US-109304P
PR	20-NOV-1998	98US-113286P
PR	22-DEC-1998	98US-113048P
PR	07-JUL-1999	99US-145658P
PR	26-JUL-1999	99US-145658P
PR	28-JUL-1999	99US-166522P
PR	18-SEP-2000	2000US-066550P

(GETH ) GENENTECH INC.

PI Ashkenazi A, Bolstein D, Desnoyers L, Bacon DL, Ferrara N;  
PI Filvarsoff E, Gong S, Gao W, Gerber H, Gerritsen ME, Goddard A,  
PI Gudowski PJ, Grimaldi JC, Gurley AL, Hillan KJ, Kihlavin IV,  
PI Maher JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
PI Williams PM, Wood WI;  
XX  
XX WPI; 2003-341586/32.  
DR  
DR P-PSDE; AB069662.

New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's disease -

Claim 2; Fig 83; 473pp; English

CC The invention describes sixty one nucleic acids encoding PRO polypeptides  
CC (secreted and transmembrane). The PRO polypeptides and nucleic acids are  
CC useful in diagnosing or treating enterocolitis, gastroentericinal

CC ulceration, skin diseases associated with abnormal keratinocyte  
 CC differentiation, e.g. psoriasis or epithelial cancers such as squamous  
 CC cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic  
 CC lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis,  
 CC asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac  
 CC injury, infertility, birth defects, premature aging, AIDS, cancer,  
 CC diabetic complications, or mutations in general. The polypeptides are  
 CC also useful for wound repair and associated therapies concerned with  
 CC re-growth of tissue. The PRO polypeptides and nucleic acid molecules  
 CC are also useful in gene therapy, and as molecular weight markers for  
 CC protein electrophoresis purposes. The anti-PRO antibodies may be used  
 CC in diagnostic assays for PRO, or for the affinity purification of PRO  
 CC from recombinant cell culture or natural sources. This sequence  
 CC encodes a novel human PRO polypeptide.

XX Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;

Query Match 100.0%; Score 2586; DB 25; Length 2586;

Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;

Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGCGCTCCGCAACCGCGCCGCCACCGCGCGCTCCCGCATCTGACCCGCGAGC 60  
 DB 1 CGCCGCGCTCCGCAACCGCGCCGCCACCGCGCGCTCCCGCATCTGACCCGCGAGC 60  
 QY 61 CGCGCGGCTCCCGCGCGGAGCGAGCATCCAGTCCGCGCGCGCGCGCGCGCGTCCA 120  
 DB 61 CGCGCGGCTCCCGCGCGGAGCGAGCATCCAGTCCGCGCGCGCGCGCGCGCGTCCA 120  
 QY 121 GTGCGGCGCGCGCGCTCGCGCGCGCGAGCGAGCATCGAGCGCGTGGCGCGACCTGTCT 180  
 DB 121 GTGCGGCGCGCGCGCTCGCGCGCGCGAGCGAGCATCGAGCGCGTGGCGCGACCTGTCT 180  
 QY 181 GCGTGTCTGCG 240  
 DB 181 GCGTGTCTGCG 240  
 QY 241 CTCAGATCAAGCCCGCGCGCGCGCTCTCAGCTACCGCGAGGAGCGACCTCATAGAGA 300  
 DB 241 CTCAGATCAAGCCCGCGCGCGCGCTCTCAGCTACCGCGAGGAGCGACCTCATAGAGA 300  
 QY 301 TGTTCGCGAGGTTGAGAACTGATGAGAGACAACGAGCAAAATTGCGCGAGCGGTGG 360  
 DB 301 TGTTCGCGAGGTTGAGAACTGATGAGAGACAACGAGCAAAATTGCGCGAGCGGTGG 360  
 QY 361 AAGAGATGAGGAGAGAAAGCTGCTAAAGCATCATCAGAGTGAACCTGGCAAACT 420  
 DB 361 AAGAGATGAGGAGAGAAAGCTGCTAAAGCATCATCAGAGTGAACCTGGCAAACT 420  
 QY 421 TACCTCCAGCTATCAATAGAACCAACAGACAGAAAGTTGAGAAATAATACATCC 480  
 DB 421 TACCTCCAGCTATCAATAGAACCAACAGACAGAAAGTTGAGAAATAATACATCC 480  
 QY 481 AATGTGACCGAGAAATTCAGAAATTAACAACAACAGAGTGAAGAAATGCTTTTCA 540  
 DB 481 AATGTGACCGAGAAATTCAGAAATTAACAACAACAGAGTGAAGAAATGCTTTTCA 540  
 QY 541 AGACAGTTATCAATCTGTGGAGACGAAAGAGCGAGAAAGAGCCAGAGTCAATATCG 600  
 DB 541 AGACAGTTATCAATCTGTGGAGACGAAAGAGCGAGAAAGAGCCAGAGTCAATATCG 600  
 QY 601 ACAGAGATCTGTGGAGCCAGAGTACTGCGAGTTTCAGAGTTCCAGTACACCTGCGAC 660  
 DB 601 ACAGAGATCTGTGGAGCCAGAGTACTGCGAGTTTCAGAGTTCCAGTACACCTGCGAC 660  
 QY 661 CATGCCGCGGCGCAGAGAGATCTGTGACCCGCGAGCATGAGTGTGTGAGACAGAGCT 720  
 DB 661 CATGCCGCGGCGCAGAGAGATCTGTGACCCGCGAGCATGAGTGTGTGAGACAGAGCT 720  
 QY 721 GTGTCTGGGGTCACTGACCAAAATGGCCACGCGGCGAGCAATGGGACCATCTGTGACA 780  
 DB 721 GTGTCTGGGGTCACTGACCAAAATGGCCACGCGGCGAGCAATGGGACCATCTGTGACA 780

QY 781 ACCAGAGGAGACTCCAGCCGCGGCTGTGCTGTGCTTCCAGAGAGGCTGTGTTCCTG 840  
 DB 781 ACCAGAGGAGACTCCAGCCGCGGCTGTGCTGTGCTTCCAGAGAGGCTGTGTTCCTG 840  
 QY 841 TGTGCAACCCCTGCGCGCGGAGGAGGAGCTTTGCAATGACCCCGCACCGGCTTCTGG 900  
 DB 841 TGTGCAACCCCTGCGCGCGGAGGAGGAGCTTTGCAATGACCCCGCACCGGCTTCTGG 900  
 QY 901 ACCCTATCACTGTGAGAGTATGAGAGCTGTGAGAGCTTGAACCGATGCTTGTGCAAGT 960  
 DB 901 ACCCTATCACTGTGAGAGTATGAGAGCTGTGAGAGCTTGAACCGATGCTTGTGCAAGT 960  
 QY 961 GCTCTCTTCCAGCCCGCACAGCAACGCTGTGTATGTGTGCAAGCCGACTTGTGTG 1020  
 DB 961 GCTCTCTTCCAGCCCGCACAGCAACGCTGTGTATGTGTGCAAGCCGACTTGTGTG 1020  
 QY 1021 GAGAGCGTGAACCAAGATGGGAGATCTGTGCGCCAGAGAGTCCCGATGATGAAAG 1080  
 DB 1021 GAGAGCGTGAACCAAGATGGGAGATCTGTGCGCCAGAGAGTCCCGATGATGAAAG 1080  
 QY 1081 TTGGAGCTTCAATGAGAGAGTGTGCGAGAGCTTGAAGACTTGAAGAGAGCTTGAATG 1140  
 DB 1081 TTGGAGCTTCAATGAGAGAGTGTGCGAGAGCTTGAAGAGCTTGAAGAGAGCTTGAATG 1140  
 QY 1141 AAGAGATGCGCGTGGGAGAGCTTGGCGGCTGCGCGCTGACCTGTGAGAGGAGAGAGA 1200  
 DB 1141 AAGAGATGCGCGTGGGAGAGCTTGGCGGCTGCGCGCTGACCTGTGAGAGGAGAGAGA 1200  
 QY 1201 TTTAGATCTGAGACCAAGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTC 1260  
 DB 1201 TTTAGATCTGAGACCAAGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTC 1260  
 QY 1261 GGTGTGTCTTGTAGCGTGTGGGCTGACAGGCTCTTCTCATCATCTTCCAGTAAGT 1320  
 DB 1261 GGTGTGTCTTGTAGCGTGTGGGCTGACAGGCTCTTCTCATCATCTTCCAGTAAGT 1320  
 QY 1321 TCCCTCTGTGCTTGAACAGATGAGAGTGTGTGCAATTTGTTCAAGCTCCCGAGCTGTT 1380  
 DB 1321 TCCCTCTGTGCTTGAACAGATGAGAGTGTGTGCAATTTGTTCAAGCTCCCGAGCTGTT 1380  
 QY 1381 CCAAGCTTCAACAGCTGTGTGCTTGGAGAGATGAGAGAGGTTAACTGAGAGAGAGTT 1440  
 DB 1381 CCAAGCTTCAACAGCTGTGTGCTTGGAGAGATGAGAGAGGTTAACTGAGAGAGAGTT 1440  
 QY 1441 GCAACCCCTGTCAAGATTAATGTGCTTGTGCTTCAACAGTGTGAGACAGCCGTTGT 1500  
 DB 1441 GCAACCCCTGTCAAGATTAATGTGCTTGTGCTTCAACAGTGTGAGACAGCCGTTGT 1500  
 QY 1501 TCTACATGCTTTGATTAATGTTTGAAGGAGAGATGAGAAACAAATGTGAGTCTCCCT 1560  
 DB 1501 TCTACATGCTTTGATTAATGTTTGAAGGAGAGATGAGAAACAAATGTGAGTCTCCCT 1560  
 QY 1561 TGATGTGTTTGGGAAATGTGAGAGAGATGCTGCTTGTGCAACATCACTGGCAA 1620  
 DB 1561 TGATGTGTTTGGGAAATGTGAGAGAGATGCTGCTTGTGCAACATCACTGGCAA 1620  
 QY 1621 AAATGCAACAAATGAATTTTCCAGAGCTTCTTCAATGGGAGATGAGTGTGCTT 1680  
 DB 1621 AAATGCAACAAATGAATTTTCCAGAGCTTCTTCAATGGGAGATGAGTGTGCTT 1680  
 QY 1681 CAGCTGTGAGATGAATGTTCTGTGCAACCTGCAATTACATGTTTATTCATCCAGCA 1740  
 DB 1681 CAGCTGTGAGATGAATGTTCTGTGCAACCTGCAATTACATGTTTATTCATCCAGCA 1740  
 QY 1741 GTGTGTCTCAGCTCTTACCTGTGTGCGAGGAGCAATTTCAATATCAATCAATTTCC 1800  
 DB 1741 GTGTGTCTCAGCTCTTACCTGTGTGCGAGGAGCAATTTCAATATCAATCAATTTCC 1800  
 QY 1801 TCTCTCAGACAGCTGTGGAGAGGAGGTCAATTGTCTCTCGTCCATCAGAGATCTCAG 1860  
 DB 1801 TCTCTCAGACAGCTGTGGAGAGGAGGTCAATTGTCTCTCGTCCATCAGAGATCTCAG 1860  
 QY 1861 GCTCAGAGACTGCAAGCTGCTTGGCCCAAGTCAACAGCTAGTGAACCAAGAGAGCTTC 1920

Db	1861	GCTCAGACACTGCAGAGCTGCTTGGCCAAAGTCAACAGCTAGTGAAGACAGAGAGATTTC	1920
Qy	1921	ATCTGGTTGTACTCTAAGCTCAAGTCTCTCTCCACTACACCCACACAGCCTTGTC	1980
Db	1921	ATCTGGTTGTACTCTAAGCTCAAGTCTCTCTCCACTACACCCACACAGCCTTGTC	1980
Qy	1981	CCAAAGAGCTCCCCAAAAGGAGAGAAATGGAAATTTTCTTGAGGATGACATCTGGA	2040
Db	1981	CCAAAGAGCTCCCCAAAAGGAGAGAAATGGAAATTTTCTTGAGGATGACATCTGGA	2040
Qy	2041	ATTAAGTCAAACTAATCTCAATCCCTCTAAAAGTAACTACTGTATGGAACAGAGT	2100
Db	2041	ATTAAGTCAAACTAATCTCAATCCCTCTAAAAGTAACTACTGTATGGAACAGAGT	2100
Qy	2101	GTTCCTCAGGTGGGCGAGCCGTCCTCTAATGAAGCAATGATATTGACACTGTCCT	2160
Db	2101	GTTCCTCAGGTGGGCGAGCCGTCCTCTAATGAAGCAATGATATTGACACTGTCCT	2160
Qy	2161	CTTTGGCAGTTGCATTAGTAACTTTGAAAGGATATGACTGAGGTAGCATACAGTTAA	2220
Db	2161	CTTTGGCAGTTGCATTAGTAACTTTGAAAGGATATGACTGAGGTAGCATACAGTTAA	2220
Qy	2221	CCTGCAGAAACAGTACTTAGTAAATTTGAGGCGAGATTATTAATGAATTTGC	2280
Db	2221	CCTGCAGAAACAGTACTTAGTAAATTTGAGGCGAGATTATTAATGAATTTGC	2280
Qy	2281	CAGTTAGCGACAGCACTGAGACAACTTATCAACAGGTGAGAAATCAAACGAGCAGGCG	2340
Db	2281	CAGTTAGCGACAGCACTGAGACAACTTATCAACAGGTGAGAAATCAAACGAGCAGGCG	2340
Qy	2341	TGTGTGAACATGTTGTATATGCGACTGCGAACACTGAACTCTACGCCCTCA	2400
Db	2341	TGTGTGAACATGTTGTATATGCGACTGCGAACACTGAACTCTACGCCCTCA	2400
Qy	2401	TGATGTTTTCAAGTGTCAATGACCTGTGCCACCAAGTATTAATCAGAGTCTTAAAGTT	2460
Db	2401	TGATGTTTTCAAGTGTCAATGACCTGTGCCACCAAGTATTAATCAGAGTCTTAAAGTT	2460
Qy	2461	TAAAGTGACATGATTTGTATAGCATGCTTCTTTGAGTTTAAATTATGTATTAACAT	2520
Db	2461	TAAAGTGACATGATTTGTATAGCATGCTTCTTTGAGTTTAAATTATGTATTAACAT	2520
Qy	2521	AAAGTGCATTTGAAATCAGACATTAATCATTCACTGCGCAAAAAAAAAAAAAA	2580
Db	2521	AAAGTGCATTTGAAATCAGACATTAATCATTCACTGCGCAAAAAAAAAAAAAA	2580
Qy	2581	AAAAAA 2586	
Db	2581	AAAAAA 2586	
RESULT 8			
ACAS8487			
ID	ACAS8487	standard; cDNA; 2586 BP.	
XX	ACAS8487;		
XX	10-JUN-2003 (first entry)		
DE	cDNA encoding human PRO polypeptide #41.		
XX	Human; secreted and transmembrane protein; PRO polypeptide; cancer;		
KW	Alzheimer's disease; ischaemia; cyostatic; nootropic; vasotropic;		
XX	neuroprotective; gene; ss.		
OS	Homo sapiens.		
XX	US2002192659-A1.		
PN	19-DEC-2002.		
PD	10-JUL-2001,2001US-0902853.		
XX			

XX 10-SEP-1998; 98WC-US18824.  
PR 14-SEP-1998; 98WC-US19177.  
PR 16-SEP-1998; 98WC-US19330.  
PR 17-SEP-1998; 98WC-US19437.  
PR 01-DEC-1998; 98WC-US25108.  
PR 08-SEP-1999; 99WC-US20594.  
PR 13-SEP-1999; 99WC-US20944.  
PR 15-SEP-1999; 99WC-US21090.  
PR 15-SEP-1999; 99WC-US21547.  
PR 03-OCT-1999; 99WC-US23889.  
PR 01-DEC-1999; 99WC-US28301.  
PR 02-DEC-1999; 99WC-US28564.  
PR 16-DEC-1999; 99WC-US30095.  
PR 20-DEC-1999; 99WC-US30911.  
PR 20-DEC-1999; 99WC-US30999.  
PR 03-JAN-2000; 2000WC-US00219.  
PR 11-FEB-2000; 2000WC-US03565.  
PR 22-FEB-2000; 2000WC-US04414.  
PR 28-JUL-2000; 2000WC-US20710.  
PR 24-AUG-2000; 2000WC-US23328.  
PR 17-SEP-1997; 97US-059113P.  
PR 17-SEP-1997; 97US-059115P.  
PR 17-SEP-1997; 97US-059117P.  
PR 18-SEP-1997; 97US-059266P.  
PR 15-OCT-1997; 97US-062125P.  
PR 17-OCT-1997; 97US-062285P.  
PR 17-OCT-1997; 97US-062287P.  
PR 21-OCT-1997; 97US-063486P.  
PR 24-OCT-1997; 97US-062814P.  
PR 24-OCT-1997; 97US-062816P.  
  
XX (GENTH ) GENENTECH INC.  
XX  
XX Ashkenazi A, Desnoyers L, Eaton DL, Ferrara N;  
PI Rikvaoroff E, Fong S, Gao W, Gerber H, Gerltsen ME, Goddard A;  
PI Godowski PJ, Grimaldi JC, Gunney AL, Hillan KJ, Kijavich IJ;  
PI Maher UP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumase D;  
PI Williams PM, Wood WI;  
XX  
XX WPI; 2003-361832/34.  
DR P-PSDB; ABU71465.  
XX  
XX New isolated nucleic acid encoding a PRO polypeptide, e.g., PRO245 or  
PT PRO1868, useful in molecular biology, chromosome and gene mapping, in  
PT generating antisense RNA and DNA, and in gene therapy  
XX  
XX Claim 2; Fig 83; 474pp; English.  
XX  
XX The present invention relates to the isolation of novel human secreted  
CC and transmembrane proteins (PRO polypeptides), and the polynucleotide  
CC sequences encoding them. The polynucleotide sequences are useful in  
CC molecular biology, as hybridisation probes, in chromosome and gene  
CC mapping, in generating antisense RNA and DNA, and in gene therapy. The  
CC polynucleotide sequences may also be used in preparing PRO polypeptides  
CC by recombinant techniques, and in generating either transgenic animals  
CC or knock-out animals which, in turn, are useful in the development and  
CC screening of therapeutically useful reagents. The PRO polypeptides or  
CC their antibodies are useful in preparing a medicament for treating a  
CC condition responsive to the polypeptide or antibody, such as cancer,  
CC Alzheimer's disease or ischaemia, and in various diagnostic assays.  
CC The present sequence encodes a human PRO polypeptide of the invention.  
XX  
XX Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;  
SQ  
Query Match 100.0%; Score 2586; DB 25; Length 2586;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps

QY	61	CCGGGCGGCTCCCGCGGGAGCGACAGATCCAGTCCGGCCCGGACCGCAACTCGGTCA	120
Db	61	CCGGGCGGCTCCCGCGGGAGCGACAGATCCAGTCCGGCCCGGACCGCAACTCGGTCA	120
QY	121	GTCCGGGCGCGCGCTGCCGGCGCAGAGCGAGATGACAGCGCTTGGGGCCCACTCGTGT	180
Db	121	GTCCGGGCGCGCGCTGCCGGCGCAGAGCGAGATGACAGCGCTTGGGGCCCACTCGTGT	180
QY	181	GCCTCTGCTGGCGCGCGGCGGTCCCCA-CGGGCCCGCGCGCTCCGACCGGCACTCGG	240
Db	181	GCCTCTGCTGGCGCGCGGCGGTCCCCA-CGGGCCCGCGCGCTCCGACCGGCACTCGG	240
QY	241	CTCCAGTCAAGCCCGGCCCCGCGCTCTCAAGTACCAGCAGAGGAGCCACCTCAATAGA	300
Db	241	CTCCAGTCAAGCCCGGCCCCGCGCTCTCAAGTACCAGCAGAGGAGCCACCTCAATAGA	300
QY	301	TGTTCCGGAGGTTTAGAGAACTGATGGAGGACAACGACACAAATTTGGCGACGGCGTGG	360
Db	301	TGTTCCGGAGGTTTAGAGAACTGATGGAGGACAACGACACAAATTTGGCGACGGCGTGG	360
QY	361	AAGAGATGAGGCGAGAGAGGCTGCTGCTAAAGCATCATCAGAAATGAACTCGGCAACT	420
Db	361	AAGAGATGAGGCGAGAGAGGCTGCTGCTAAAGCATCATCAGAAATGAACTCGGCAACT	420
QY	421	TACCTTCCAGCTTATCAAAATGAGACCAACAGACACGAGGTTGGAAATTAATACATCC	480
Db	421	TACCTTCCAGCTTATCAAAATGAGACCAACAGACACGAGGTTGGAAATTAATACATCC	480
QY	481	ATGTGCACCGAGAAATTCACAAGATPAAACCAACAACGACTGGAACAAATGGCTTTGAG	540
Db	481	ATGTGCACCGAGAAATTCACAAGATPAAACCAACAACGACTGGAACAAATGGCTTTGAG	540
QY	541	AGACAGTTATCACTCTGTGGGAGACGAAGAAAGCAAGAGGCCACGATGCATCATCG	600
Db	541	AGACAGTTATCACTCTGTGGGAGACGAAGAAAGCAAGAGGCCACGATGCATCATCG	600
QY	601	ACGAGACCTGTGGGCGCAGCATGTACTGTGCACTTGGCAGCTCCAGTACACTCGACGC	660
Db	601	ACGAGACCTGTGGGCGCAGCATGTACTGTGCACTTGGCAGCTCCAGTACACTCGACGC	660
QY	661	CATGCCGGGCGCAGAGATGCTCTTGCAACCCGGGACAGTGAAGTCTGTGGAGCAAGCTGT	720
Db	661	CATGCCGGGCGCAGAGATGCTCTTGCAACCCGGGACAGTGAAGTCTGTGGAGCAAGCTGT	720
QY	721	GTGTCTGGGGTACACAGCAACAAATGCGCCACAGGGGGCAGAAATGGGACCATCTAGTGA	780
Db	721	GTGTCTGGGGTACACAGCAACAAATGCGCCACAGGGGGCAGAAATGGGACCATCTAGTGA	780
QY	781	ACCAGAGGGACTGCCAGCCGGGGCTGTGTGTCTTCCAGAGAGGCGCTGTTCCTGT	840
Db	781	ACCAGAGGGACTGCCAGCCGGGGCTGTGTGTCTTCCAGAGAGGCGCTGTTCCTGT	840
QY	841	TGTGACACACCCCTGCCCGCTGAGGGCGAGCTTTGCCATGACCCCGCGACGGCGCTTTGG	900
Db	841	TGTGACACACCCCTGCCCGCTGAGGGCGAGCTTTGCCATGACCCCGCGACGGCGCTTTGG	900
QY	901	ACCTCATCACTGTGGAGGTAGAGCCTGTAGTGAAGCCTTGGACCGATGCCCTTGTGCAATG	960
Db	901	ACCTCATCACTGTGGAGGTAGAGCCTGTAGTGAAGCCTTGGACCGATGCCCTTGTGCAATG	960
QY	961	GCCTCTCTGCGCAGGCCCAACAGCCACAGCTGTGTGTATGTGTGCAAGCGGACCTTCGTGG	1020
Db	961	GCCTCTCTGCGCAGGCCCAACAGCCACAGCTGTGTGTATGTGTGCAAGCGGACCTTCGTGG	1020
QY	1021	GGAGCGGTGACCAAGATGGGGAGATCTGCTGCCAGAGAGGTCCCCGATGTAGTATGAG	1080
Db	1021	GGAGCGGTGACCAAGATGGGGAGATCTGCTGCCAGAGAGGTCCCCGATGTAGTATGAG	1080
QY	1081	TTGGAGCTTCAATGAGAGAGGTGCGCAGAGCTGAGAGACTTGGAGAGAGACTTGAATG	1140
Db	1081	TTGGAGCTTCAATGAGAGAGGTGCGCAGAGCTGAGAGACTTGGAGAGAGACTTGAATG	1140

QY	1141	AAGGATGAGGCGCTGGGGGAGCCTCGSSCTCCGCCCTGACCTGCGGAGGGGAGAGA	1200
Db	1141	AAGGATGAGGCGCTGGGGGAGCCTCGGCGCTCCGCCCTGACCTGCGGAGGGGAGAGA	1200
QY	1201	TTTAGATCTGGACCGAGCGCTGTGGGTATGTGCATAATGAATAGCTAATTAATTTCGCCA	1260
Db	1201	TTTAGATCTGGACCGAGCGCTGTGGGTATGTGCATAATGAATAGCTAATTAATTTCGCCA	1260
QY	1261	GGTGTGTGCTTTAAGCGTGGGCTGACCAAGCGCTTCTTCTACATCTCTTCCGATAGTT	1320
Db	1261	GGTGTGTGCTTTAAGCGCTGGGCTGACCAAGCGCTTCTTCTACATCTCTTCCGATAGTT	1320
QY	1321	TCCCGCTCGGCTTACAGCATAAGAGTGTGTGTGCAATTTGTTCAAGTCCCGCAGCGTCTCT	1380
Db	1321	TCCCGCTCGGCTTACAGCATAAGAGTGTGTGTGCAATTTGTTCAAGTCCCGCAGCGTCTCT	1380
QY	1381	CCAGGCTTACAGTCTGTGTGTGTGGGAGAGTCAAGGCGGTTAACTGACGAGACAGTTT	1440
Db	1381	CCAGGCTTACAGTCTGTGTGTGTGGGAGAGTCAAGGCGGTTAACTGACGAGAGCAATTT	1440
QY	1441	GCACCCCGCTGCGAGATTAATGAGTGTGCTTTGCGCTCTACAGTTGGGCGACAGCGCTTGT	1500
Db	1441	GCACCCCGCTGCGAGATTAATGAGTGTGCTTTGCGCTCTACAGTTGGGCGACAGCGCTTGT	1500
QY	1501	TCTACATGCTTTGATTAATGTTTGAGGGGAGAGATGAGAAACAATGTGAGTCTCCCTC	1560
Db	1501	TCTACATGCTTTGATTAATGTTTGAGGGGAGAGATGAGAAACAATGTGAGTCTCCCTC	1560
QY	1561	TGATTTGGTTTGGGGGAATGTGGAGAGAGTCCCGCTTTCGAAACATCAACCTGGGCAA	1620
Db	1561	TGATTTGGTTTGGGGGAATGTGGAGAGAGTCCCGCTTTCGAAACATCAACCTGGGCPA	1620
QY	1621	AAATGCAACAATTAATTTTCCACGACAGTCTTTCACATGGGCAATAGGTAAAGCTGTGCTT	1680
Db	1621	AAATGCAACAATTAATTTTCCACGACAGTCTTTCACATGGGCAATAGGTAAAGCTGTGCTT	1680
QY	1681	CAGCTGTTCAGATGAAATGTTCTGTTCACCTTCGATTAATGTGTTTATTCATCCGCA	1740
Db	1681	CAGCTGTTCAGATGAAATGTTCTGTTCACCTTCGATTAATGTGTTTATTCATCCAGCA	1740
QY	1741	GTGTTGCTCAGGCTCCCTACGCTGTGGCGAGGAGCATTTTTCATFATCCAAATCAATTCGCC	1800
Db	1741	GTGTTGCTCAGGCTCCCTACGCTGTGGCGAGGAGCATTTTTCATFATCCAAATCAATTCGCC	1800
QY	1801	TCTCTCAGCAAGCGCTGGGAGAGGGGGTCAATTTTCTCTCTGTCATCAGGATCTCAGAG	1860
Db	1801	TCTCTCAGCAAGCGCTGGGAGAGGGGGTCAATTTTCTCTCTGTCATCAGGATCTCAGAG	1860
QY	1861	GCTCAGAGACTGCAAGCTGTGCTTCCCAAGTCACACACTGATGTGAAGCCAGAGCAATTTTC	1920
Db	1861	GCTCAGAGACTGCAAGCTGTGCTTCCCAAGTCACACACTGATGTGAAGCCAGAGCAATTTTC	1920
QY	1921	ATCTGATGTGTACTCTTAAGCTCACTGTCTCTCTCACATACCCACACAGCGCTTGTGCCA	1980
Db	1921	ATCTGATGTGTACTCTTAAGCTCACTGTCTCTCTCACATACCCACACAGCGCTTGTGCCA	1980
QY	1981	CCAAAAGTGTCTCCCGAAAAGGAGAGAGATGGGATTTTTCTTGAGGATGACACTGTGGGA	2040
Db	1981	CCAAAAGTGTCTCCCGAAAAGGAGAGAGATGGGATTTTTCTTGAGGATGACACTGTGGGA	2040
QY	2041	ATTAAAGGTCAACTAATTTCTCACTCCCTCTAAAGTAACCTACTGTGTAGGACAGCAGT	2100
Db	2041	ATTAAAGGTCAACTAATTTCTCACTCCCTCTAAAGTAACCTACTGTGTAGGACAGCAGT	2100
QY	2101	GTTCCTCAGTGTGGGGGAGCGCTTCTTCTAATGAAGACAATGATTTGACCTGTCCCT	2160
Db	2101	GTTCCTCAGTGTGGGGGAGCGCTTCTTCTAATGAAGACAATGATTTGACCTGTCCCT	2160
QY	2161	CTTTGGCAGTTGCAATTAGTAACTTTGAAAGGTATATGACTGAGCGTGTGACATCAGGTTAA	2220
Db	2161	CTTTGGCAGTTGCAATTAGTAACTTTGAAAGGTATATGACTGAGCGTGTGACATCAGGTTAA	2220
QY	2221	CCTGAGAGAACGTAAGTAATTTAGGGCGAGAGTTATTAATGAATTTTGCAGAAAT	2280

```

Db      2221 CCTGCGAAACGCTCTTGGTATTTGAGGCGAGATTAATGAAATTTGCAAAAT 2280
QY      2281 CACTTAGCAGCACTGAGAGCAATTAATCAACCGTGGAGAAATCAACCGAGAGGCG 2340
Db      2281 CACTTAGCAGCACTGAGAGCAATTAATCAACCGTGGAGAAATCAACCGAGAGGCG 2340
QY      2341 TGTGTGAAACATGCTGTATATGATGCACTGCGAACACTGACCTTACGCACTTCAAAA 2400
Db      2341 TGTGTGAAACATGCTGTATATGATGCACTGCGAACACTGACCTTACGCACTTCAAAA 2400
QY      2401 TGAATGTTTCAGTGTGATGATGCACTGTTGCAACGATGATTAATCAAGAGTTCTTAAAGT 2460
Db      2401 TGAATGTTTCAGTGTGATGATGCACTGTTGCAACGATGATTAATCAAGAGTTCTTAAAGT 2460
QY      2461 TAAAGTTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
Db      2461 TAAAGTTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
QY      2521 AAGTTCATTTAGAAATCAAGCATTAATCACTCACTCACTCACTCACTCACTCACTCACTCACT 2580
Db      2521 AAGTTCATTTAGAAATCAAGCATTAATCACTCACTCACTCACTCACTCACTCACTCACTCACT 2580
QY      2581 AAAAAA 2586
Db      2581 AAAAAA 2586

RESULT 9
ACAS8813
ID ACAS8813 standard; cDNA, 2586 BP.
XX
AC ACAS8813;
XX
DT 10-JUN-2003 (first entry)
XX
DE cDNA encoding human secreted polypeptide PRO295.
XX
XX Human; ss; gene; gene therapy; tumour; cancer.
XX
OS Homo sapiens.
XX
PN US2003013855-A1.
XX
PD 16-JAN-2003.
XX
PF 03-MAY-2002; 2002US-0063616.
XX
PR 30-DEC-1998; 98KR-0062142.
PR 08-MAR-1999; 99MO-US05028.
PR 14-MAY-1999; 99MO-US10733.
PR 30-DEC-1999; 99MO-US31274.
PR 18-FEB-2000; 2000WO-US04341.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 21-MAR-2000; 2000WO-US07532.
PR 22-MAY-2000; 2000WO-US14042.
PR 02-JUN-2000; 2000WO-US15264.
PR 24-AUG-2000; 2000WO-US2328.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US11820.
PR 14-MAY-1999; 99US-0311832.
PR 25-AUG-1999; 99US-0380137.
PR 25-AUG-1999; 99US-0380138.
PR 25-AUG-1999; 99US-0380139.
PR 25-AUG-1999; 99US-0380142.
PR 15-SEP-1999; 99US-0397342.
PR 18-OCT-1999; 99US-0403297.
PR 12-NOV-1999; 99US-0423844.
PR 22-AUG-2000; 2000US-0644848.

```

```

BR      18-SEP-2000; 2000US-0664510.
PR      18-SEP-2000; 2000US-0665350.
PR      08-NOV-2000; 2000US-0709238.
PR      20-DEC-2000; 2000US-0747259.
PR      22-MAR-2001; 2001US-0816744.
PR      10-MAY-2001; 2001US-0854208.
PR      10-MAY-2001; 2001US-0854280.
PR      30-MAY-2001; 2001US-0870574.
PR      05-JUN-2001; 2001US-0874503.
PR      29-JUN-2001; 2001US-0869599.
PR      18-JUL-2001; 2001US-0908827.
PR      06-DEC-2001; 2001US-0006867.
XX
XX (GENTECH ) GENENTECH INC.
XX
PA Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Garney AL, Macanabe CK, Wood WI;
XX
XX WPI; 2003-330485/31.
DR      P-PSDB; ABU71509.
XX
XX
XX New isolated antibody specifically binding a PRO polypeptide, useful
PT for the preparation of a medicament for treating disorders with the
PT aberrant expression or activity of the PRO polypeptide, such as tumor
PT conditions and cancer.
XX
XX
XX Example 4; Page 71-72; 406bp; English.
PS
XX
XX The invention relates to an antibody that binds to a polypeptide with a
CC fully defined sequence given in the specification. The methods and
CC compositions (containing antibodies that specifically bind a PRO
CC polypeptide) of the present invention are useful for the preparation of a
CC medicament for the treatment of disorders associated with the aberrant
CC expression or activity of the PRO polypeptide, such as tumor conditions
CC and cancer. They can also be used to generate transgenic or knockout
CC animals useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptide and encoding nucleic acids can be used as
CC molecular weight markers for protein electrophoresis, chromosome
CC identification and tissue typing. The PRO polypeptides are useful to
CC induce angiogenesis e.g wound healing, in the treatment of sports-related
CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The
CC antibodies may be used in various diagnostic, competitive binding and/or
CC immunoprecipitation assays. The present sequence represents a cDNA
CC encoding a PRO polypeptide of the invention.
XX
XX
SQ      Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 2586; DB 25; Length 2586;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 CGCGCGCTCCCGCAACCGCGGCGCCGCCACCGCGCGCTCCCGCACTGACCCGAGC 60
Db      1 CGCGCGCTCCCGCAACCGCGGCGCCGCCACCGCGCGCTCCCGCACTGACCCGAGC 60
QY      61 CGCGCGCTCCCGCGGAGCGAGATCACTCCGCGCCCGCGAGCGCAACTCGGTCA 120
Db      61 CGCGCGCTCCCGCGGAGCGAGATCACTCCGCGCCCGCGAGCGCAACTCGGTCA 120
QY      121 GTCGGCGCGCGGCTCGCGGCGAGCGAGATGACGCGGCTTGGGCGCACTCTGCTGT 180
Db      121 GTCGGCGCGCGGCTCGCGGCGAGCGAGATGACGCGGCTTGGGCGCACTCTGCTGT 180
QY      181 GCGTGTGCTGCGCGCGCGGCTCCCAAGCGCGCGCGCGCGCGCTCGGAGCGGAGCTCGG 240
Db      181 GCGTGTGCTGCGCGCGCGGCTCCCAAGCGCGCGCGCGCGCGCTCGGAGCGGAGCTCGG 240
QY      241 CTCGAGTCAGACCCCGCGCGCTCTGAGCTACCGGAGAGAGAGGCAACCTCAATAGA 300
Db      241 CTCGAGTCAGACCCCGCGCGCTCTGAGCTACCGGAGAGAGAGGCAACCTCAATAGA 300
QY      301 TGTTCGCGAGAGTTGAGGAATGATGAGAGACGACGACCAAAATTGCGCAGCGCGGTGG 360

```

Db 301 TGTTCGCGAGGTTGAGAACTGATGAGAGACCGCAGCAAAATTCGCGACGGGTGG 360  
QY AAGAGATGAGGCGAGAAAGAGCTGTCTAAAGCATCATCAGAAGTGAACCTGGCAAACT 420  
Db 361 AAGAGATGAGGCGAGAAAGAGCTGTCTAAAGCATCATCAGAAGTGAACCTGGCAAACT 420  
QY 421 TACCTCCGAGCTATCAATGAGACCAACAGACAGCAAGGTTGGAAATTAATACATCC 480  
Db 421 TACCTCCGAGCTATCAATGAGACCAACAGACAGCAAGGTTGGAAATTAATACATCC 480  
QY 481 ATGTGACCGAGAAATTCACAAAGATTAACCAACAGACAGCTGAGCAAAATGTCTTTTGG 540  
Db 481 ATGTGACCGAGAAATTCACAAAGATTAACCAACAGACAGCTGAGCAAAATGTCTTTTGG 540  
QY 541 AGCAATTTATCAATCTGTGGGAGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
Db 541 AGCAATTTATCAATCTGTGGGAGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
QY 601 ACAGAGACTGTGGGCGCAGACATGTGACAGTTTGCAGCTTCCAGTACACTGCGACG 660  
Db 601 ACAGAGACTGTGGGCGCAGACATGTGACAGTTTGCAGCTTCCAGTACACTGCGACG 660  
QY 661 CATGCCGGGGCCAGAGAGATGCTGTGCAACCGGAGCATGAGTGTGTGGAGACAGCTGT 720  
Db 661 CATGCCGGGGCCAGAGAGATGCTGTGCAACCGGAGCATGAGTGTGTGGAGACAGCTGT 720  
QY 721 GTGTCTGGGGTCACTGACCAAAATGCGCAGCAGGGGAGCAATGGGACATCTGTGACA 780  
Db 721 GTGTCTGGGGTCACTGACCAAAATGCGCAGCAGGGGAGCAATGGGACATCTGTGACA 780  
QY 781 ACCAGAGGAGCTGCGACCGCGGGCTGTGTGTGCTTCCAGAGAGGCTGTGTTCCCTG 840  
Db 781 ACCAGAGGAGCTGCGACCGCGGGCTGTGTGTGCTTCCAGAGAGGCTGTGTTCCCTG 840  
QY 841 TGTGCAACACCCCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900  
Db 841 TGTGCAACACCCCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900  
QY 901 ACCTCATCACTGTGGAGCTAGAGCCTGATGAGCCTTGGACCGATGCTTGTGCGAGTG 960  
Db 901 ACCTCATCACTGTGGAGCTAGAGCCTGATGAGCCTTGGACCGATGCTTGTGCGAGTG 960  
QY 961 GCTCTCTGTGCGACGCGCCACAGCAGCAGCCTGTGTGTGTGCGAGCAGCAGCAGCAG 1020  
Db 961 GCTCTCTGTGCGACGCGCCACAGCAGCAGCCTGTGTGTGTGCGAGCAGCAGCAGCAG 1020  
QY 1021 GAGACCGGTGACCAAGATGGGGAGATCTGTCTGCCAGAGAGGTTCCCGCATGATGAAG 1080  
Db 1021 GAGACCGGTGACCAAGATGGGGAGATCTGTCTGCCAGAGAGGTTCCCGCATGATGAAG 1080  
QY 1081 TTGGCAGCTTTCATGAGAGAGTGTGCGCAGAGAGTGGAGAGCTTGGAGAGAGAGCTG 1140  
Db 1081 TTGGCAGCTTTCATGAGAGAGTGTGCGCAGAGAGTGGAGAGCTTGGAGAGAGAGCTG 1140  
QY 1141 AAGAGATGAGGCGTGGGAGAGCTGTGCGGCTGCGCAGCTGACATGTGCGGAGGAGAG 1200  
Db 1141 AAGAGATGAGGCGTGGGAGAGCTGTGCGGCTGCGCAGCTGACATGTGCGGAGGAGAG 1200  
QY 1201 TTTAGATCTGAGACAGAGCTGTGGGTGATGTGCAATGAATAGCTAATTTATTTCCCA 1260  
Db 1201 TTTAGATCTGAGACAGAGCTGTGGGTGATGTGCAATGAATAGCTAATTTATTTCCCA 1260  
QY 1261 GGTGTGTGCTTTGAGGCTGAGCAGAGCTTCTTCTCAATCTTCTTCCAGTAAGTT 1320  
Db 1261 GGTGTGTGCTTTGAGGCTGAGCAGAGCTTCTTCTCAATCTTCTTCCAGTAAGTT 1320  
QY 1321 TCCCTCTGTGCTTGTGACAGATGAGTGTGTGCAATTTGTTCAGCTCCCGCAGGCTGTCT 1380  
Db 1321 TCCCTCTGTGCTTGTGACAGATGAGTGTGTGCAATTTGTTCAGCTCCCGCAGGCTGTCT 1380  
QY 1381 CCGAGCTTCAAGTCTGTGTGCTTGGGAGTCAAGGAGGTTAACTGAGAGAGAGTTT 1440  
Db 1381 CCGAGCTTCAAGTCTGTGTGCTTGGGAGTCAAGGAGGTTAACTGAGAGAGAGTTT 1440

Db 1381 CCGAGCTTCAAGTCTGTGTGCTTGGGAGTCAAGGAGGTTAACTGAGAGAGAGTTT 1440  
QY 1441 GCCACCCCTGTCCAGATTAATTTGCTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 1500  
Db 1441 GCCACCCCTGTCCAGATTAATTTGCTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 1500  
QY 1501 TCTACATGCTTGTGATTAATTTGTTGAGGGGAGGAGATGAGAAATGATGAGTCTGCTC 1560  
Db 1501 TCTACATGCTTGTGATTAATTTGTTGAGGGGAGGAGATGAGAAATGATGAGTCTGCTC 1560  
QY 1561 TGAATGTTTGGGAGAAATGTGAGAGAGATGCTGCTTGTGCAAAATCACTGAGGCA 1620  
Db 1561 TGAATGTTTGGGAGAAATGTGAGAGAGATGCTGCTTGTGCAAAATCACTGAGGCA 1620  
QY 1621 AAATGCAACAAATGAATTTTCCAGAGCTTCTTCCATGAGGAGTATGATGCTGTGCTT 1680  
Db 1621 AAATGCAACAAATGAATTTTCCAGAGCTTCTTCCATGAGGAGTATGATGCTGTGCTT 1680  
QY 1681 CAGCTGTTGAGATGAATGTTCTGTTCACCTGCAATTCATGATGTTTATTCACAGCA 1740  
Db 1681 CAGCTGTTGAGATGAATGTTCTGTTCACCTGCAATTCATGATGTTTATTCACAGCA 1740  
QY 1741 GTGTGCTCAGCTTCTTACCTGTGCGAGGAGCATTTTCAATTCAGATCAATTTCC 1800  
Db 1741 GTGTGCTCAGCTTCTTACCTGTGCGAGGAGCATTTTCAATTCAGATCAATTTCC 1800  
QY 1801 TCTCTCAGCAGGCTGGGAGGAGGAGGAGTATGTTCTCTGCTGCTCATCAGGAGTCTCAG 1860  
Db 1801 TCTCTCAGCAGGCTGGGAGGAGGAGGAGTATGTTCTCTGCTGCTCATCAGGAGTCTCAG 1860  
QY 1861 GCTCAGAGACTGCAAGCTGCTTGCACAGTCAACAGTATGTAAGACACAGAGCAATTC 1920  
Db 1861 GCTCAGAGACTGCAAGCTGCTTGCACAGTCAACAGTATGTAAGACACAGAGCAATTC 1920  
QY 1921 ATCTGATGATGATCTTAAGTCAAGTGTCTTCCAGTCAACAGCTTGTGAGGAGGAG 1980  
Db 1921 ATCTGATGATGATCTTAAGTCAAGTGTCTTCCAGTCAACAGCTTGTGAGGAGGAG 1980  
QY 1981 CCAAAAGTGTCTCCCAAAAGAGAGAGATGAGATTTTCTTGAAGGATGACATCTGGA 2040  
Db 1981 CCAAAAGTGTCTCCCAAAAGAGAGAGATGAGATTTTCTTGAAGGATGACATCTGGA 2040  
QY 2041 ATTAAGGTCAAACTTAATTTCAATCCTCTTAATGAAGTAACTGTTGAGGAGGAG 2100  
Db 2041 ATTAAGGTCAAACTTAATTTCAATCCTCTTAATGAAGTAACTGTTGAGGAGGAG 2100  
QY 2101 GTTCTCAGATGTGGGAGCAGCTGCTTCTTAATGAAGCAATGATATGCACTGTCCCT 2160  
Db 2101 GTTCTCAGATGTGGGAGCAGCTGCTTCTTAATGAAGCAATGATATGCACTGTCCCT 2160  
QY 2161 CTTTGGAGTTGATTAATGTAATTTGAAAGTATGATGAGAGCTGAGAGCTGAGAGGTTA 2220  
Db 2161 CTTTGGAGTTGATTAATGTAATTTGAAAGTATGATGAGAGCTGAGAGCTGAGAGGTTA 2220  
QY 2221 CTTGCAAGAAACAGTACTTAAGTATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2280  
Db 2221 CTTGCAAGAAACAGTACTTAAGTATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2280  
QY 2281 CACTTACAGCAACTGAAGCAATTTATCAACAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340  
Db 2281 CACTTACAGCAACTGAAGCAATTTATCAACAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340  
QY 2341 TGTGTGAACATGTTGATTAATGAGAGCTGAGCACTGAGACTGAGCACTGAGCACTG 2400  
Db 2341 TGTGTGAACATGTTGATTAATGAGAGCTGAGCACTGAGACTGAGCACTGAGCACTG 2400  
QY 2401 TGAATGTTTCAAGTGTATGAGAGCTGTTGCGACATGATTAATTCAGAGTCTTAAAGTT 2460  
Db 2401 TGAATGTTTCAAGTGTATGAGAGCTGTTGCGACATGATTAATTCAGAGTCTTAAAGTT 2460  
QY 2461 TAAAGTTGACATGATGATTAAGAGTCTTCTTGAAGTAAATTAATTAATTAATTAAT 2520  
Db 2461 TAAAGTTGACATGATGATTAAGAGTCTTCTTGAAGTAAATTAATTAATTAATTAAT 2520



```

QY      2521  AGGTGATTAGAAATCAAGCATTAATCACTTCAACTGCAGCAAAAAAAAAAAAAAAAAAAAA 2580
Db      2521  AGGTGATTAGAAATCAAGCATTAATCACTTCAACTGCAGCAAAAAAAAAAAAAAAAAAAAA 2580
QY      2581  AAAAAA 2586
Db      2581  AAAAAA 2586

RESULT 10
ACb60194
ID      ACA60194 standard; cDNA; 2586 BP.
XX
XX      ACA60194;
XX
XX      12-JUN-2003 (first entry)
XX
XX      Human cDNA for secreted/transmembrane protein PRO25.
XX
XX      Human; ss; gene; secreted protein; transmembrane protein; PRO;
XX      gene therapy; chromosome identification; chromosome marker.
XX
XX      Homo sapiens.
XX
XX      US2003003530-A1.
XX
XX      02-JAN-2003.
XX
XX      11-JUL-2001; 2001US-0904011.
XX
XX      10-SEP-1998; 98WO-US16824.
XX      14-SEP-1998; 98WO-US19177.
XX      16-SEP-1998; 98WO-US19330.
XX      17-SEP-1998; 98WO-US19437.
XX      01-DEC-1998; 98WO-US25108.
XX      08-SEP-1999; 99WO-US20594.
XX      13-SEP-1999; 99WO-US20944.
XX      15-SEP-1999; 99WO-US21090.
XX      15-SEP-1999; 99WO-US21547.
XX      05-OCT-1999; 99WO-US23089.
XX      29-NOV-1999; 99WO-US28214.
XX      30-NOV-1999; 99WO-US28313.
XX      01-DEC-1999; 99WO-US28301.
XX      02-DEC-1999; 99WO-US28564.
XX      02-DEC-1999; 99WO-US28565.
XX      16-DEC-1999; 99WO-US30095.
XX      20-DEC-1999; 99WO-US30911.
XX      20-DEC-1999; 99WO-US30919.
XX      05-JAN-2000; 2000WO-US00219.
XX      11-FEB-2000; 2000WO-US03565.
XX      22-FEB-2000; 2000WO-US04414.
XX      24-FEB-2000; 2000WO-US05004.
XX      02-MAR-2000; 2000WO-US05841.
XX      20-MAR-2000; 2000WO-US07377.
XX      30-MAR-2000; 2000WO-US08439.
XX      22-MAY-2000; 2000WO-US14042.
XX      02-JUN-2000; 2000WO-US15264.
XX      28-JUL-2000; 2000WO-US20710.
XX      24-AUG-2000; 2000WO-US23328.
XX      17-SEP-1997; 97US-0591139.
XX      17-SEP-1997; 97US-0591159.
XX      17-SEP-1997; 97US-0591179.
XX      17-SEP-1997; 97US-0591199.
XX      17-SEP-1997; 97US-0591219.
XX      17-SEP-1997; 97US-0591229.
XX      17-SEP-1997; 97US-0591849.
XX      18-SEP-1997; 97US-0592639.
XX      18-SEP-1997; 97US-0592669.
XX      15-OCT-1997; 97US-0621259.
XX      17-OCT-1997; 97US-0622859.
XX      17-OCT-1997; 97US-0622879.
XX      21-OCT-1997; 97US-0634869.

```

```

PR      24-OCT-1997; 97US-0628149.
PR      24-OCT-1997; 97US-0628169.
PR      24-OCT-1997; 97US-0630459.
PR      24-OCT-1997; 97US-0631209.
PR      24-OCT-1997; 97US-0631219.
PR      24-OCT-1997; 97US-0631279.
PR      24-OCT-1997; 97US-0631289.
PR      27-OCT-1997; 97US-0633279.
PR      27-OCT-1997; 97US-0633299.
PR      28-OCT-1997; 97US-0635419.
PR      28-OCT-1997; 97US-0635449.
PR      28-OCT-1997; 97US-0635499.
PR      28-OCT-1997; 97US-0635509.
PR      28-OCT-1997; 97US-0635569.
PR      29-OCT-1997; 97US-0634359.
PR      29-OCT-1997; 97US-0637049.
PR      29-OCT-1997; 97US-0637329.
PR      29-OCT-1997; 97US-0637349.
PR      29-OCT-1997; 97US-0637359.
PR      29-OCT-1997; 97US-0637389.
PR      29-OCT-1997; 97US-0642159.
PR      31-OCT-1997; 97US-0638709.
PR      03-NOV-1997; 97US-0641039.
PR      07-NOV-1997; 97US-0642489.
PR      12-NOV-1997; 97US-0648099.
PR      17-NOV-1997; 97US-0651869.
PR      18-NOV-1997; 97US-0658469.
PR      21-NOV-1997; 97US-0661209.
PR      21-NOV-1997; 97US-0663649.
PR      24-NOV-1997; 97US-0664539.
PR      24-NOV-1997; 97US-0664669.
PR      24-NOV-1997; 97US-0665119.
PR      24-NOV-1997; 97US-0667709.
PR      18-SEP-2000; 2000US-0665350.
XX
XX      (GENTH ) GENENTECH INC.
XX
XX      Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N,
XX      Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
XX      Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kilaavin J,
XX      Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D,
XX      Williams PM, Wood WI;
XX      WPI; 2003-329602/31.
XX      P-PSDB; AB071931.
XX
XX      New transmembrane polypeptides and nucleic acids encoding the
XX      polypeptides, useful in gene therapy, in chromosome identification, as
XX      chromosome markers, in generating probes and in tissue typing
XX
XX      Claim 2, Fig 83; 484pp; English.
XX
XX      The invention relates to an isolated nucleic acid with at least 80%
XX      nucleic acid sequence identity to a nucleotide sequence encoding one of
XX      61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
XX      PRO protein extracellular domain. Also included are a vector comprising
XX      the PRO nucleic acid, a host cell comprising the vector, producing a PRO
XX      polypeptide (by culturing the host cell for the expression of the PRO
XX      polypeptide, and recovering the host cell from the cell culture),
XX      an isolated PRO polypeptide (having at least 80% sequence identity
XX      to: (a) an amino acid sequence selected from the 61 PRO proteins;
XX      (b) an amino acid sequence encoded by a nucleic acid molecule deposited
XX      with an ATCC number (detailed in the specification); or (c) an
XX      extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking
XX      its associated signal peptide), a chimeric molecule comprising a PRO
XX      polypeptide of fused to a heterologous amino acid sequence, an anti-PRO
XX      antibody, detecting a PRO245 or PRO1868 in a sample suspected of
XX      containing the polypeptide, linking a bioactive molecule to a cell
XX      expressing a PRO245 or PRO1868 and modulating at least one biological
XX      activity of a cell expressing a PRO245 or PRO1868. Nucleic acids which

```



```

QY 1921 ATCTGGTGTGACTTAAGCTCAGTGTCTCTCCACTACCCACACAGCCTTGATCCA 1980
DB 1921 ATCTGGTGTGACTTAAGCTCAGTGTCTCTCCACTACCCACACAGCCTTGATCCA 1980
QY 1981 CCAAAAGTGTCTCCCAAAAGGAGAGAAATGGGATTTTCTTAAAGCATGCACTGTGGA 2040
DB 1981 CCAAAAGTGTCTCCCAAAAGGAGAGAAATGGGATTTTCTTAAAGCATGCACTGTGGA 2040
QY 2041 ATTAAGGTCAAACTAATTTCTCACATCCCTCTAAAGAACTACTGTAGAAACAGACAGT 2100
DB 2041 ATTAAGGTCAAACTAATTTCTCACATCCCTCTAAAGAACTACTGTAGAAACAGACAGT 2100
QY 2101 GTTCTCAGAGTGGGGGACCGCTCTCTTAATGAAGACATATATGACACTGTCCCT 2160
DB 2101 GTTCTCAGAGTGGGGGACCGCTCTCTTAATGAAGACATATATGACACTGTCCCT 2160
QY 2161 CTATTGGCAGTTGCATTAGTAATTTGAAAGATATGACTGAGCGTATACAGGTTAA 2220
DB 2161 CTATTGGCAGTTGCATTAGTAATTTGAAAGATATGACTGAGCGTATACAGGTTAA 2220
QY 2221 CTGCGAGAAACAGTACTTAAAGTAATTTGAGGGCGAGGATTATTAATGAATTTGCAAAAT 2280
DB 2221 CTGCGAGAAACAGTACTTAAAGTAATTTGAGGGCGAGGATTATTAATGAATTTGCAAAAT 2280
QY 2281 CACTTACGACCACTGAAGACATTTATCAACACGCGGAGAAATGAATGAACCGGACGAGGCG 2340
DB 2281 CACTTACGACCACTGAAGACATTTATCAACACGCGGAGAAATGAATGAACCGGACGAGGCG 2340
QY 2341 TGTGTGAACAGTGTGTATATGCGACTGCGAACACTGAATCTTACCGCACTCCACAAA 2400
DB 2341 TGTGTGAACAGTGTGTATATGCGACTGCGAACACTGAATCTTACCGCACTCCACAAA 2400
QY 2401 TGAATGTTTGAAGTGTGCATGAGTGTGCGACCATGTATTCACCCGAGTTCTTAAAGT 2460
DB 2401 TGAATGTTTGAAGTGTGCATGAGTGTGCGACCATGTATTCACCCGAGTTCTTAAAGT 2460
QY 2461 TAAAGTTGCATGATGTATTAAGCATGCTTCTTGAAGTTAAATTAATTAATTAACAT 2520
DB 2461 TAAAGTTGCATGATGTATTAAGCATGCTTCTTGAAGTTAAATTAATTAATTAACAT 2520
QY 2521 AAATGTGATTTAAGTAATCAAGCATTAATCACTTCAACTGCAAAAAA 2580
DB 2521 AAATGTGATTTAAGTAATCAAGCATTAATCACTTCAACTGCAAAAAA 2580
QY 2581 AAAAAA 2586
DB 2581 AAAAAA 2586

```

```

RESULT 11
ID ACA60366 standard; cDNA; 2586 BP.
AC ACA60366;
XX
XX
XX 11-JUN-2003 (first entry)
XX
XX
XX Novel human secreted and transmembrane protein PRO295 cDNA.
XX
XX Human: secreted and transmembrane polypeptide; gene; seq.
XX chromosome mapping; gene mapping; transgenic animal; knockout animal;
XX therapeutic agent screening; chromosome identification; tissue typing;
XX gene therapy.
XX
XX Homo sapiens.
XX
XX US2003018183-A1.
XX
XX 23-JAN-2003.
XX
XX 01-MAY-2002; 2002US-0063512.
XX
XX 06-DEC-2001; 2001US-0006867.
XX

```

```

XX (GETH ) GENENTECH INC.
PA
XX
XX Eaton DL, Filvarcoff E, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gunney AL, Watanabe CK, Wood WI,
XX WPI; 2003-330984/31.
XX P-PsDB; ABU71955.
XX
XX New secreted and transmembrane PRO polypeptides and nucleic acid
XX molecules encoding the polypeptides, useful in gene therapy or
XX PT preparing a medicament for treating a condition that is responsive to
XX the PRO polypeptide or antibody
XX
XX Disclosure; Fig 7; 409pp; English.
XX
XX The invention describes novel isolated PRO polypeptides. The PRO
XX polypeptides or anti-PRO antibodies are useful in preparing a medicament
XX for treating a condition that is responsive to the PRO polypeptide or
XX antibody. The PRO nucleotide sequences may be used as hybridisation
XX probes in chromosome and gene mapping, or in generating antisense RNA
XX and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,
XX in assays to identify other proteins or molecules involved in binding
XX reaction, to generate transgenic animals or knockout animals, which in
XX turn are useful in the development and screening of therapeutically
XX useful reagents, for chromosome identification, and tissue typing. The
XX PRO polypeptides and nucleic acid molecules are also useful in gene
XX therapy, and as molecular weight markers for protein electrophoresis
XX purposes. The anti-PRO antibodies may be used in diagnostic assays for
XX CC PRO, or for the affinity purification of PRO from recombinant cell
XX CC culture or natural sources. This sequence encodes a novel human
XX secreted and transmembrane PRO polypeptide.
XX
XX Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;
XX

```

```

Query Match 100.0%; Score 2586; DB 25; Length 2586;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 CGCGGCGCTCCCGGACCCGCGCCGACACCGCGCGCTCCCGCATGTGACCCGAGC 60
DB 1 CGCGGCGCTCCCGGACCCGCGCCGCGCCGCGCGCTCCCGCATGTGACCCGAGC 60
QY 61 CGCGGCGCTCCCGGAGCGAGCATGCTCCGCGCCGCGAGCGCACTCGATCCA 120
DB 61 CGCGGCGCTCCCGGAGCGAGCATGCTCCGCGCCGCGAGCGCACTCGATCCA 120
QY 121 GTCGGGGCGGCGCTGCGGGCGGAGCGAGATGCAAGCGGCTTGGGGCCACTGCTGT 180
DB 121 GTCGGGGCGGCGCTGCGGGCGGAGCGAGATGCAAGCGGCTTGGGGCCACTGCTGT 180
QY 181 GCTGCTGCTGCGGGCGGCTCCCAAGCGGCGCCGCGCGCTCCCAAGCGGCGACTCGG 240
DB 181 GCTGCTGCTGCGGGCGGCTCCCAAGCGGCGCCGCGCGCTCCCAAGCGGCGACTCGG 240
QY 241 CTCAAGTCAAGCCCGGCGGCTTCAAGCTACCGCGAGAGAGGCGCACTCTCAATGAGA 300
DB 241 CTCAAGTCAAGCCCGGCGGCTTCAAGCTACCGCGAGAGAGGCGCACTCTCAATGAGA 300
QY 301 TGTTCGCGGAGGTGAGGAACTGATGAGAGACGACGACAAATTTGCGACCGCGGTGG 360
DB 301 TGTTCGCGGAGGTGAGGAACTGATGAGAGACGACGACAAATTTGCGACCGCGGTGG 360
QY 361 AAGAGATGAGGCGAGAGAGCTGCTGTAAGCATCATCAAGATGAGAACTGCGAAACT 420
DB 361 AAGAGATGAGGCGAGAGAGCTGCTGTAAGCATCATCAAGATGAGAACTGCGAAACT 420
QY 421 TACCTCCAGCTATCACAATGAGCAACAACAGACAGAAAGTTGAAATTAATACGATCC 480
DB 421 TACCTCCAGCTATCACAATGAGCAACAACAGACAGAAAGTTGAAATTAATACGATCC 480
QY 481 ATGTGACCGGAAATTTCAAGATTAACAAACAACAGACTGAGCAATGCTTTTONG 540
DB 481 ATGTGACCGGAAATTTCAAGATTAACAAACAACAGACTGAGCAATGCTTTTONG 540

```



[illegible]

Db	301	TTGTTCCGCGAGGTTGAGGAATCTAATGGAGGACACGCGACCAATTTGCGAGCGGGTGG	360
Qy	361	AAGAGATGAGGCGAGAAAGAGCTGCTCTAAGCATCATCAAGATGAACTGGCAAACT	420
Db	361	AAGAGATGAGGCGAGAAAGAGCTGCTCTAAGCATCATCAAGATGAACTGGCAAACT	420
Qy	421	TACCTCCCACTATCACAATGAGACCAACAGACAGAAAGTTGAAATATACATCC	480
Db	421	TACCTCCCACTATCACAATGAGACCAACAGACAGAAAGTTGAAATATACATCC	480
Qy	481	ATGTGCAACCGAAGAAATTCACAAATTAACCAACCACTGGAACAATGTCTTTTCAG	540
Db	481	ATGTGCAACCGAAGAAATTCACAAATTAACCAACCACTGGAACAATGTCTTTTCAG	540
Qy	541	AGACAGTTATACACTCTGTGGGAGACGAAAGGACGAAAGAGCAAGATGCATATCG	600
Db	541	AGACAGTTATACACTCTGTGGGAGACGAAAGGACGAAAGAGCAAGATGCATATCG	600
Qy	601	ACGAGAACTGTGGGCCCCAGCATGTACTGCCAAGTTTGCAGCTTCCAAATCACCTGGCAGC	660
Db	601	ACGAGAACTGTGGGCCCCAGCATGTACTGCCAAGTTTGCAGCTTCCAAATCACCTGGCAGC	660
Qy	661	CATGCCCGGGCCAGAGAGATGCTCTGCACCCGGGACAGTGAATGTCTGTGAGAACCAAGCTGT	720
Db	661	CATGCCCGGGCCAGAGAGATGCTCTGCACCCGGGACAGTGAATGTCTGTGAGAACCAAGCTGT	720
Qy	721	GTGTCTGGGGTCACTGACCAAAATGGCCACAGGGGACCAATGGGAAACCATCTGTACA	780
Db	721	GTGTCTGGGGTCACTGACCAAAATGGCCACAGGGGACCAATGGGAAACCATCTGTACA	780
Qy	781	ACCAAGAGGAACTGSCCAACCGGGGCTGTGTGTCTTCCAGAGAGGCTGTGTTCCTGTG	840
Db	781	ACCAAGAGGAACTGSCCAACCGGGGCTGTGTGTCTTCCAGAGAGGCTGTGTTCCTGTG	840
Qy	841	TGTGCACAACCCCTGSCCGGTGGAGGGGCGAGCTTTCACATGACCCCGGACAGCGGCTTCTGTG	900
Db	841	TGTGCACAACCCCTGSCCGGTGGAGGGGCGAGCTTTCACATGACCCCGGACAGCGGCTTCTGTG	900
Qy	901	ACCTCATCACTCTGGGAGCTTAAAGCTTATGAGGCTTTGAAACGATGCCCTTTGTGCCAATG	960
Db	901	ACCTCATCACTCTGGGAGCTTAAAGCTTATGAGGCTTTGAAACGATGCCCTTTGTGCCAATG	960
Qy	961	GCCCTCCTCTGACAGCCCGACAGCCACAGAGCCTGTGTATGTGTGACAGCCGACCTTCCGTG	1020
Db	961	GCCCTCCTCTGACAGCCCGACAGCCACAGAGCCTGTGTATGTGTGACAGCCGACCTTCCGTG	1020
Qy	1021	GGAGCCGTGACCAAGATGAGGAGATCTGTCTGTCCCAAGAGAGTCCCGATATGATGAAG	1080
Db	1021	GGAGCCGTGACCAAGATGAGGAGATCTGTCTGTCCCAAGAGAGTCCCGATATGATGAAG	1080
Qy	1081	TTTGCAGATTCATGAGAGAGGTGTGGCCAGAGAGCTGAGAGAACTGGAGAGAGGCTGATCG	1140
Db	1081	TTTGCAGATTCATGAGAGAGGTGTGGCCAGAGAGCTGAGAGAACTGGAGAGAGGCTGATCG	1140
Qy	1141	AAGAGATGCGCTGAGGAGAGCTTGCAGCTGTCCGCTGCACTCTCTGGAGAGGAGAACGA	1200
Db	1141	AAGAGATGCGCTGAGGAGAGCTTGCAGCTGTCCGCTGCACTCTCTGGAGAGGAGAACGA	1200
Qy	1201	TTTATGATCTGACACAGAGCTGTGGGTAGATGTGCATAATGAATACTAATTAATTTCCCA	1260
Db	1201	TTTATGATCTGACACAGAGCTGTGGGTAGATGTGCATAATGAATACTAATTAATTTCCCA	1260
Qy	1261	GGTGTGTGCTTTAAGCGGTGGCTGACAGGCTTTTCTCTATCATCTTCTTCCAGTAAGTT	1320
Db	1261	GGTGTGTGCTTTAAGCGGTGGCTGACAGGCTTTTCTCTATCATCTTCTTCCAGTAAGTT	1320
Qy	1321	TCCCTCTGTGCTTACAGACAGATGATGTGTGCAATTTGTTCAAGCTTCCCGCAGGCTGTCT	1380
Db	1321	TCCCTCTGTGCTTACAGACAGATGATGTGTGCAATTTGTTCAAGCTTCCCGCAGGCTGTCT	1380
Qy	1381	CCAGGCTTCAACATCTGTGCTTGGAGAGTCAAGCAGGTTAACTGCAGAGCAAGTTT	1440
Db	1381	CCAGGCTTCAACATCTGTGCTTGGAGAGTCAAGCAGGTTAACTGCAGAGCAAGTTT	1440

DB 1381 CGAGCTTCACAGTGTGCTGGGAGAGTCAGCAGGGTTAACTCAGAGACGTTT 1440  
QY 1441 GCACCCCTGTCAGATTAATGAGTCTTTGCTTACAGTTGGCAGACGCCGTTGT 1500  
DB 1441 GCACCCCTGTCAGATTAATGAGTCTTTGCTTACAGTTGGCAGACGCCGTTGT 1500  
QY 1501 TGTACATGAGCTTGTATATGTTTGAAGGAGAGAAATGAAACATGTGAGTCTCCCTC 1560  
DB 1501 TGTACATGAGCTTGTATATGTTTGAAGGAGAGAAATGAAACATGTGAGTCTCCCTC 1560  
QY 1561 TGAATGTTTTGGGAAATGTGAGAGAGTGCCCTGCTTTGCAAAACATCACTGGCAA 1620  
DB 1561 TGAATGTTTTGGGAAATGTGAGAGAGTGCCCTGCTTTGCAAAACATCACTGGCAA 1620  
QY 1621 AATATGAAATGAATTTTCCAGCAGTCTTTCCATGAGGATNGTAACTGTGCTT 1680  
DB 1621 AATATGAAATGAATTTTCCAGCAGTCTTTCCATGAGGATNGTAACTGTGCTT 1680  
QY 1681 CAGCTGTCAGATGAATGTTCTGTTCACCTGCATTAATGTTTATTCATCCAGCA 1740  
DB 1681 CAGCTGTCAGATGAATGTTCTGTTCACCTGCATTAATGTTTATTCATCCAGCA 1740  
QY 1741 GTGTTGCTCAGTCTCTACCTCTGTGTCAGGAGCAGATTTTCATATCCAAATTCCTC 1800  
DB 1741 GTGTTGCTCAGTCTCTACCTCTGTGTCAGGAGCAGATTTTCATATCCAAATTCCTC 1800  
QY 1801 TCTTCAGACAGCCTGGGAGGAGGAGTCAATGTTCCGTCATCAAGGATCCAGAG 1860  
DB 1801 TCTTCAGACAGCCTGGGAGGAGGAGTCAATGTTCCGTCATCAAGGATCCAGAG 1860  
QY 1861 GCTCAGAGACTGCAAGCTCTGCTCCCAAGTCAACAGCTAGTGAAGACCAAGCAGTTTC 1920  
DB 1861 GCTCAGAGACTGCAAGCTCTGCTCCCAAGTCAACAGCTAGTGAAGACCAAGCAGTTTC 1920  
QY 1921 ATCTGTTGTACTTAAGCTCAGTCTCTCCATCCCAAGCAGCCTGTTGTCGA 1980  
DB 1921 ATCTGTTGTACTTAAGCTCAGTCTCTCCATCCCAAGCAGCCTGTTGTCGA 1980  
QY 1981 CCAAAAGTCTCCCAAAAGGAGAGAAATGAGATTTTCTTGAGGATGACATCTGGA 2040  
DB 1981 CCAAAAGTCTCCCAAAAGGAGAGAAATGAGATTTTCTTGAGGATGACATCTGGA 2040  
QY 2041 AATTAAGTCAATCTAATTTCTCAATCCCTCTAAAGTAACTAGTGAAGACAGCAGT 2100  
DB 2041 AATTAAGTCAATCTAATTTCTCAATCCCTCTAAAGTAACTAGTGAAGACAGCAGT 2100  
QY 2101 GTTCTCAGAGTGGGGAGCCGCTCTTAATGAAGCAATGATTAATGACACTGCTCCT 2160  
DB 2101 GTTCTCAGAGTGGGGAGCCGCTCTTAATGAAGCAATGATTAATGACACTGCTCCT 2160  
QY 2161 CTTTGGCAATTTAGTAACTTTGAAAGGTATATGACTGAGGCTAGCATACAGTTAA 2220  
DB 2161 CTTTGGCAATTTAGTAACTTTGAAAGGTATATGACTGAGGCTAGCATACAGTTAA 2220  
QY 2221 CCTGCAGAAACAGTACTTATGTTAGGCGCAGATTAATAATGAATTTGCAAAAT 2280  
DB 2221 CCTGCAGAAACAGTACTTATGTTAGGCGCAGATTAATAATGAATTTGCAAAAT 2280  
QY 2281 CACTTATGCGCAACTGAAACATTAATCAACAGTGGGAAATCAACCGAGAGGGC 2340  
DB 2281 CACTTATGCGCAACTGAAACATTAATCAACAGTGGGAAATCAACCGAGAGGGC 2340  
QY 2341 TGTGTGAACATGTTGTATATGAGCACTGCAACATGATTAATCAAGAGTTCTTAAAGTT 2400  
DB 2341 TGTGTGAACATGTTGTATATGAGCACTGCAACATGATTAATCAAGAGTTCTTAAAGTT 2400  
QY 2401 TGAATGTTTCAAGTGTCAATGAGCTGTGTCACATGATTAATCAAGAGTTCTTAAAGTT 2460  
DB 2401 TGAATGTTTCAAGTGTCAATGAGCTGTGTCACATGATTAATCAAGAGTTCTTAAAGTT 2460  
QY 2461 TAAAGTGCACATGATTTGATTAAGCAGTCTTCTTTGAGTTTAAATATGATTAACAT 2520  
DB 2461 TAAAGTGCACATGATTTGATTAAGCAGTCTTCTTTGAGTTTAAATATGATTAACAT 2520

QY 2521 AAGTTCATTAGAAATCAAGCATTAATCACTTCAACTGCAAAAAAAAAAAAAAAAAA 2580  
DB 2521 AAGTTCATTAGAAATCAAGCATTAATCACTTCAACTGCAAAAAAAAAAAAAAAAAA 2580  
QY 2581 AAAAAA 2586  
DB 2581 AAAAAA 2586  
  
RESULT 13  
ACA05532 standard; cDNA; 2586 BP.  
XX  
AC ACA05532;  
XX  
DT 29-MAY-2003 (first entry)  
XX  
DE cDNA encoding human secreted protein PRO295.  
XX  
KW Human; gene therapy; mucosal lesion; ulcer; enterocolitis; skin disease;  
KW psoriasis; cancer; lung cancer; colon cancer; nerve cell disease;  
KW Alzheimer's disease; Parkinson's disease; Usner syndrome; angiodenesis;  
KW atrophid areata; inflammatory disease; asthma; rheumatoid arthritis;  
KW ischaemia; ss; gene.  
XX  
OS Homo sapiens.  
XX  
PN US2003023054-A1.  
XX  
PD 30-JAN-2003.  
XX  
PF 16-JUL-2001; 2001US-096742.  
XX  
PR 10-SEP-1998; 98MO-US18624.  
PR 14-SEP-1998; 98MO-US19177.  
PR 16-SEP-1998; 98MO-US19330.  
PR 17-SEP-1998; 98MO-US19437.  
PR 01-DEC-1998; 98MO-US25108.  
PR 08-SEP-1999; 99MO-US20594.  
PR 13-SEP-1999; 99MO-US20944.  
PR 15-SEP-1999; 99MO-US21090.  
PR 15-SEP-1999; 99MO-US21547.  
PR 05-OCT-1999; 99MO-US23069.  
PR 29-NOV-1999; 99MO-US28214.  
PR 30-NOV-1999; 99MO-US28313.  
PR 01-DEC-1999; 99MO-US28301.  
PR 02-DEC-1999; 99MO-US28564.  
PR 02-DEC-1999; 99MO-US28565.  
PR 16-DEC-1999; 99MO-US30095.  
PR 20-DEC-1999; 99MO-US30911.  
PR 20-DEC-1999; 99MO-US30999.  
PR 05-JAN-2000; 2000MO-US00219.  
PR 11-FEB-2000; 2000MO-US03565.  
PR 22-FEB-2000; 2000MO-US04414.  
PR 24-FEB-2000; 2000MO-US05004.  
PR 02-MAR-2000; 2000MO-US05841.  
PR 20-MAR-2000; 2000MO-US07377.  
PR 30-MAR-2000; 2000MO-US08439.  
PR 22-MAY-2000; 2000MO-US14042.  
PR 02-JUN-2000; 2000MO-US15264.  
PR 28-JUL-2000; 2000MO-US20710.  
PR 24-AUG-2000; 2000MO-US23328.  
PR 17-SEP-1997; 97US-059113P.  
PR 17-SEP-1997; 97US-059115P.  
PR 17-SEP-1997; 97US-059117P.  
PR 17-SEP-1997; 97US-059119P.  
PR 17-SEP-1997; 97US-059121P.  
PR 17-SEP-1997; 97US-059122P.  
PR 17-SEP-1997; 97US-059124P.  
PR 18-SEP-1997; 97US-059263P.  
PR 18-SEP-1997; 97US-059266P.  
PR 15-OCT-1997; 97US-062125P.



PR	17-OCT-1997	97US-062285P
PR	17-OCT-1997	97US-062287P
PR	21-OCT-1997	97US-062486P
PR	24-OCT-1997	97US-062481P
PR	24-OCT-1997	97US-062816P
PR	24-OCT-1997	97US-063045P
PR	24-OCT-1997	97US-063120P
PR	24-OCT-1997	97US-063121P
PR	24-OCT-1997	97US-063127P
PR	24-OCT-1997	97US-063128P
PR	27-OCT-1997	97US-063327P
PR	27-OCT-1997	97US-063329P
PR	28-OCT-1997	97US-063541P
PR	28-OCT-1997	97US-063542P
PR	28-OCT-1997	97US-063544P
PR	28-OCT-1997	97US-063545P
PR	28-OCT-1997	97US-063550P
PR	28-OCT-1997	97US-063564P
PR	29-OCT-1997	97US-063435P
PR	29-OCT-1997	97US-063704P
PR	29-OCT-1997	97US-063732P
PR	29-OCT-1997	97US-063734P
PR	29-OCT-1997	97US-063735P
PR	29-OCT-1997	97US-063738P
PR	29-OCT-1997	97US-064215P
PR	31-OCT-1997	97US-063870P
PR	31-OCT-1997	97US-064103P
PR	03-NOV-1997	97US-064248P
PR	07-NOV-1997	97US-064809P
PR	12-NOV-1997	97US-065186P
PR	18-NOV-1997	97US-065846P
PR	21-NOV-1997	97US-065693P
PR	21-NOV-1997	97US-066120P
PR	24-NOV-1997	97US-066364P
PR	24-NOV-1997	97US-066453P
PR	24-NOV-1997	97US-066466P
PR	24-NOV-1997	97US-066511P
PR	24-NOV-1997	97US-066770P
PR	24-NOV-1997	97US-066772P
PR	25-NOV-1997	97US-066840P
PR	12-DEC-1997	97US-069425P
PR	10-JUN-1998	98US-088026P
PR	10-SEP-1998	98US-099603P
PR	14-SEP-1998	98US-100262P
PR	17-SEP-1998	98US-100858P
PR	13-OCT-1998	98US-104080P
PR	20-NOV-1998	98US-109304P
PR	22-DEC-1998	98US-113296P
PR	07-JUL-1999	99US-143048P
PR	26-JUL-1999	99US-143698P
PR	28-JUL-1999	99US-146222P
PR	18-SEP-2000	2000US-066535P

PA (GETH ) GENENTECH INC.  
XX  
XX  
PI Ashkenazi A, Borstein D, Deeneyers L, Eaton DL, Ferrara N;  
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan LJ, Kijavini LJ;  
PI Mather JP, Pan U, Paoni NF, Roy MA, Stewart TA, Tumas D;  
PI Williams PM, Wood WJ;  
XX  
XX WPI; 2003-331485/31.  
DR P-PSDB; ABU67385.  
XX  
XX  
PT Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g.  
PT PRO245 or PRO1868, useful in chromosome and gene mapping, in generating  
PT antisense RNA and DNA, and in treating cancer and Alzheimer's disease -  
XX  
XX Example 38; Fig 83; 481pp; English.  
XX  
XX The invention relates to sixty one nucleic acids encoding PRO  
CC polypeptides (secreted and transmembrane). The polynucleotide is useful  
CC in molecular biology, including uses as hybridisation probes, in

CC chromosome and gene mapping, in generating antisense RNA and DNA, and in  
CC gene therapy. The polynucleotide may also be used in preparing PRO  
CC polypeptide. By recombinant techniques, and in generating either  
CC transgenic animals or knock-out animals which, in turn, are useful in the  
CC development and screening of therapeutically useful reagents. The PRO  
CC polypeptide or the antibody is used in preparing a medicament for  
CC treating a condition responsive to the polypeptide or antibody, such as  
CC mucosal lesions e.g. ulcers and enterocolitis, skin disease e.g.  
CC psoriasis, cancer e.g. lung cancer and colon cancer, nerve cell disease  
CC e.g. Alzheimer's disease and Parkinson's disease, Usher syndrome,  
CC atropia areata, angiodermatitis, inflammatory disease e.g. asthma and  
CC rheumatoid arthritis, ischaemia, and in various diagnostic assays. The  
CC present sequence represents an cDNA which encodes a PRO polypeptide.

XX Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;

Query Match	100.0%	Score 2586	DB 25	Length 2586
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2586	0	Mismatches	0	Gaps 0

QY	1	CGCCGCGCTCCCGCAGCCCGCGCCCGCCACCGCGCCCGCTCCCGCATCTCCACCCGACG	60
Ds	1	CGCCGCGCTCCCGCAGCCCGCGCCCGCCACCGCGCCCGCTCCCGCATCTCCACCCGACG	60
QY	61	CGCGCGGCTCCCGCGGAGGCGAGCAGATTCAGTCCGCGCGCGACGCACTCGGTCA	120
Ds	61	CGCGCGGCTCCCGCGGAGGCGAGCAGATTCAGTCCGCGCGCGACGCACTCGGTCA	120
QY	121	GTGCGGCGCGCGCGCTGCGCGCGCGCAGAGCGGAGATGCGAGCGCGCTTGTGGGCGCCACCTGCTGT	180
Ds	121	GTGCGGCGCGCGCGCTGCGCGCGCGCAGAGCGGAGATGCGAGCGCGCTTGTGGGCGCCACCTGCTGT	180
QY	181	GCTGCTGCTGCGCGCGCGCGGTCCCGCAGGCCCCCGCGCGCTTCGACGCGCATCTCG	240
Ds	181	GCTGCTGCTGCGCGCGCGCGGTCCCGCAGGCCCCCGCGCGCTTCGACGCGCATCTCG	240
QY	241	CTGCAATCAAGCCCGCGCCCGCTCTCAACTCCCGCGAGAGAGAGGCCACCTCAATGAGA	300
Ds	241	CTGCAATCAAGCCCGCGCCCGCTCTCAACTCCCGCGAGAGAGGCCACCTCAATGAGA	300
QY	301	TGTTCCGCGAGGTTGAGGACTGATGAGAGCACGCGACCAAAATTGCGAGCGCGGTG	360
Ds	301	TGTTCCGCGAGGTTGAGGACTGATGAGAGCACGCGACCAAAATTGCGAGCGCGGTG	360
QY	361	AAGAATGAGAGCGAGAAGAGCTGCTGTAAGATCATCAGAAAGTGAACCTGCGAACT	420
Ds	361	AAGAATGAGAGCGAGAAGAGCTGCTGTAAGATCATCAGAAAGTGAACCTGCGAACT	420
QY	421	TACCTCCAGCTATCACAATGAGCCACACAGACGAAAGTTGAAATATATCATCC	480
Ds	421	TACCTCCAGCTATCACAATGAGCCACACAGACGAAAGTTGAAATATATCATCC	480
QY	481	ATGTGACCGAGAAATTCACAGATTAACCAACCAACCGACCTGACCAATGCTCTTTGAG	540
Ds	481	ATGTGACCGAGAAATTCACAGATTAACCAACCAACCGACCTGACCAATGCTCTTTGAG	540
QY	541	AGAAGTATCACATCTGTGGAGCGAAGAGCGAAGAGCACGAGTGATCATCG	600
Ds	541	AGAAGTATCACATCTGTGGAGCGAAGAGCGAAGAGCACGAGTGATCATCG	600
QY	601	ACGAGACTGTGGGCCCGCAGCATGATCTGCGCAGTTTGCCAGTTTCAGTACACCGCGACG	660
Ds	601	ACGAGACTGTGGGCCCGCAGCATGATCTGCGCAGTTTGCCAGTTTCAGTACACCGCGACG	660
QY	661	CATGCCGCGGCGCAGAGGATCTCTGACCCGCGACAGTGAAGTGTGTGAGAACCAAGCTGT	720
Ds	661	CATGCCGCGGCGCAGAGGATCTCTGACCCGCGACAGTGAAGTGTGTGAGAACCAAGCTGT	720
QY	721	GTGTTCGCGGCTCATCTGACCAAAATGCGCACCGAGGCGAGCAATGGGACCATCTGTGACA	780
Ds	721	GTGTTCGCGGCTCATCTGACCAAAATGCGCACCGAGGCGAGCAATGGGACCATCTGTGACA	780
QY	781	ACGAGAGGACTGCGCAGCCGCGGCGTGTGCTTCCAGAGAGCGCTGTCTTCCCTG	840

```

Db 781 ACCAAGAGGAGCTGCAGCCGGGCTGTGTGTGCTTCCAGAGAGAGCTGTCTGTCCCTG 840
Qy 781 TGTGCAACCCCTGCCCGTGGAGGGGCGAGCTTTGGCAATGACCCCGCCAGCGGCTTCGG 900
Db 841 TGTGCAACCCCTGCCCGTGGAGGGGCGAGCTTTGGCAATGACCCCGCCAGCGGCTTCGG 900
Qy 901 ACCCTATCACTGGAGAGCTAGAGCTGTATGAGAGCTTGTGACCGATGCCCTTGTGCAAGT 960
Db 901 ACCCTATCACTGGAGAGCTAGAGCTGTATGAGAGCTTGTGACCGATGCCCTTGTGCAAGT 960
Qy 961 GCTCTCTCTGCGAGCCCAAGCCCAAGCTGTGTATGTGTGCAAGCCGACCTTCGTGG 1020
Db 961 GCTCTCTCTGCGAGCCCAAGCCCAAGCTGTGTATGTGTGCAAGCCGACCTTCGTGG 1020
Qy 1021 GGAGCCGTGACCAAGATGGGAGAGATCTGTGCTCCAGAGAGGTCCCGATGATGTAAG 1080
Db 1021 GGAGCCGTGACCAAGATGGGAGAGATCTGTGCTCCAGAGAGGTCCCGATGATGTAAG 1080
Qy 1081 TTGGCAGCTTCAATGAGAGAGTGGCCGAGAGAGCTGAGAGACTTGGAGAGAGCTGACTG 1140
Db 1081 TTGGCAGCTTCAATGAGAGAGTGGCCGAGAGAGCTGAGAGACTTGGAGAGAGCTGACTG 1140
Qy 1141 AAGAGATGGCGCTGGGGGAGAGCTGGCGGCTGCCGCGCTGCACTGCTGGGAGGGGAGAGA 1200
Db 1141 AAGAGATGGCGCTGGGGGAGAGCTGGCGGCTGCCGCGCTGCACTGCTGGGAGGGGAGAGA 1200
Qy 1201 TTTAGATCTGGAACAGAGCTGTGGGATGATGTGCAATAGAAATAGCTAAATTTATTTCCCA 1260
Db 1201 TTTAGATCTGGAACAGAGCTGTGGGATGATGTGCAATAGAAATAGCTAAATTTATTTCCCA 1260
Qy 1261 GGTGTGTGCTTTAGAGGTGGGCTGACAGAGCTTCTTCTCAATCTTCTTCCAGTAAGT 1320
Db 1261 GGTGTGTGCTTTAGAGGTGGGCTGACAGAGCTTCTTCTCAATCTTCTTCCAGTAAGT 1320
Qy 1321 TCCCTCTGTGGCTTGAAGAGATGAGTGTGTGCAATTTGTTCAGCTCCCGAGGCTGTCT 1380
Db 1321 TCCCTCTGTGGCTTGAAGAGATGAGTGTGTGCAATTTGTTCAGCTCCCGAGGCTGTCT 1380
Qy 1381 CCAAGCTTCAAGCTGTGTGCTGGAGAGTCAAGGAGGTTAACTGAGAGAGAGT 1440
Db 1381 CCAAGCTTCAAGCTGTGTGCTGGAGAGTCAAGGAGGTTAACTGAGAGAGAGT 1440
Qy 1441 GCCACCCCTGTCCAGATTAATGGCTGTGTGCTCTTCAACAGTGTGCAAGCCGTTGT 1500
Db 1441 GCCACCCCTGTCCAGATTAATGGCTGTGTGCTCTTCAACAGTGTGCAAGCCGTTGT 1500
Qy 1501 TCTACATGGCTTTGAATTTGTGAGGGAGAGATGGAACATGTGAGATCTCCCTC 1560
Db 1501 TCTACATGGCTTTGAATTTGTGAGGGAGAGATGGAACATGTGAGATCTCCCTC 1560
Qy 1561 TGAATGATTTGGGAAATGTGAGAAAGTGGCCCTGTTTCCAAACATCAACTGGCA 1620
Db 1561 TGAATGATTTGGGAAATGTGAGAAAGTGGCCCTGTTTCCAAACATCAACTGGCA 1620
Qy 1621 AAATGCAACAAATGAATTTTCCAGCAGTCTTTTCCATGGGCAATGATGAGTGTGCTT 1680
Db 1621 AAATGCAACAAATGAATTTTCCAGCAGTCTTTTCCATGGGCAATGATGAGTGTGCTT 1680
Qy 1681 CACCTGTGAGATGAATTTCTGTTCACCCCTGATTCATGTGTTTATTCATCAGCA 1740
Db 1681 CACCTGTGAGATGAATTTCTGTTCACCCCTGATTCATGTGTTTATTCATCAGCA 1740
Qy 1741 GGTGTGTGCTGCTTCACTGTGTGCGAGAGAGCAATTTTCAATATCAAGATCAATTTCC 1800
Db 1741 GGTGTGTGCTGCTTCACTGTGTGCGAGAGAGCAATTTTCAATATCAAGATCAATTTCC 1800
Qy 1801 TCTCTCAGCAGAGCTGGGAGAGGGGCTGATTTCTTCTCCTGTCATCAGAGATCTCAGAG 1860
Db 1801 TCTCTCAGCAGAGCTGGGAGAGGGGCTGATTTCTTCTCCTGTCATCAGAGATCTCAGAG 1860
Qy 1861 GCTCAGAGCTGCAAGCTGTGCTTCCCAAGTCAACAGCTATGTAAGACCAAGAGCTTTC 1920

```

```

Db 1861 GCTCAGAGCTGCAAGCTGCTTCCCAAGTCAACAGCTATGTAAGACCAAGAGCTTTC 1920
Qy 1921 ATCTGTTGATCTTAAGCTAGATGCTCTCTTCCATACCCCAACAGCTTGTGCA 1980
Db 1921 ATCTGTTGATCTTAAGCTAGATGCTCTCTTCCATACCCCAACAGCTTGTGCA 1980
Qy 1981 CCAAAAGTCTCCCAAAAGAGAGAAATGGGATTTTCTTGAAGCATGCAATCTGTA 2040
Db 1981 CCAAAAGTCTCCCAAAAGAGAGAAATGGGATTTTCTTGAAGCATGCAATCTGTA 2040
Qy 2041 ATTAAGTCAAACTAATTTCTCAATCCCTCTAAAGTAATACTGTGTGAACAGAGCT 2100
Db 2041 ATTAAGTCAAACTAATTTCTCAATCCCTCTAAAGTAATACTGTGTGAACAGAGCT 2100
Qy 2101 GTTCTCAGATGTGGGAGAGCCGCTCTTCTTAATGAAGCAATGATTTGACATGTCCT 2160
Db 2101 GTTCTCAGATGTGGGAGAGCCGCTCTTCTTAATGAAGCAATGATTTGACATGTCCT 2160
Qy 2161 CTTTGGCAGTTGATTAATTAATTTGAAAGGTATATGATGAGCTGAGCTAGCATACAGTTAA 2220
Db 2161 CTTTGGCAGTTGATTAATTAATTTGAAAGGTATATGATGAGCTGAGCTAGCATACAGTTAA 2220
Qy 2221 CTTGCAAGAAACAGTACTTAAGTATTTGAGGGGAGAGATTAATGAATTTGCAAAAT 2280
Db 2221 CTTGCAAGAAACAGTACTTAAGTATTTGAGGGGAGAGATTAATGAATTTGCAAAAT 2280
Qy 2281 CACTTACAGCAACTGAAGCAATTAATCAACGCTGAGAAATCAACCCGAGAGAGG 2340
Db 2281 CACTTACAGCAACTGAAGCAATTAATCAACGCTGAGAAATCAACCCGAGAGAGG 2340
Qy 2341 TGTGTGAACATGTTGTAATATGAGCTGCAAGCACTGAATCTTCAAGCTTCCCAAA 2400
Db 2341 TGTGTGAACATGTTGTAATATGAGCTGCAAGCACTGAATCTTCAAGCTTCCCAAA 2400
Qy 2401 TGAATTTTCAAGTGTCAATGAGACTGTTCGACCATGATTAATCAAGAGTCTTAAAGT 2460
Db 2401 TGAATTTTCAAGTGTCAATGAGACTGTTCGACCATGATTAATCAAGAGTCTTAAAGT 2460
Qy 2461 TAAAGTTCACATGATTTGATTAAGCAATGCTTCTTGAAGTTTAAATGATTAACAT 2520
Db 2461 TAAAGTTCACATGATTTGATTAAGCAATGCTTCTTGAAGTTTAAATGATTAACAT 2520
Qy 2521 AAGTTCATTTAAGAAATCAAGCATTAATCACTTCACTGCAAAAAA 2580
Db 2521 AAGTTCATTTAAGAAATCAAGCATTAATCACTTCACTGCAAAAAA 2580
Qy 2581 AAAAAA 2586
Db 2581 AAAAAA 2586

RESULT 14
ABX96211
ID ABX96211 standard; cDNA; 2586 bp.
XX
XX ABX96211;
XX
XX 13-MAY-2003 (first entry)
XX
XX Human secreted/transmembrane protein cDNA, #43.
XX
XX Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;
XX diagnostic; biosensor; bioreactor; therapeutic; hyperplasia;
XX endometriosis; cancer; tumor; ischemia; coronary arterial disease;
XX polycystic kidney disease; renal failure; inflammatory response; asthma;
XX rheumatoid arthritis; psoriasis; multiple sclerosis; gene therapy;
XX cytostatic; gynecological; cardiac; nephrotoxic; hepatocytic;
XX antiinflammatory.
XX
XX Homo sapiens.
XX
XX US2002160374-A1.
XX

```



Dh 301 TGTTCGGAGGTTGAGGACTGATGAGAGACCGCAGCAAAATTGGCCAGCGCGTGG 360  
Qy 361 AAGAGATGAGGCGAGAGAGAGCTGTGCTTAAAGCATCATCAGAAAGTGAACCTGGCAAACT 420  
Db 361 AAGAGATGAGGCGAGAGAGAGCTGTGCTTAAAGCATCATCAGAAAGTGAACCTGGCAAACT 420  
Qy 421 TACCTCCAGCTATCACTATGAGACCAACAGACAGCAAGGTTGAAATTAATACATCC 480  
Db 421 TACCTCCAGCTATCACTATGAGACCAACAGACAGCAAGGTTGAAATTAATACATCC 480  
Qy 481 ATGTGACCGAGAAATTCACAGATTAACCAACAGACAGCTGAGCAAAATGTCTTTTGG 540  
Db 481 ATGTGACCGAGAAATTCACAGATTAACCAACAGACAGCTGAGCAAAATGTCTTTTGG 540  
Qy 541 AAGACATTAATCACTGTGAG 600  
Db 541 AAGACATTAATCACTGTGAG 600  
Qy 601 ACAGAGACTGTGGGCGCAGCATGTATCTGCACTTTGCACTTTCAGATACATCTCCAGC 660  
Db 601 ACAGAGACTGTGGGCGCAGCATGTATCTGCACTTTGCACTTTCAGATACATCTCCAGC 660  
Qy 661 CATGCCGAGGCGAGAGATGCTCTGCACTCCGAGACATGATGTGTGAGAGACAGCTGT 720  
Db 661 CATGCCGAGGCGAGAGATGCTCTGCACTCCGAGACATGATGTGTGAGAGACAGCTGT 720  
Qy 721 GTGTCTGGGGTCACTGCACTCAAAATGAGGCGACAGAGGAGAGAGAGAGAGAGAGAGAG 780  
Db 721 GTGTCTGGGGTCACTGCACTCAAAATGAGGCGACAGAGGAGAGAGAGAGAGAGAGAGAG 780  
Qy 781 ACCAGAGGAGCTGCGAGAGCGGAGGCTGTGTGCTTCCAGAGAGGCTGTCTTCCCTG 840  
Db 781 ACCAGAGGAGCTGCGAGAGCGGAGGCTGTGTGCTTCCAGAGAGGCTGTCTTCCCTG 840  
Qy 841 TGTGACACCCCTGCGGAG 900  
Db 841 TGTGACACCCCTGCGGAG 900  
Qy 901 ACCTCATCACTTGGAG 960  
Db 901 ACCTCATCACTTGGAG 960  
Qy 961 GCTCTCTGCGAG 1020  
Db 961 GCTCTCTGCGAG 1020  
Qy 1021 GAGAGCGTGAACAAAGATGGGAGAGATCTGTGCTCCAGAGAGAGAGAGAGAGAGAG 1080  
Db 1021 GAGAGCGTGAACAAAGATGGGAGAGATCTGTGCTCCAGAGAGAGAGAGAGAGAGAG 1080  
Qy 1081 TTGGCAGCTTCACTGAG 1140  
Db 1081 TTGGCAGCTTCACTGAG 1140  
Qy 1141 AAGAGATGAGGCTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200  
Db 1141 AAGAGATGAGGCTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200  
Qy 1201 TTTAGATCTGAGACAGAGCTGTGGGATGATGTGCAATGAAATGCTAATTTATTCCTCA 1260  
Db 1201 TTTAGATCTGAGACAGAGCTGTGGGATGATGTGCAATGAAATGCTAATTTATTCCTCA 1260  
Qy 1261 GGTGTGCTTTAG 1320  
Db 1261 GGTGTGCTTTAG 1320  
Qy 1321 TCCCTCTGAGCTTGAAG 1380  
Db 1321 TCCCTCTGAGCTTGAAG 1380  
Qy 1381 CAGAGCTTCAAGCTGTGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
Db 1381 CAGAGCTTCAAGCTGTGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440

Qy 1441 GCCACCCCTGTCCAGATTAATGGCTGTGCTTGCCTTACCAAGTTGGCAGACAGCCGTTGT 1500  
Db 1441 GCCACCCCTGTCCAGATTAATGGCTGTGCTTGCCTTACCAAGTTGGCAGACAGCCGTTGT 1500  
Qy 1501 TCTACATGCTTGTATTAATGTTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560  
Db 1501 TCTACATGCTTGTATTAATGTTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560  
Qy 1561 TGAATGTTTGGGAG 1620  
Db 1561 TGAATGTTTGGGAG 1620  
Qy 1621 AAATGCAACAAATGAATTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680  
Db 1621 AAATGCAACAAATGAATTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680  
Qy 1681 CAGCTGTTGAG 1740  
Db 1681 CAGCTGTTGAG 1740  
Qy 1741 GTGTGCTCAGCTCTCACTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
Db 1741 GTGTGCTCAGCTCTCACTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
Qy 1801 TCTCTCAGACAGCTGAG 1860  
Db 1801 TCTCTCAGACAGCTGAG 1860  
Qy 1861 GCTTACAGAGCTGCAAGCTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920  
Db 1861 GCTTACAGAGCTGCAAGCTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920  
Qy 1921 ATCTGTTGAGACTTAAGCTCAGTGTCTCTCCTCACTACCCACACAGGCTTGTGCGA 1980  
Db 1921 ATCTGTTGAGACTTAAGCTCAGTGTCTCTCCTCACTACCCACACAGGCTTGTGCGA 1980  
Qy 1981 CCAGAAAGTGTCTCCCAAG 2040  
Db 1981 CCAGAAAGTGTCTCCCAAG 2040  
Qy 2041 ATTAAGGTCAAACTAATCTCACTCCCTTAAAGAGTAATCTAGTAAAGAGAGAGAGAG 2100  
Db 2041 ATTAAGGTCAAACTAATCTCACTCCCTTAAAGAGTAATCTAGTAAAGAGAGAGAGAG 2100  
Qy 2101 GTTCTCAAGTGTGGGAG 2160  
Db 2101 GTTCTCAAGTGTGGGAG 2160  
Qy 2161 CTTTGGCAGTGTGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 2220  
Db 2161 CTTTGGCAGTGTGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 2220  
Qy 2221 CTTGAG 2280  
Db 2221 CTTGAG 2280  
Qy 2281 CACTTACAG 2340  
Db 2281 CACTTACAG 2340  
Qy 2341 TGTGTGAACATGTTGTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400  
Db 2341 TGTGTGAACATGTTGTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400  
Qy 2401 TGAATGTTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 2460  
Db 2401 TGAATGTTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 2460  
Qy 2461 TAAAGTGAACATTAATTAAG 2520  
Db 2461 TAAAGTGAACATTAATTAAG 2520

QY 2521 AAGTGCATTAGAAATCAGCATTAATCACTTCACTGCAAAAAA 2580  
 DB 2521 AAGTGCATTAGAAATCAGCATTAATCACTTCACTGCAAAAAA 2580  
 QY 2581 AAAAAA 2586  
 DB 2581 AAAAAA 2586  
 RESULT 15  
 ABX71642  
 ID ABX71642 standard; cDNA; 2586 BP.  
 XX  
 AC ABX71642;  
 XX  
 DT 10-MAR-2003 (first entry)  
 XX  
 DE Human cDNA encoding secreted/transmembrane protein PRO295.  
 XX  
 KW Human; PRO; secreted protein; transmembrane protein; enterocolitis;  
 KW gastrointestinal ulceration; skin disease; ss; gene;  
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;  
 KW squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;  
 KW amyotrophic lateral sclerosis; inflammatory disease;  
 KW rheumatoid arthritis; asthma; multiple sclerosis; organ failure;  
 KW atherosclerosis; cardiac injury; infertility; birth defect;  
 KW premature aging; AIDS; acquired immunodeficiency syndrome; cancer;  
 KW diabetic complication; wound repair.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002132240-A1.  
 XX  
 PD 19-SEP-2002.  
 XX  
 PF 18-JUL-2001; 2001US-0909320.  
 XX  
 PR 10-SEP-1998; 98MO-US18824.  
 PR 14-SEP-1998; 98MO-US19177.  
 PR 16-SEP-1998; 98MO-US19330.  
 PR 17-SEP-1998; 98MO-US19437.  
 PR 01-DEC-1998; 98MO-US25108.  
 PR 08-SEP-1999; 99MO-US20944.  
 PR 13-SEP-1999; 99MO-US21090.  
 PR 13-SEP-1999; 99MO-US21547.  
 PR 15-SEP-1999; 99MO-US23089.  
 PR 05-OCT-1999; 99MO-US28301.  
 PR 01-DEC-1999; 99MO-US28564.  
 PR 02-DEC-1999; 99MO-US28565.  
 PR 16-DEC-1999; 99MO-US30095.  
 PR 20-DEC-1999; 99MO-US30911.  
 PR 20-DEC-1999; 99MO-US30911.  
 PR 06-JAN-2000; 2000MO-US00219.  
 PR 11-FEB-2000; 2000MO-US03565.  
 PR 22-FEB-2000; 2000MO-US04414.  
 PR 28-JUL-2000; 2000MO-US20710.  
 PR 24-AUG-2000; 2000MO-US23328.  
 PR 17-SEP-1997; 97US-059113P.  
 PR 17-SEP-1997; 97US-059115P.  
 PR 17-SEP-1997; 97US-059117P.  
 PR 15-OCT-1997; 97US-062125P.  
 PR 17-OCT-1997; 97US-062285P.  
 PR 17-OCT-1997; 97US-062287P.  
 PR 21-OCT-1997; 97US-063486P.  
 PR 24-OCT-1997; 97US-062814P.  
 PR 24-OCT-1997; 97US-062816P.  
 XX  
 PA (GENETH ) GENENTECH INC.  
 XX  
 AS Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
 PI Filvaroff E, Fong S, Gao W, Garber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavlin IJ;

PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams EM, Wood WI;  
 XX  
 DR WPI; 2003-147434/14.  
 XX  
 DR P-PSDB; ABUS4387.  
 XX  
 PT New PRO polypeptides and nucleic acid molecules, useful in diagnosing  
 PT or treating inflammatory diseases, organ failure, atherosclerosis,  
 PT cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or  
 PT Parkinson's disease -  
 XX  
 PS Claim 2; Fig 83; 473bp; English.  
 XX  
 CC The invention relates to an isolated PRO polypeptide having at least 80%  
 CC amino acid sequence identity to: (a) any one of 61 fully defined amino  
 CC acid sequences given in the specification (appearing as ABUS4347-  
 CC ABUS4407); (b) an amino acid sequence encoded by the nucleotide sequence  
 CC deposited under American Type Culture Collection (accession numbers  
 CC listed in the specification); (c) any one of the PRO sequences which  
 CC lacks its associated signal peptide; (d) an extracellular domain of the  
 CC PRO polypeptide with its associated signal peptide; or (e) an  
 CC extracellular domain of the PRO polypeptide which lacks its associated  
 CC signal peptide. Also include are the nucleic acids encoding the PRO  
 CC polypeptides, vectors, host cells and anti-PRO antibodies.  
 CC The PRO polypeptides and nucleic acids are useful in diagnosing  
 CC or treating enterocolitis, gastrointestinal ulceration, skin diseases  
 CC associated with abnormal keratinocyte differentiation, e.g. psoriasis  
 CC or epithelial cancers such as squamous cell carcinoma, Alzheimer's  
 CC disease, Parkinson's disease, amyotrophic lateral sclerosis,  
 CC inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple  
 CC sclerosis, organ failure, atherosclerosis, cardiac injury, infertility,  
 CC birth defects, premature aging, AIDS, cancer, diabetic complications,  
 CC or mutations in general. The polypeptides are also useful for wound  
 CC repair and associated therapies concerned with re-growth of tissue. The  
 CC nucleotide sequences may be used as hybridisation probes in chromosome  
 CC and gene mapping, or in generating antisense RNA and DNA. PRO nucleic  
 CC acids are also useful in preparing PRO polypeptides, in assays to  
 CC identify other proteins or molecules involved in binding reaction, to  
 CC generate transgenic animals or knockout animals, which in turn are  
 CC useful in the development and screening of therapeutically useful  
 CC reagents, for chromosome identification, and tissue typing. The PRO  
 CC polypeptides and nucleic acid molecules are also useful in gene  
 CC therapy, and as molecular weight markers for protein electrophoresis  
 CC purposes. The anti-PRO antibodies may be used in diagnostic assays for  
 CC PRO, or for the affinity purification of PRO from recombinant cell  
 CC culture or natural sources. The present sequence encodes a PRO  
 CC polypeptide.  
 XX  
 SQ Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;  
 QY  
 Query Match 100.0%; Score 2586; DB 25; Length 2586;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGCCGGGCTCCGCAACCGGCGCCGCGCGCTCCGATTCGACCCGACG 60  
 DB 1 CGCCGGGCTCCGCAACCGGCGCCGCGCGCTCCGATTCGACCCGACG 60  
 QY 61 CGCGGGGCTCCCGCGGAGGAGCAGATCCAGTCCGCGCCGCGGAGTCCGATCA 120  
 DB 61 CGCGGGGCTCCCGCGGAGGAGCAGATCCAGTCCGCGCCGCGGAGTCCGATCA 120  
 QY 121 GTCGGGGCGCGGCTGCGGGCGCAGAGCGGAGATCAGCGGCTTGGGGCCACTGGCTGT 180  
 DB 121 GTCGGGGCGCGGCTGCGGGCGCAGAGCGGAGATCAGCGGCTTGGGGCCACTGGCTGT 180  
 QY 181 GCGTGTGCTGCGCGCGCGGCGGCGCCCGCGCGCGCTCCGAGCGGAGCTCGG 240  
 DB 181 GCGTGTGCTGCGCGCGCGGCGGCGCCCGCGCGCGCTCCGAGCGGAGCTCGG 240  
 QY 241 CTCGACATCAAGCCGCGCGCGCTTCAGGTACCCGCGAGAGAGGCCACCTCAATGAGA 300  
 DB 241 CTCGACATCAAGCCGCGCGCGCTTCAGGTACCCGCGAGAGAGGCCACCTCAATGAGA 300

QY 301 TGTTCGCGAGGTTGAGGAACTGATGAGAGACAACGAGACAATTTGCGACGCGGTGG 360  
Db 301 TGTTCGCGCGAGGTTGAGGAACTGATGAGAGACAACGAGACAATTTGCGACGCGGTGG 360  
QY 361 AAGAGATGAGGAGAGAGAGAGCTGTGCTTAAGCATCATCAGAAGTGAACCTGGGAAACT 420  
Db 361 AAGAGATGAGGAGAGAGAGAGCTGTGCTTAAGCATCATCAGAAGTGAACCTGGGAAACT 420  
QY 421 TACCTCCAGCTTATCACAATGAGACCAACAAGAGTTGGAAATTAATCATCC 480  
Db 421 TACCTCCAGCTTATCACAATGAGACCAACAAGAGTTGGAAATTAATCATCC 480  
QY 481 ATGTGACCGAGAAATTCAATAATTAACCAACAACGAGTTGGAATTAATCATCC 540  
Db 481 ATGTGACCGAGAAATTCAATAATTAACCAACAACGAGTTGGAATTAATCATCC 540  
QY 541 AGACAGTTATCACATCTGTGAGAGACGAAGAGGAGAGAGACGAGTGCATCATCG 600  
Db 541 AGACAGTTATCACATCTGTGAGAGACGAAGAGGAGAGAGACGAGTGCATCATCG 600  
QY 601 ACAGAGACTGTGGGCCCCAGATGTAATGCGAGTTTCCAGCTTCCAGTACACCTGCGACG 660  
Db 601 ACAGAGACTGTGGGCCCCAGATGTAATGCGAGTTTCCAGCTTCCAGTACACCTGCGACG 660  
QY 661 CATGCCGAGGACAGAGGATGCTCTGACACCGGAGCAGTGAAGTGTGAGACAGCTGT 720  
Db 661 CATGCCGAGGACAGAGGATGCTCTGACACCGGAGCAGTGAAGTGTGAGACAGCTGT 720  
QY 721 GTGTCTGGGGTCACTGCAACCAAAATGAGCAACAGGGGAGCAATGGAGCATCTGTGACA 780  
Db 721 GTGTCTGGGGTCACTGCAACCAAAATGAGCAACAGGGGAGCAATGGAGCATCTGTGACA 780  
QY 781 ACCAGAGGAGCTGCGACCGGGGCTGTGCTGCTTCCAGAGAGGCTGTGTTCCCTG 840  
Db 781 ACCAGAGGAGCTGCGACCGGGGCTGTGCTGCTTCCAGAGAGGCTGTGTTCCCTG 840  
QY 841 TGTGACACCCCTGCGCGTGGAGAGGAGAGCTTTGCCATGACCCCGACGCGGCTTCTGG 900  
Db 841 TGTGACACCCCTGCGCGTGGAGAGGAGAGCTTTGCCATGACCCCGACGCGGCTTCTGG 900  
QY 901 ACCTCATCACTGAGAGCTAGAGCTGATGAGAGCTTGAACGAGTGCCTTGTGCGAAGT 960  
Db 901 ACCTCATCACTGAGAGCTAGAGCTGATGAGAGCTTGAACGAGTGCCTTGTGCGAAGT 960  
QY 961 GCCTCTCTGCGACGCCCAACAGCAACGCTGTGTATGTGTGCAAGCCGACTTCTGTGG 1020  
Db 961 GCCTCTCTGCGACGCCCAACAGCAACGCTGTGTATGTGTGCAAGCCGACTTCTGTGG 1020  
QY 1021 GAGAGCGGTGACCAAGATGGGGAATCTGTCTGCCAGAGAGTCCCGCATAGATGAAAG 1080  
Db 1021 GAGAGCGGTGACCAAGATGGGGAATCTGTCTGCCAGAGAGTCCCGCATAGATGAAAG 1080  
QY 1081 TTGGCAGCTTCAATGAGAGAGTGCAGAGAGCTGAGAGACTTGAAGAGAGACCTGACTG 1140  
Db 1081 TTGGCAGCTTCAATGAGAGAGTGCAGAGAGCTGAGAGACTTGAAGAGAGACCTGACTG 1140  
QY 1141 AAGAGATGGGCTGGGAGAGCTGTGCGGCTGCGGCTGCACTGCTGAGGAGGAGAAAGAA 1200  
Db 1141 AAGAGATGGGCTGGGAGAGCTGTGCGGCTGCGGCTGCACTGCTGAGGAGGAGAAAGAA 1200  
QY 1201 TTTAGATCTGAGACCAAGAGCTGTGGGTAGATGTGCAATAGAAATTAATTTTCCCA 1260  
Db 1201 TTTAGATCTGAGACCAAGAGCTGTGGGTAGATGTGCAATAGAAATTAATTTTCCCA 1260  
QY 1261 GGTGTGTGCTTTAGGGGTGGGCTGACCAAGCTTCTTCTTAATCTTTTCCAGTAAGTT 1320  
Db 1261 GGTGTGTGCTTTAGGGGTGGGCTGACCAAGCTTCTTCTTAATCTTTTCCAGTAAGTT 1320  
QY 1321 TCCCTCTGTGCTTGAAGAGCATGAGTGTGTGATTTGTTCAAGTCCCGACGCGTGTCT 1380  
Db 1321 TCCCTCTGTGCTTGAAGAGCATGAGTGTGTGATTTGTTCAAGTCCCGACGCGTGTCT 1380

QY 1381 CCAGGCTTCAACAGTCTGTGCTTGGAGAGTCAAGCAGGTTAACTGACGAGAGTTT 1440  
Db 1381 CCAGGCTTCAACAGTCTGTGCTTGGAGAGTCAAGCAGGTTAACTGACGAGAGTTT 1440  
QY 1441 GCGACCCCTGTCCAGATTAATTTGGCTGTGCTTACCAAGTTGGAGAGACGCGTGTGT 1500  
Db 1441 GCGACCCCTGTCCAGATTAATTTGGCTGTGCTTACCAAGTTGGAGAGACGCGTGTGT 1500  
QY 1501 TCTACATGCTTTGATTAATTTGTTAGGAGAGAGATGAGAAACAATGTGAGTCTCCCTC 1560  
Db 1501 TCTACATGCTTTGATTAATTTGTTAGGAGAGAGATGAGAAACAATGTGAGTCTCCCTC 1560  
QY 1561 TGAATGGTTTTGGGGAATGAGAGAGATGCGCTTGTGCAAAATCAATCACTGGCAA 1620  
Db 1561 TGAATGGTTTTGGGGAATGAGAGAGATGCGCTTGTGCAAAATCAATCACTGGCAA 1620  
QY 1621 AATGCAACAATGAAATTTTCAAGCAGTCTTCCATGAGGCAATGATTAAGTGTGCTT 1680  
Db 1621 AATGCAACAATGAAATTTTCAAGCAGTCTTCCATGAGGCAATGATTAAGTGTGCTT 1680  
QY 1681 CAGCTGTGAGATGAAATGTTCTGTTCAACCTGCAATTAATGTTTATTCATCCAGCA 1740  
Db 1681 CAGCTGTGAGATGAAATGTTCTGTTCAACCTGCAATTAATGTTTATTCATCCAGCA 1740  
QY 1741 GTGTGCTCAGCTCTTACTCTGTGCGAGGAGCAGATTTTCATATCCAAATCAATTTCC 1800  
Db 1741 GTGTGCTCAGCTCTTACTCTGTGCGAGGAGCAGATTTTCATATCCAAATCAATTTCC 1800  
QY 1801 TCTTTCAGCAGACGCTGGGAGAGGGGATGATTTCTCTGTCATAGGAAATCTCAGAG 1860  
Db 1801 TCTTTCAGCAGACGCTGGGAGAGGGGATGATTTCTCTGTCATAGGAAATCTCAGAG 1860  
QY 1861 GCTCAGAGACTGCAAGGTGCTGCGCCAAAGTCAACAGCTAGTGAAGACAGAGATTC 1920  
Db 1861 GCTCAGAGACTGCAAGGTGCTGCGCCAAAGTCAACAGCTAGTGAAGACAGAGATTC 1920  
QY 1921 ATCTGTGAGACTTAAGTCAAGTCTCTCTCACTAATCCCAACAGCTTGTGCGCA 1980  
Db 1921 ATCTGTGAGACTTAAGTCAAGTCTCTCTCACTAATCCCAACAGCTTGTGCGCA 1980  
QY 1981 CCAAAATGCTCCCAAAAAGAGAGAAATGGGATTTTCTTGAAGCATCAATCTGGA 2040  
Db 1981 CCAAAATGCTCCCAAAAAGAGAGAAATGGGATTTTCTTGAAGCATCAATCTGGA 2040  
QY 2041 ATTAAAGTCAAACTAATCTCAATCTCTTAATAAGTAACTAAGTAAAGCAAGAGT 2100  
Db 2041 ATTAAAGTCAAACTAATCTCAATCTCTTAATAAGTAACTAAGTAAAGCAAGAGT 2100  
QY 2101 GTTCTCAAGTGGGAGAGCGGCTTCTTAATGAGAGCAATGATTAAGCACTGTCCT 2160  
Db 2101 GTTCTCAAGTGGGAGAGCGGCTTCTTAATGAGAGCAATGATTAAGCACTGTCCT 2160  
QY 2161 CTTTGGCAGTTGATTAAGTCTTTGAAAGTATGACAGAGCTGATGAGAGCTGTTAA 2220  
Db 2161 CTTTGGCAGTTGATTAAGTCTTTGAAAGTATGACAGAGCTGATGAGAGCTGTTAA 2220  
QY 2221 CTTGCAAAAACAGTACTTAAGTATTTGAGGAGAGATTAATTAAGTAAATTTGCAAAAT 2280  
Db 2221 CTTGCAAAAACAGTACTTAAGTATTTGAGGAGAGATTAATTAAGTAAATTTGCAAAAT 2280  
QY 2281 CACTTACAGCAACTGAAGCAATTAATCAACAGTGGAGAAATCAACCGAGAGGCG 2340  
Db 2281 CACTTACAGCAACTGAAGCAATTAATCAACAGTGGAGAAATCAACCGAGAGGCG 2340  
QY 2341 TGTGTGAAACATGGTGTATTAATGCGACCTGCGAACTGAACTTGAAGCACTCCACAAA 2400  
Db 2341 TGTGTGAAACATGGTGTATTAATGCGACCTGCGAACTGAACTTGAAGCACTCCACAAA 2400  
QY 2401 TGAATGTTTTAGGTTGATGAGAGCTGTTCCACATGATTAATCAAGAGTTCTTAAAGTT 2460  
Db 2401 TGAATGTTTTAGGTTGATGAGAGCTGTTCCACATGATTAATCAAGAGTTCTTAAAGTT 2460  
QY 2461 TAAAGTTGACATGATGATTAAGCATGCTTCTTGAAGTTTAATTAATGATTAAGCAT 2520



Db	2461	TAAGTTGACATGATGTATATAGCATGCTTCTTGAGTTTAATTAATATAACAT	2520
QY	2521	AAATTGCAATTAGAAATCAAGCATAAATCACTCAACTGCAAAAAA	2580
Db	2521	AAATTGCAATTAGAAATCAAGCATAAATCACTCAACTGCAAAAAA	2580
QY	2581	AAAAAA	2586
Db	2581	AAAAAA	2586

Search completed: February 19, 2004, 18:41:11  
Job time : 701 secs



[illegible]

RESULT 1		ALIGNMENTS	
LOCUS	EX418715		
DEFINITION	EX418715 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone	1201 bp	linear
ACCESSION	CS0DF008YIN2.5-PRIME, mRNA sequence.		EST 15-MAY-2003
VERSION	EX418715		
KEYWORDS	EX418715.1 GI:30769505		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	1 (bases 1 to 1201)		
COMMENT	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.		
	Full-length cDNA libraries and normalization		
	Unpublished		
	Contact: Genoscope		
	Genoscope - Centre National de Sequencage		
	BP 191 91006 EVRY cedex - France		
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr		
	Library was constructed by Life Technologies, a division of		
	Invitrogen. This sequence belongs to sequence cluster 6027.r For		
	more information about this cluster, see		
	http://www.genoscope.cns.fr/		
	cgi-bin/cluster.cgi?seq=CS0DF008D06QPI&cluster=6027.r. Contact :		
	Feng Liang Email : fliang@lifetech.com URL :		
	http://Fulllength.invitrogen.com/Invitrogen Corporation 1600		
	Faraday Avenue Genoscope sequence ID : CS0DF008D06QPI.		
FEATURES	location/Qualifiers		
source	1..1201		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="CS0DF008YIN2"		
	/tissue_type="FETAL BRAIN"		
	/dev_stage="fetal"		
	/clone_lib="Homo sapiens FETAL BRAIN"		
	/notes="Organ: brain; Vector: PCMVSPORT 6; 1st strand cDNA		
	was primed with a NotI-oligo(dT) primer. Five prime end		
	enriched, double-strand cDNA was digested with Not I and		
	cloned into the Not I and EcoRV sites of the PCMVSPORT 6		
	vector. Library was not normalized."		
BASE COUNT	266 a 347 c 379 g 195 t 14 others		
ORIGIN			
	Query Match	39.7%; Score 1026; DB 13; Length 1201;	
	Best Local Similarity	96.9%; Pred. No. 4,7e-125;	
	Matches 1089; Conservative	9; Mismatches 21; Indels 5; Gaps 5;	
QY	55	CGCAGCCCGCGGCGCTCCCGCGCGGAGCGACGACGATCCGCGCCGCGACCGCACTC	114
DB	67	CGCAGCCCGCGGCGCTCCCGCGCGGAGCGACGACGATCCGCGCCGCGACCGCACTC	126
QY	115	GGTCAGTCGCGGCGCGCGCTCGCGCGCGAGACGAGATGACGAGCGGCTTGGGGGCACCC	174
DB	127	GGTCAGTCGCGGCGCGCGCTCGCGCGCGAGACGAGATGACGAGCGGCTTGGGGGCACCC	186
QY	175	TGCTGTGCTGCTGTGTGCGCGCGCGGCGGTCCCGACGCGCCCCCGGCTTCCGACGGCGA	234
DB	187	TGCTGTGCTGCTGTGTGCGCGCGCGGCGGTCCCGACGCGCCCCCGGCTTCCGACGGCGA	246
QY	235	CCTCGGCTTCAGTCAAGCCCGCGCGCTCTCAGTACCCGAGAGAGAGACCACTTCA	294
DB	247	CCTCGGCTTCAGTCAAGCCCGCGCGCTCTCAGTACCCGCA-GAGAGAGCACTTCA	305
QY	295	ATGAGATGTTCCGCGAGGTTGAGAACTATGAGAGACGCGACGCAAAATTGGCAGCG	354
DB	306	ATGAGATGTTCCGCGAGGTTGAGAACTATGAGAGACGCGACGCAAAATTGGCAGCA-CG	364

[illegible]

JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D.
	Email: rcapds-remail.nih.gov
	Tissue Procurement: ATCC
	cDNA Library Preparation: Rubin Laboratory
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
	DNA Sequencing by: Agencourt Bioscience Corporation
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
	http://image.llnl.gov
	plate: LNCM139 row: p column: 22
FEATURES	High quality sequence stop: 743.
SOURCE	Location/Qualifiers
	1..1002
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="IMAGE:5952261"
	/tissue_type="ductal carcinoma, cell line"
	/lab_host="DH103 (phage-resistant)"
	/clone_idb="NIH_MGC_110"
	/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
	Note: This is a NIH_MGC Library."
BASE COUNT	204 a 258 c 288 g 252 t
ORIGIN	
Query Match	36.5%; Score 945; DB 13; Length 1002;
Best Local Similarity	97.7%; Pred. No.-2e-114;
Matches 980; Conservative	0; Mismatches 20; Indels 3; Gaps 2;
QY	849 CCCCTGCCCTGGAGGGCGAGCTTTGGCAAGACCCGCCAGCCGCTTCMGACTCATC 908
DB	1 CCCTGCCCCGTGAAGGGCGAGCTTTGGCAAGACCCGCCAGCCGCTTCMGACTCATC 60
QY	909 ACCTGAGAGCTAAGAGCTGATGAGAGCTTGGACCAGTACCCTTGTCAGTAGGCTCTC 968
DB	61 ACCTGGAGCTAAGAGCTGATGAGAGCTTGGACCAGTACCCTTGTCAGTAGGCTCTC 120
QY	969 TGCCAGGCCCAKAGCCAKAGACCTTGTAATGTGTGCAAGCCGACCTTCGTGGGAGCCGT 1028
DB	121 TGCAGGCCCAKAGCCAKAGACCTTGTAATGTGTGCAAGCCGACCTTCGTGGGAGCCGT 180
QY	1029 GACCAAGATGGAGAGATCCTGCTGCCAGAGAGCTCCCGCATGAGTAAATTGGAGC 1088
DB	181 GACCAAGATGGAGAGATCCTGCTGCCAGAGAGCTCCCGCATGAGTAAATTGGAGC 240
QY	1089 TTCAATGAGAAGAGGTGCGCCCKAGAGCTGAGAGACTTGGAGAGAGCTGATGAGAGATG 1148
DB	241 TTCAATGAGAAGAGGTGCGCCCKAGAGCTGAGAGACTTGGAGAGAGCTGATGAGAGATG 300
QY	1149 GCCTGGGGAGAGCTGCGCTGCGCGCGCTGCACTGCTGGAGAGGAGAGATTTAATC 1208
DB	301 GCCTGGGGAGAGCTGCGCTGCGCGCGCTGCACTGCTGGAGAGGAGAGATTTAATC 360
QY	1209 TGAACCAAGGCTGTGGGTGAGATGTGCAATAAATAAGTAAATTTATTTCCCAGGATGTG 1268
DB	361 TGAACCAAGGCTGTGGGTGAGATGTGCAATAAATAAGTAAATTTATTTCCCAGGATGTG 420
QY	1269 CTTTAAAGCGTGAGCTGACAAGGCTTCTTCTTACATCTTCTCCAGTAAGTTTCCCTCT 1328
DB	421 CTTTAAAGCGTGAGCTGACAAGGCTTCTTCTTACATCTTCTCCAGTAAGTTTCCCTCT 480
QY	1329 GGCTTGAACAACATGAGGATGTGTGCAATTGTTCAGTCCGCCAGGCGGTCTCCAGGCTT 1388
DB	481 GGCTTGAACAACATGAGGATGTGTGCAATTGTTCAGTCCGCCAGGCGGTCTCTCAGGCTT 540
QY	1389 CACAGCTGTGCTTGGAGAGTCAAGCAGGATTAACTGACAGAGCATTTTGCCACCC 1448

Db	541	CACAGTGTGGTGCCTGGGAGAGCTCAGCGAAGGGTTAACTGCAGGAGAGCTTTGCCA	600
Qy	1449	TGTCACAGATTATTTGGCTGTGCTTTGCCCTTACACAGATTGGCAGACAGCCGTTTGTCTACATG	1508
Db	601	TGTCACAGATTATTTGGCTGTGCTTTGCCCTTACACAGATTGGCAGACAGCCGTTTGTCTACATG	660
Qy	1509	GCTTGAATTAATTTTGTGAAGGGAGAGATGGAACAATGTGAGAGTCCTCCCTCATTTGTT	1568
Db	661	GCTTGAATTAATTTTGTGAAGGGAGAGATGGAACAATGTGAGAGTCCTCCCTCATTTGTT	720
Qy	1569	TTTGGGGAATATGTGAGAGAGATGGCCCTGCTTTGCAACATCAACTGGCAAAATGCA	1628
Db	721	TTTGGGGAATATGTGAGAGAGA-TGCCCTGCTTTGCAACATCAACTGGCAAAATGCA	779
Qy	1629	CAATGAATTTTTCACGCGAGTCTTTTCATGGGCAATGATTAAGCTGTGCTTCAGCTGTT	1688
Db	780	CAATGAATTTTTCACGCGAGTCTTTTCATGGGCAATGATTAAGCTGTGCTTCACGCTGTT	839
Qy	1689	GCAATGAATATGTTCTGTTCACCCCTGCATACATGTGTATTTCATCCAGCAGTGTGCT	1748
Db	840	GCAATGAATATGTTCTGTTCACCCCTGCATACATGTGTATTTCATCCAGCAGTGTGCT	899
Qy	1749	CAGTCTCTACTCTGTGTGCAGGAGAGATTTTCAATATCCAGATCAATTCCTCTCTCAG	1808
Db	900	CAATCTCTACTCTGTGTGCAGGAGAGATTTTCAATATCCAGATCAATTCCTCTCTCAG	959
Qy	1809	CACAGCTGAGG--AGGGGATCATGTTCTCTCTGATCATAG	1849
Db	960	AAAACTCTGGGGAGAGGGGCTTGTGTCTCTCTCCGCCAATAG	1002

FEATURES	Location/Qualifiers
source	1. .936

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5208328"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1fb="N1H MGC_110"
/note="Organ: pancreas; Vector: pOT8; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACAG(G). Library constructed by
Ling Hong in the laboratory of Gerald W. Rubin (University

```

BASE COUNT  
ORIGIN

186 a 234 c 275 g 240 t 1 others.

of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH-MGC library."

Query Match	Similarity	99.4%	Score	916.6	DB 13	Length	936
Best Local	Similarity	99.4%	Pred.	1.1e-110			
Matches	930	Conservative	0	Mismatches	5	Indels	1
QY	849	CCCCTGCCCCGTGAGGCGCAGCTTTGTCATGACCCCGCCACAGCGGCTTCTGAGACTTCATC	908				
Db	1	CCCCGTGCCCCGTGAGGCGCGAGCTTTGTCATGACCCCGCCACAGCGGCTTCTGAGACTTCATC	60				
QY	909	ACCGGGAGAGCTAGAGCCTGATGAGACCTTGAACCCGATGAGCCCTTGTGCAAGTGGCCTCTC	968				
Db	61	ACCTGGAGAGCTAGAGCCTGATGAGACCTTGGACCGATGCGCTTGTGCAAGTGGCCTCTC	120				
QY	969	TGACAGCCCCACAGCCACAGCCTGTGTATGTGTGCAAGCCGACCTTGTGGGAGCCGT	1028				
Db	121	TGACAGCCCCACAGCCACAGCCTGTGTATGTGTGCAAGCCGACCTTGTGGGAGCCGT	180				
QY	1029	GACCAAGATGGGGAGATCTGCTGCGCCAGAGAGGTCCCGCATGATGATGATGATGAGC	1088				
Db	181	GACCAAGATGGGGAGATCTGCTGCGCCAGAGAGGTCCCGCATGATGATGATGATGAGC	240				
QY	1089	TTCATGAGAGAGGTGTGCGCCACAGAGCTGAGAGCCTGAGAGAGAGCTGATGAGAGATG	1148				
Db	241	TTCATGAGAGAGGTGTGCGCCACAGAGCTGAGAGAGCTGAGAGAGAGCTGATGAGAGATG	300				
QY	1149	GCGCTGGGGGGAGCCTTGCGGCTGCGCGCGCTGCACTGCTGGGAGGGAGAGATTAGATC	1208				
Db	301	GCGCTGGGGGGAGCCTTGCGGCTGCGCGCGCTGCACTGCTGGGAGGGAGAGATTAGATC	360				
QY	1209	TGACACAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTATTTCCCGAGGTGTG	1268				
Db	361	TGACACAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTATTTCCCGAGGTGTG	420				
QY	1269	CTTTAGGCGTGGGGTGACACAGGCTTCTCCATCACTCTTCCAGTAAAGTTTCCCCTCT	1328				
Db	421	CTTTAGGCGTGGGGTGACACAGGCTTCTCCATCACTCTTCCAGTAAAGTTTCCCCTCT	480				
QY	1329	GGCTTGAACAGATAGGTGTGTGATTTGTTCAGCTCCCGCAGGCTGTCTCCAGGCTT	1388				
Db	481	GGCTTGAACAGATAGGTGTGTGATTTGTTCAGCTCCCGCAGGCTGTCTCCAGGCTT	540				
QY	1389	CACAGCTGTGGCTTGGAGAGGTAGGAGAGGGGTAAACTGGAGGAGAGTTGGCACCCC	1448				
Db	541	CACAGCTGTGGCTTGGAGAGGTAGGAGAGGGGTAAACTGGAGGAGAGTTGGCACCCC	600				
QY	1449	TGTCCAGATTATTTGGCTGTGTGCTTACACAGTTGGCAGACAGCCGTTGTCTACATG	1508				
Db	601	TGTCCAGATTATTTGGCTGTGTGCTTACACAGTTGGCAGACAGCCGTTGTCTACATG	660				
QY	1509	GCTTGAATATTTGTTAGGGGAGAGATGGAACATATGAGATCTCCCTCATTTGGT	1568				
Db	661	GCTTGAATATTTGTTAGGGGAGAGATGGAACATATGAGATCTCCCTCATTTGGT	720				
QY	1569	TTTGGGGAAATGTGGAGAGAGTCCCTGTCTTGCAAACATCAACTGGCAAAATATGCA	1628				
Db	721	TTTGGGGAAATGTGGAGAGAGTCCCTGTCTTGCAAACATCAACTGGCAAAATATGCA	780				
QY	1629	CAATGAAATTTTCCAGCGAGTTCTTTCATGAGGATAGTAAAGCTGAGCTTCAAGCTT	1688				
Db	781	CAATGAAATTTTCCAGCGAGTTCTTTCATGAGGATAGTAAAGCTGAGCTTCAAGCTT	840				
QY	1689	GCAGATGAATGTTCTGTTCACCCCTGCATTCATATGTGTTATTCATCCAGCATGTGCT	1748				
Db	841	GCAGATGAATGTTCTGTTCACCCCTGCATTCATATGTGTTATTCATCCAGCATGTGCT	900				
QY	1749	CAGCTCTCACTCTGT--GCCAGGGGACAGATTTTCAAT	1783				
Db	901	CAGCTCTCACTCTGTGGAGGGGACAGATTTTCAAT	936				

RESULT 4  
BO690888 951 bp mRNA linear EST 15-JUL-2002  
LOCUS AGENCOURT 8034028 NIH\_MGC\_110 Homo sapiens CDNA clone IMAGE:6208256  
DEFINITION 5', mRNA sequence.  
ACCESSION BO690888 GI:21816204  
VERSION BO690888.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
1 (bases 1 to 951)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
AUTHORS Contact: Robert Strausberg, Ph.D.  
TITLE Email: cgabbs-remail.nih.gov  
JOURNAL Tissue Procurement: ATCC  
COMMENT CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM2365 row: k column: 09  
High quality sequence stop: 698.  
Location/Qualifiers  
1. 951  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6208256"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;  
Site 2: EcoRI; CDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-CDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."  
BASE COUNT 191 a 239 c 276 g 244 t 1 others  
ORIGIN  
Query Match 35.4%; Score 914.8; DB 13; Length 951;  
Best Local Similarity 98.9%; Pred. No. 1.8e-110;  
Matches 941; Conservative 0; Mismatches 8; Indels 2; Gaps 2;  
QY 849 CCCCTGCCGTGAGGCGAGCTTTGGCATGATCCCGCCAGCGCGCTTCTGACCTCATC 908  
DB 1 CCCCTGCCGTGAGGCGAGCTTTGGCATGATCCCGCCAGCGCGCTTCTGACCTCATC 60  
QY 909 ACCTGGGAGCTAGAGCTGTATGAGACCTTGGACCGATGCCCTTGTGCGAGCTTCTC 968  
DB 61 ACCTGGGAGCTAGAGCTGTATGAGACCTTGGACCGATGCCCTTGTGCGAGCTTCTC 120  
QY 969 TGGCAGCCCGACAGCCAGCCTGTATGTATGTGCAAGCCGACTTCTGAGGAGACCTT 1028  
DB 121 TGGCAGCCCGACAGCCAGCCTGTATGTATGTGCAAGCCGACTTCTGAGGAGACCTT 180  
QY 1029 GACCAATATGGGAGATCTCTGCTGCCAGAGAGGTCCCGATGATGATGAAGTTGGCAGC 1088  
DB 181 GACCAATATGGGAGATCTCTGCTGCCAGAGAGGTCCCGATGATGATGAAGTTGGCAGC 240  
QY 1089 TTGATGAGAGAGGTGGCCAGAGCTGAGAGACCTGAGAGAGAGCTGATGAAGAGATG 1148  
DB 241 TTGATGAGAGAGGTGGCCAGAGCTGAGAGACCTGAGAGAGAGCTGATGAAGAGATG 300

QY 1149 GCGCTGGGGAGAGCTTGGGCTGCCCGCTGCACTGCTGGGAGAGGAGATTTAGATC 1208  
DB 301 GCGCTGAGGAGAGCTTGGGCTGCCCGCTGCACTGCTGGGAGAGGAGATTTAGATC 360  
QY 1209 TGACACAGAGCTGTGTGAGATGTGCAATAGAAATAGTAAATTTATTTCCAGAGTGTG 1268  
DB 361 TGACACAGAGCTGTGTGAGATGTGCAATAGAAATAGTAAATTTATTTCCAGAGTGTG 420  
QY 1269 CTTTACGCTGTGGGTACAGAGCTTCTTCTTACATCTTCTTCCAGTAATTTCCCTCT 1328  
DB 421 CTTTACGCTGTGGGTACAGAGCTTCTTCTTACATCTTCTTCCAGTAATTTCCCTCT 480  
QY 1329 GCGTTGACAGATGAGTGTGTGATGATTTGTGAGTCCCGCCAGAGCTTCTTCCAGAGCTT 1388  
DB 481 GCGTTGACAGATGAGTGTGTGATGATTTGTGAGTCCCGCCAGAGCTTCTTCCAGAGCTT 540  
QY 1389 CACAGCTGTGTGTGGAGAGATGAGCAGAGGTTAAACTGACAGAGCAGTTTGCACACC 1448  
DB 541 CACAGCTGTGTGTGGAGAGATGAGCAGAGGTTAAACTGACAGAGCAGTTTGCACACC 600  
QY 1449 TGTCCAGATTTATGCTGTGCTTGTGCTTACAGTGTGACAGAGCCGTTGTTACATG 1508  
DB 601 TGTCCAGATTTATGCTGTGCTTGTGCTTACAGTGTGACAGAGCCGTTGTTACATG 660  
QY 1509 GCTTGTATTAATTTGTTGAGGAGAGAGATGAAACAAATGTGAGTCTTCTTGTATTTGT 1568  
DB 661 GCTTGTATTAATTTGTTGAGGAGAGAGATGAAACAAATGTGAGTCTTCTTGTATTTGT 720  
QY 1569 TTTGGGGAAATGTGAGAAAGATGACCTGCTTGCATTAACATCACTTGGCAAAATGCA 1628  
DB 721 TTTGGGGAAATGTGAGAAAGATGACCTGCTTGCATTAACATCACTTGGCAAAATGCA 780  
QY 1629 CAATGATTTTCCAGCAGATTTCTTCCATGAGGATAGTAAAGTGTGCTTCAAGTGT 1688  
DB 781 CAATGATTTTCCAGCAGATTTCTTCCATGAGGATAGTAAAGTGTGCTTCAAGTGT 840  
QY 1689 GCAATGAAATGTTCTGTCTTCACTTGCATTAACATGTTATATCAACGAGATGTGTC 1747  
DB 841 GCAATGAAATGTTCTGTCTTCACTTGCATTAACATGTTATATCAACGAGATGTGTC 900  
QY 1748 TCAGTCTTACCTCTGTGCCA-GGGCAGCAATTTTCATATCCAGATCAAT 1797  
DB 901 TCAGTCTTACCTCTGTGCCA-GGGCAGCAATTTTCATATCCAGATCAAT 951  
RESULT 5  
BO686792 932 bp mRNA linear EST 15-JUL-2002  
LOCUS AGENCOURT 8343587 NIH\_MGC\_110 Homo sapiens CDNA clone IMAGE:6250382  
DEFINITION 5', mRNA sequence.  
ACCESSION BO686792 GI:21812108  
VERSION BO686792.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
1 (bases 1 to 932)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
AUTHORS Contact: Robert Strausberg, Ph.D.  
TITLE Email: cgabbs-remail.nih.gov  
JOURNAL Tissue Procurement: ATCC  
COMMENT CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM2393 row: f column: 15  
High quality sequence stop: 710.  
Location/Qualifiers



```

source
1. .932
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6250179"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT      184 a      235 c      279 g      234 t
ORIGIN
Query Match      33.9%; Score 877.6; DB 13; Length 932;
Best Local Similarity 98.8%; Pred. No. 1.3e-105;
Matches 905; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

QY 847 CACCCCTGCCGTGAGAGGCGAGCTTTGCCATGACCCCGCAGCCGACTTCTGACCTCA 906
DB 18 CACCCCTGCCGTGAGAGGCGAGCTTTGCCATGACCCCGCAGCCGACTTCTGACCTCA 77
QY 907 TCACCTGGAGAGCTAGAGCTGATGAGCCTTGAGACCGATGCCCTTGTCAGTGGCCCTCC 966
DB 78 TCACCTGGAGAGCTAGAGCTGATGAGCCTTGAGACCGATGCCCTTGTCAGTGGCCCTCC 137
QY 967 TCTGCCAGCCCGCAGCCAGCCAGCTGTGTATGTGTGCAAGCCGACCTTCTGAGGAGCC 1026
DB 138 TCTGCCAGCCCGCAGCCAGCCAGCTGTGTATGTGTGCAAGCCGACCTTCTGAGGAGCC 197
QY 1027 GTTACCAAGATGGGAGAGATCTCTCTCCCAAGAGAGTCCCCCATGATGATGAAGTTGGCA 1086
DB 198 GTTACCAAGATGGGAGAGATCTCTCTCCCAAGAGAGTCCCCCATGATGATGAAGTTGGCA 257
QY 1087 GCTTCAAGAGAGAGTGGCCGCAAGAGCTGAGAGAGCTGAGAGAGAGCTGATGAGAGAGA 1146
DB 258 GCTTCAAGAGAGAGTGGCCGCAAGAGCTGAGAGAGCTGAGAGAGAGCTGATGAGAGAGA 317
QY 1147 TGGCGCTGGGAGAGCTGCGGCTGCGCGCTGCACTGCTGGGAGGGAAGATTGTAGA 1206
DB 318 TGGCGCTGGGAGAGCTGCGGCTGCGCGCTGCACTGCTGGGAGGGAAGATTGTAGA 377
QY 1207 TCTGAGACAGAGCTGTGAGATGTCATATAGAAATAGCTAATTTATTTCCCAAGGTGTG 1266
DB 378 TCTGAGACAGAGCTGTGAGATGTCATATAGAAATAGCTAATTTATTTCCCAAGGTGTG 437
QY 1267 TGTCTTAGGCGCTGGGCTGACCAAGCTTCTTCTCACTCTTCTTCCAGTAAGTTCCCT 1326
DB 438 TGTCTTAGGCGCTGGGCTGACCAAGCTTCTTCTCACTCTTCTTCCAGTAAGTTCCCT 497
QY 1327 CTGGCTTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1386
DB 498 CTGGCTTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 557
QY 1387 TTCAAGTCTGTGCTTGGAGAGAGTCAAGGAGGTTAACTGAGAGAGAGTTGGCACC 1446
DB 558 TTCAAGTCTGTGCTTGGAGAGAGTCAAGGAGGTTAACTGAGAGAGAGTTGGCACC 617
QY 1447 CCTGTCCAGATTAATTTGGCTCTTGGCTCTTACCAAGTTGAGAGAGCGTTTGTCTTACA 1506
DB 618 CCTGTCCAGATTAATTTGGCTCTTGGCTCTTACCAAGTTGAGAGAGCGTTTGTCTTACA 677
QY 1507 TGGCTTTGATTAATTTGTTGAGGAGAGAGATGGAACAAATGAGAGTCTTCTTGATTTG 1566
DB 678 TGGCTTTGATTAATTTGTTGAGGAGAGAGATGGAACAAATGAGAGTCTTCTTGATTTG 737
QY 1567 GTTTTGGGAGAAATGTGAGAGAGAGTCCCTGCTTTGCAACATCAACTGGCAAAATTC 1626

```

```

DB 738 GTTTTGGGAGAAATGTGAGAGAGAGTCCCTGCTTTC-ACATCAACTCGGCAAAATTC 796
QY 1627 AACAAATGAATTTTCCACGAGATTTCTTTCATGGGATAGTAAGCTGTGCTTCACTG 1686
DB 797 AACAAATGAATTTTCCACGAGATTTCTTTCATGGGATAGTAAGCTGTGCTTCACTG 856
QY 1687 TTGCAATGAATTTTCTGTCACCTGTCATTCATGTTTATTTCA-TCCAGCATGTT 1745
DB 857 TTGCAATGAATTTTCTGTCACCTGTCATTCATGTTTATTTCACTTCAGCGTTGT 916
QY 1746 GCTCAGCTCTTACCTC 1761
DB 917 GCTCAGCTCTTACCTC 932

RESULT 6
B0689559 926 bp mRNA linear EST 15-JUL-2002
LOCUS AGENCOURT 8345000 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250179
DEFINITION 5', mRNA sequence.
ACCESSION B0689559.1 GI:21814875
VERSION B0689559.1 GI:21814875
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ARCC
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2392 row: n column: 04
High quality sequence stop: 584.
Location/Qualifiers
1. .926
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6250179"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_110"
/notes="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT      181 a      232 c      272 g      237 t
ORIGIN
Query Match      33.9%; Score 876.2; DB 13; Length 926;
Best Local Similarity 97.9%; Pred. No. 2e-105;
Matches 906; Conservative 0; Mismatches 17; Indels 2; Gaps 2;

QY 849 CCCCCTGCCGTGAGAGGCGAGCTTTGCCATGACCCCGCAGCCGACTTCTGACCTATC 908
DB 1 CCCCCTGCCGTGAGAGGCGAGCTTTGCCATGACCCCGCAGCCGACTTCTGACCTATC 60
QY 909 ACCTGGAGAGCTAGAGAGCTTGTGAGAGAGCTTGTGAGAGAGCTTGTGAGAGAGCTTCTC 968
DB 61 ACCTGGAGAGCTAGAGAGCTTGTGAGAGAGCTTGTGAGAGAGCTTGTGAGAGAGCTTCTC 120

```

QY 969 TGGCAGCCCCCAGCCAGCCTGCTGTATGTGTGAAAGCCAGCCTTGTGGAGCCGT 1028  
DB 121 TGCACAGCCCCCAGCCAGCCTGCTGTATGTGTGAAAGCCAGCCTTGTGGAGCCGT 180  
QY 1029 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGATGAATGATGGCAGC 1088  
DB 181 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGATGAATGATGGCAGC 240  
QY 1089 TTCATGAGAGAGGTGCGCGAGAGCTGAGAGACTTGGAGAGAGAGCTGATGAAGAGATG 1148  
DB 241 TTCATGAGAGAGGTGCGCGAGAGCTGAGAGACTTGGAGAGAGAGCTGATGAAGAGATG 300  
QY 1149 GCGCTGAGAGAGCTGCGCGAGAGCTGAGAGACTTGGAGAGAGAGAGATTTAGATC 1208  
DB 301 GCGCTGAGAGAGCTGCGCGAGAGCTGAGAGACTTGGAGAGAGAGAGATTTAGATC 360  
QY 1209 TGGACCAAGCTGTGGATGATGTGCAATAGAAATAGCTAATTTATTTCCCAAGTGTGTG 1268  
DB 361 TGGACCAAGCTGTGGATGATGTGCAATAGAAATAGCTAATTTATTTCCCAAGTGTGTG 420  
QY 1269 CTTTAGAGAGAGCTGCGCGAGAGCTTCTCTCAATCTTCTCCAGTAGATTTCCCTCT 1328  
DB 421 CTTTAGAGAGAGCTGCGCGAGAGCTTCTCTCAATCTTCTCCAGTAGATTTCCCTCT 480  
QY 1329 GCGCTGACAGCATGAGAGTGTGTGCAATTTGTCAGCTCCCGAGAGCTGTTCTCAAGCTT 1388  
DB 481 GCGCTGACAGCATGAGAGTGTGTGCAATTTGTCAGCTCCCGAGAGCTGTTCTCAAGCTT 540  
QY 1389 CACAGCTGTGTGTGGAGAGCTCAGCAGAGGTTAACTGCGAGAGCATTTGGCCACCC 1448  
DB 541 CACAGCTGTGTGTGGAGAGCTCAGCAGAGGTTAACTGCGAGAGCATTTGGCCACCC 600  
QY 1449 TGGCAGATTAATGAGCTGCTTCTCTCAATCTTCTCCAGTAGATTTCCCTCT 1508  
DB 601 TGGCAGATTAATGAGCTGCTTCTCTCAATCTTCTCCAGTAGATTTCCCTCT 660  
QY 1509 GCTTTGATTAATTTGTGGAGAGAGAGATGAAACAATGTGAGTCTCCCTGATGTGT 1568  
DB 661 GCTTTGATTAATTTGTGGAGAGAGAGATGAAACAATGTGAGTCTCCCTGATGTGT 720  
QY 1569 TTTGGGGAATGAG 1628  
DB 721 TTTGGGGAATGAG 779  
QY 1629 CAAATGATTTTTCACAGCAGTCTTTCATGAGCATAGAGTGTGCTTCAAGCTGT 1688  
DB 780 CAAATGATTTTTCACAGCAGTCTTTCATGAGCATAGAGTGTGCTTCAAGCTGT 839  
QY 1689 GCAAGATGAAATGTTGTTGTCACAGCAGTCTTTCATGAGCATAGAGTGTGCTTCAAGCTGT 1747  
DB 840 GCAAGATGAAATGTTGTTGTCACAGCAGTCTTTCATGAGCATAGAGTGTGCTTCAAGCTGT 899  
QY 1748 TCAGCTCTTACTCTGTGCGCAGGCT 1772  
DB 900 TCAGCTCTTACTCTGTGCGCAGGCT 924

RESULT 7  
BO691927 912 bp mRNA linear EST 15-JUL-2002  
LOCUS AGENCOURT 8034941 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6207089  
DEFINITION 5', mRNA sequence.  
ACCESSION BO691927.1 GI:21817255  
VERSION BO691927.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 912)  
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: LNCM2362 row: 5 column: 18  
High quality sequence stop: 654.  
Location/Qualifiers  
source 1..912  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6207089"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH MGC 110"  
/note="Organ: pancreas; Vector: pOT87; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Library constructed by  
ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC library."

BASE COUNT 180 a 228 c 270 g 231 t 3 others  
ORIGIN

Query Match 33.7%; Score 872.2; DB 13; Length 912;  
Best Local Similarity 98.6%; Pred. No. 6.8e-105;  
Matches 899; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 849 CCCCTGCCCGTGGAGAGAGCTTGGCATGACCCGCGAGCGGCTTGGACCTCATC 908  
DB 1 CCCCTGCCCGTGGAGAGAGCTTGGCATGACCCGCGAGCGGCTTGGACCTCATC 60  
QY 909 ACCTGGAGCTAGAGCTGTAGAGAGCTTGGACCGATGCCCTTGTGCAAGTGCCTCTC 968  
DB 61 ACCTGGAGCTAGAGCTGTAGAGAGCTTGGACCGATGCCCTTGTGCAAGTGCCTCTC 120  
QY 969 TGGCAGCCCCCAGCCAGCAGCTGTGTATGTGTGCAAGCGACCTTCGTGGAGAGCGT 1028  
DB 121 TGGCAGCCCCCAGCCAGCAGCTGTGTATGTGTGCAAGCGACCTTCGTGGAGAGCGT 180  
QY 1029 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGAAGTGGCAGC 1088  
DB 181 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGAAGTGGCAGC 240  
QY 1089 TTCATGAGAGAGGTGCGCGAGAGCTTGGAGAGAGAGCTGATGAAGAGATG 1148  
DB 241 TTCATGAGAGAGGTGCGCGAGAGCTTGGAGAGAGAGCTGATGAAGAGATG 300  
QY 1149 GCGCTGAGAGAGCTGCGCGAGAGCTGAGAGACTTGGAGAGAGAGAGATTTAGATC 1208  
DB 301 GCGCTGAGAGAGCTGCGCGAGAGCTGAGAGACTTGGAGAGAGAGAGATTTAGATC 360  
QY 1209 TGGACCAAGCTGTGGATGATGTGCAATAGAAATAGCTAATTTATTTCCCAAGTGTGTG 1268  
DB 361 TGGACCAAGCTGTGGATGATGTGCAATAGAAATAGCTAATTTATTTCCCAAGTGTGTG 420  
QY 1269 CTTTAGAGAGAGCTGCGCGAGAGCTTCTCTCAATCTTCTCCAGTAGATTTCCCTCT 1328  
DB 421 CTTTAGAGAGAGCTGCGCGAGAGCTTCTCTCAATCTTCTCCAGTAGATTTCCCTCT 480  
QY 1329 GCGCTGACAGCATGAGAGTGTGTGCAATTTGTCAGCTCCCGAGAGCTGTTCTCAAGCTT 1388  
DB 481 GCGCTGACAGCATGAGAGTGTGTGCAATTTGTCAGCTCCCGAGAGCTGTTCTCAAGCTT 540  
QY 1389 CACAGCTGTGTGTGGAGAGCTCAGCAGAGGTTAACTGCGAGAGCATTTGGCCACCC 1448

Db 541 CACAGCTGCTGCTGGAGAGTCAAGAGGCTTAACTGACAGAGCATTTGCCACCCC 600  
 1449 TGTCCAGATTATGCTGCTTTGCTCCTTACCAAGTTGGCAGACAGCCGTTTGTCTACATG 1508  
 Db 601 TGTCCAGATTATGCTGCTTTGCTCCTTACCAAGTTGGCAGACAGCCGTTTGTCTACATG 660  
 1509 GCTTTGATTAATGTTGAGGGAGAGAGATGAAACAATGTGAGAGTCCCTCTAATGGT 1568  
 Db 661 GCTTTGATTAATGTTGAGGGAGAGAGATGAAACAATGTGAGAGTCCCTCTAATGGT 720  
 1569 TTTGGGAAATGTGAGAGAGTGTGCTGCTTTGCAAAATCACTGGCAAAAATGCA 1628  
 Db 721 TTTGGGAAATGTGAGAGAGTGTGCTGCTTTGCAAAATCACTGGCAAAAATGCA 779  
 1629 CAAATGAATTTCCAGCAGTCTTTCCATGAGGATAGTAAGCTGTCCTTCACTGTT 1688  
 Db 780 CAAATGAATTTCCAGCAGTCTTTCCATGAGGATAGTAAGCTGTCCTTCACTGTT 839  
 1689 GCAGATGAATGTTGCTGCTTCACTGCTGATTAATGATGTTT-ATTGATCCAGAGTGTGC 1747  
 Db 840 GCAGATGAATGTTGCTGCTTCACTGCTGATTAATGATGTTT-ATTGATCCAGAGTGTGC 899  
 1748 TTAGCTCTCTACC 1759  
 Db 900 TTAGCTCTCTACC 911

RESULT 8 AL535720 977 bp mRNA linear EST 31-MAY-2003  
 LOCUS AL535720 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
 DEFINITION CS0DF016YJ11 5-PRIME, mRNA sequence.  
 ACCESSION AL535720  
 VERSION AL535720.2 GI:31260722  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 977)  
 L1,W.B., Gruber,C., Jessee,J. and Polayes,D.  
 Full-length cDNA libraries and normalization  
 Unpublished  
 On Feb 13, 2001 this sequence version replaced gi:12799213.  
 CONTACT Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 6027.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF016CB06QPL&cluster=6027.r. Contact :  
 Feng Liang Email : fliang@life.techn.com URL :  
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0DF016CB06QPL.  
 Location/Qualifiers  
 1..977  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DF016YJ11"  
 /rname="FETAL BRAIN"  
 /dev\_stage="fetal"  
 /clone\_lib="Homo sapiens FETAL BRAIN"  
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-strand cDNA was digested with NotI and  
 cloned into the NotI and EcoRV sites of the pCMVSPORT 6  
 vector. Library was not normalized."

BASE COUNT  
 ORIGIN

222 a 294 c 296 g 165 t

Query Match 33.7%; Score 872; DB 9; Length 977;  
 Best Local Similarity 99.9%; Pred. No. 78-105; Mismatches 0; Indels 1; Gaps 1;  
 Matches 883; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 126 GGGCGGCGCTGCGGGCGCAGAGCGAGATGACGCGCTTGGGGCCACCTGCTGCTG 185  
 Db 95 GGGCGGCGCTGCGGGCGCAGAGCGAGATGACGCGCTTGGGGCCACCTGCTGCTG 154  
 186 CTCTGCGCGCGCGGCTCCCAAGCGCCCGCGCCGCTCCGACGCGCCTCGGCTGCA 245  
 Db 155 CTCTGCGCGCGCGGCTCCCAAGCGCCCGCGCCGCTCCGACGCGCCTCGGCTGCA 214  
 246 GTCAAGCCCGCGCGCGCTCTCAGCTACCCGAGAGAGAGCCACCTCAATAGATGTT 305  
 Db 215 GTCAAGCCCGCGCGCGCTCTCAGCTACCCGAGAGAGAGCCACCTCAATAGATGTT 274  
 306 CGGAGGTTGAGGAATGATGAGAGCAGCAGCACAATTTGGCAGCGCGGTTGAGAG 365  
 Db 275 CGGAGGTTGAGGAATGATGAGAGCAGCAGCACAATTTGGCAGCGCGGTTGAGAG 333  
 366 ATGAGGCAAGAAAGCTGCTGCTAAGCATATCAGAGTGAACCTGGCAACTTACCT 425  
 Db 334 ATGAGGCAAGAAAGCTGCTGCTAAGCATATCAGAGTGAACCTGGCAACTTACCT 393  
 426 CCAGCTATCAATAGAGCAACACAGACAGAGGTTGAAATTAATCATCATCTG 485  
 Db 394 CCAGCTATCAATAGAGCAACACAGACAGAGGTTGAAATTAATCATCATCTG 453  
 486 CACGGAATTTCAACAAGTTAACTCAACCAACAGACTGACCAATGCTTTTCAGAGCA 545  
 Db 454 CACGGAATTTCAACAAGTTAACTCAACCAACAGACTGACCAATGCTTTTCAGAGCA 513  
 546 GTTATCATCTGTGAGAGCAGAAAGGAGAGAGCCAGATGATCATTCAGAGAG 605  
 Db 514 GTTATCATCTGTGAGAGCAGAAAGGAGAGAGCCAGATGATCATTCAGAGAG 573  
 606 GACTGTGGGCGCCAGCATGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 665  
 Db 574 GACTGTGGGCGCCAGCATGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 633  
 666 CGGGGCGAGAGATGCTTGGACCTGGGAGAGTGAAGTCTGTGAGAGCAAGCTGTGTC 725  
 Db 634 CGGGGCGAGAGATGCTTGGACCTGGGAGAGTGAAGTCTGTGAGAGCAAGCTGTGTC 693  
 726 TGGGGTCACTGACCAAAATGGCCACAGGGGAGAGATGGAGCATCTGTGCAACAG 785  
 Db 694 TGGGGTCACTGACCAAAATGGCCACAGGGGAGAGATGGAGCATCTGTGCAACAG 753  
 786 AGGAGCTGCAGCGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 845  
 Db 754 AGGAGCTGCAGCGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 813  
 846 ACACCCCTGCGCGCTGAGAGGGCGAGCTTTGTCATGACCCGCGCAGCGGCTTGTGAC 905  
 Db 814 ACACCCCTGCGCGCTGAGAGGGCGAGCTTTGTCATGACCCGCGCAGCGGCTTGTGAC 873  
 906 ATCACTGTGAGCTAGAGCTGTGATGAGCTTGTGAGCTTGTGAGCTTGTGAGCTTGT 965  
 Db 874 ATCACTGTGAGCTAGAGCTGTGATGAGCTTGTGAGCTTGTGAGCTTGTGAGCTTGT 933  
 966 CTCTGCGAGCGCCAGAGCCACAGCCAGCTGCTGATAGTGTGCAAGCC 1009  
 Db 934 CTCTGCGAGCGCCAGAGCCACAGCTGCTGATAGTGTGCAAGCC 977

RESULT 9 BU149689 949 bp mRNA linear EST 03-SEP-2002  
 LOCUS BU149689  
 DEFINITION AGENCOURT\_8049944 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6083782  
 5', mRNA sequence.  
 ACCESSION BU149689  
 VERSION BU149689.1 GI:22663221

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 949)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: rgs@bgl.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:  
http://image.liml.gov  
Plate: LIM2314 row: h column: 23  
High quality sequence start: 19  
High quality sequence stop: 678.  
Location/Qualifiers  
1. 949  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6083782"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOT87; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald W. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT 188 a 236 c 288 g 237 t  
ORIGIN

Query Match 33.6%; Score 870; DB 13; Length 949;  
Best Local Similarity 98.1%; Pred. No. 1,3e-104;  
Matches 901; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

848 ACCCTGCGCGTGGAGGGCGAGCTTTGGCCATGACCCCGACGCGGCTTCTGACCTCAT 907  
31 ACCCTGCGCGTGGAGGGCGAGCTTTGGCCATGACCCCGACGCGGCTTCTGACCTCAT 90  
908 CACCTGGAGCTAAGAGCTTATGAGAGCTTGGACGATGCTTTGGCCAGTGGCTTCT 967  
91 CACCTGGAGCTAAGAGCTTATGAGAGCTTGGACGATGCTTTGGCCAGTGGCTTCT 150  
968 CTGGCAGCCCGACGACGACCTGTGTATGTGTGCAAGCCGACCTTCTGGGGAGCCG 1027  
151 CTGGCAGCCCGACGACGACCTGTGTATGTGTGCAAGCCGACCTTCTGGGGAGCCG 210  
1028 TGACCAAGATGGAGAGATCTGCTGCCAGAGAGAGTCCCGATGATGAAGTTGGCAG 1087  
211 TGACCAAGATGGAGAGATCTGCTGCCAGAGAGAGTCCCGATGATGAAGTTGGCAG 270  
1088 CTTTATGAGAGAGTGTGGCCGACGAGCTTGGAGAGAGCTTGAATGAAGAT 1147  
271 CTTTATGAGAGAGTGTGGCCGACGAGCTTGAAGAGAGCTTGAATGAAGAT 330  
1148 GCGCGTGGGGAGAGCTGCGGCGCTGCCGCTGCACTGCGAGAGAGAGATTAGAT 1207  
331 GCGCGTGGGGAGAGCTGCGGCGCTGCCGCTGCACTGCGAGAGAGAGATTAGAT 390  
1208 CTGAGCAGAGCTGTGGTATGATGTGCAATTAATTAATTTTCCCAAGGTGT 1267  
391 CTGAGCAGAGCTGTGGTATGATGTGCAATTAATTAATTTTCCCAAGGTGT 450

QY 1268 GCTTTAGCGGTGGGCTGACAGGCTTCTTCTACATCTTCTTCCAGTAAGTTCCCTC 1327  
DB 451 GCTTTAGCGGTGGGCTGACAGGCTTCTTCTACATCTTCTTCCAGTAAGTTCCCTC 510  
QY 1328 TGGCTTACAGATAGAGTGTGTGATTTGTAGCTTCCCGCAGGCTTCTCCAGGCT 1387  
DB 511 TGGCTTACAGATAGAGTGTGTGATTTGTAGCTTCCCGCAGGCTTCTCCAGGCT 570  
QY 1388 TCACAGTGTGTGCTTGGAGAGAGTGCAGAGGTTAACTCAGAGAGAGATTGCCACC 1447  
DB 571 TCACAGTGTGTGCTTGGAGAGAGTGCAGAGGTTAACTCAGAGAGAGATTGCCACC 630  
QY 1448 CTGTCCAGATTAATTTGGCTTGGCTTGTGCTTACAGTGTGACAGAGCGTTGTCTACAT 1507  
DB 631 CTGTCCAGATTAATTTGGCTTGTGCTTGTGCTTACAGTGTGACAGAGCGTTGTCTACAT 690  
QY 1508 GCGTTTGAATTAATTTTGGAGGAGAGATGGAACAAATGTGAGTCTCCCTGTATTGG 1567  
DB 691 GCGTTTGAATTAATTTTGGAGGAGAGATGGAACAAATGTGAGTCTCCCTGTATTGG 750  
QY 1568 TTTTGGGGAATGTGAGAGAGAGTCCCTGCTTGGCAACATCACTGGCAAAAATGCA 1627  
DB 751 TTTTGGGGAATGTGAGAGAGAGTCCCTGCTTGGCAACATCACTGGCAAAAATGCA 810  
QY 1628 ACAATGAATTTTCCAGCAG-TTCTTTCATGGGATAGGTAAGCTGTGCTTCAAGCTG 1686  
DB 811 ACAATGAATTTTCCAGCAGTTCTTTCATGGGATAGGTAAGCTGTGCTTCAAGCTG 870  
QY 1687 TTGCAGATGAATTTTCTGTTTCACTTGCATTAATGTC-TTATTATCCAGCAGTGT 1745  
DB 871 TTGCAGATGAATTTTCTGTTTCACTTGCATTAATGTC-TTATTATCCAGCAGTGT 930  
QY 1746 GCTCAGCTCTTCACTCTG 1763  
DB 931 GCTCAGCTCTTCACTCTG 948

RESULT 10  
AL566024/c  
LOCUS  
DEFINITION  
AL566024 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
CS0DP016Y011 3-PRIME, mRNA sequence.  
ACCESSION  
AL566024  
VERSION  
AL566024.1 GI:12917976  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
COMMENT  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr; Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 6027.r For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DP016CE06NP1&cluster=6027.r. Contact :  
Peng Liang Email: fliang@life.techn.com URL:  
http://fulllength.invitrogen.com/ invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID: CS0DP016CE06NP1.  
Location/Qualifiers  
1. 959  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DP016Y011"  
/tissue\_type="FETAL BRAIN"  
/dev\_stage="fetal"

```

/clone_lib="Homo sapiens FETAL BRAIN"
/Note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT      241 a      195 c      221 g      266 t      36 others
ORIGIN
Query Match      33.3%; Score 862.2; DB 9; Length 959;
Best Local Similarity 93.4%; Pred. No. 1.3e-103;
Matches 897; Conservative 31; Mismatches 28; Indels 4; Gaps 3;
QY 1576 AATTGTGAGAAAGAGGCGCTGTTTGCAAACTCACTGCGCAAAATGACAAAGCA 1635
DB 959 AATGTGAGAAAGAGGCGCTGTTTGCAAACTCACTGCGCAAAATGACAAAGCA 900
QY 1636 ATTTCCACGAGCTTTTCATGAGGAGTAAGTGAAGTGGCTTCAGCTTTGAGATG 1695
DB 899 ATTTCCACGAGCTTTTCATGAGGAGTAAGTGAAGTGGCTTCAGCTTTGAGATG 840
QY 1696 AATGTTCTGTACCTGATTAATGTTTATTCATCCAGAGTGTGCTCAGCTCC 1755
DB 839 AATGTTCTGTACCTGATTAATGTTTATTCATCCAGAGTGTGCTCAGCTCC 780
QY 1756 TACCTGTGCGAGGAGAGATTTTCATATCCAAATCAATCCCTCTCAGCAGAGC 1815
DB 779 TACCTGTGCGAGGAGAGATTTTCATATCCAAATCAATCCCTCTCAGCAGAGC 720
QY 1816 TGGGAGGGGGGATATTGTTCTCTGTCATCAAGGATTCAGAGGCTCAGAGCTGCA 1875
DB 719 TGGGAGGGGGGATATTGTTCTCTGTCATCAAGGATTCAGAGGCTCAGAGCTGCA 660
QY 1876 GCTGCTTGGCCAGTACACAGTATGAAAGCAGAGAGTTTCACTGATGATGATC 1935
DB 659 GCTGCTTGGCCAGTACACAGTATGAAAGCAGAGAGTTTCACTGATGATGATC 600
QY 1936 TAAGCTAGTGTCTCTCCACTACCCACACAGCCTTGGTGCACAAAGTGTCTCCC 1995
DB 599 TAAGCTAGTGTCTCTCCACTACCCACACAGCCTTGGTGCACAAAGTGTCTCCC 540
QY 1996 AAAGAGAGAGAGATGGGATTTTTC--TGAGGAGTACATCTGGAATTAAGTCAAC 2053
DB 539 AAAGAGAGAGAGATGGGATTTTTC--TGAGGAGTACATCTGGAATTAAGTCAAC 480
QY 2054 TAAATCTACATCCCTCTAAAGTAATACTGTTAGAAAGCAGAGTCTTCCAGAGT 2113
DB 479 TAAATCTACATCCCTCTAAAGTAATACTGTTAGAAAGCAGAGTCTTCCAGAGT 420
QY 2114 GGGGAGGCGCTCTCTTAATGAAGACATGATATGACCTGCTTTGGCAGTGC 2173
DB 419 GGGGAGGCGCTCTCTTAATGAAGACATGATATGACCTGCTTTGGCAGTGC 360
QY 2174 ATTAGTAATCTTGAAGAGTATAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2233
DB 359 ATTAGTAATCTTGAAGAGTATAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300
QY 2234 TACTTAGTAATCTTGAAGAGTATAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2293
DB 299 TACTTAGTAATCTTGAAGAGTATAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 240
QY 2294 CTGAAGACATTTACACACGAGTGAAGAAATCAACCGAGGAGGCTGTGGAACATG 2353
DB 239 CTGAAGACATTTACACACGAGTGAAGAAATCAACCGAGGAGGCTGTGGAACATG 180
QY 2354 GTTGTATATGCACTGCGAAGCACTGAACCTTACGCAATATATGTTTTCAGG 2413
DB 179 GATATATATGCACTGCGAAGCACTGAACCTTACGCAATATATGTTTTCAGG 120
QY 2414 TGTATGAGAGTGTGCGACAGTATATTCAGAGTCTTAAAGTTTAAAGTTCAGAT 2473
DB 119 TGTATGAGAGTGTGCGACAGTATATTCAGAGTCTTAAAGTTTAAAGTTCAGAT 61

```

```

QY 2474 GATTGATTAAGCATGCTTTCTTTGAGTTTAAATATGATATAACATTAAGTTCATTAG 2533
DB 60 GATT-TATAAGCATGCTTTCTTTGAGTTTAAATATGATATAACATTAAGTTCATTAG 2
RESULT 11
AL572550/c 1201 bp mRNA 1near EST 31-MAY-2003
LOCUS AL572550 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSOD1008YN07 3-PRIME, mRNA sequence.
ACCESSION AL572550
VERSION AL572550
KEYWORDS GI:31293927
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization.
JOURNAL Unpublished
COMMENT On Feb 16, 2001 this sequence version replaced gi:12930928.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6027.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD1008G04NP1&cluster=6027.r. Contact:
Feng Liang Email: fliang@life.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOD1008G04NP1.
FEATURES
Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1008YN07"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/Note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 311 a 254 c 261 g 311 t 64 others
ORIGIN
Query Match 33.2%; Score 858.4; DB 9; Length 1201;
Best Local Similarity 95.6%; Pred. No. 3.8e-103;
Matches 970; Conservative 14; Mismatches 18; Indels 13; Gaps 10;
QY 1509 GCTTTGTAATTTGTTGAGGAGAGAGATGAAGAAACATGAGTCCCTGATTTGT 1568
DB 1031 GCTTTGTAATTTGTTGAGGAGAGAGATGAAGAAACATGAGTCCCTGATTTGT 976
QY 1569 TTTGGGAAATGAGAAAGAGTCCCTGTTGGCAACATCAACCTGGAAATATGCA 1628
DB 975 TTT-GGGAAATGAGAAAGAGTCCCTGTTGGCAACATCAACCTGGAAATATGCA 918
QY 1629 CAATGAAATTTTCCACGAGTCTTTTCATGAGGAGATAGTAACTGTGCTCAGCTGT 1688
DB 917 CAATGAAATTTTCCACGAGTCTTTTCATGAGGAGATAGTAACTGTGCTCAGCTGT 860
QY 1689 GCAATGAAATTTTCTGTTACCTGATTAACATGCTTATTCAT-CCAGCAGTGTGC 1747
DB 859 GCAATGAAATTTTCTGTTACCTGATTAACATGCTTATTCAT-CCAGCAGTGTGC 800
QY 1748 TCACTCTCTA-CCTCTGTGCGAGGAGAGATTTTCAATATCAAGATCAATTCCTCTCTC 1806
DB 799 TCACTCTCTA-CCTCTGTGCGAGGAGAGATTTTCAATATCAAGATCAATTCCTCTCTC 740

```





Db 661 GCTTGAATATGTTGAGGGGAGAGATGGAACAATGTGAGTCTCCCTCGATTGCT 720

QY 1569 TTT-GGGGAAATGTGAGAAAGAGTGCCTGCTTGTGCAACATCAACCTGGCAAAATGCA 1627

Db 721 TTTGGGGGAAATGTGAGAAAGAGTGCCTGCTTGTGCAACATCAACCTGGCAAAATGTC 780

QY 1628 ACAATGAAATTTTCCAGCAGTCTTTCATGAGGAGCATAGTAAGTGTGCTTCAGCTGT 1687

Db 781 ACAATGAAATTTTCCAGCAGTCTTTCATGAGGAGCATAGTAAGTGTGCTTCAGCTGT 840

QY 1688 TGCAGTGAATGTTCTGTTCCACCTGCAATTACATGCTGTTTATTCACGAG 1741

Db 841 TGCAGTGAATGTTCTGTTCCACCTGCAATTACATGCTGTTTATTCACGAG 893

RESULT 13

LOCUS B0686834 934 bp mRNA linear EST 15-JUL-2002

DEFINITION AGENCOURT\_8345:189 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6250143

ACCESSION B0686834

VERSION B0686834

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapsd-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov

Plate: LNCM2392 row: 1 column: 16

High quality sequence stop: 607.

Location/Qualifiers

1. .934

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6250143"

/tissue\_type="ductal carcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_1b="NIH MGC 110"

/note="Organ: pancreas; Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH\_MGC library."

BASE COUNT 185 a 234 c 276 g 231 t 8 others

ORIGIN

Query Match 33.0%; Score 852.4; DB 13; Length 934;

Best Local Similarity 97.0%; Pred. No. 2.6e-102;

Matches 906; Conservative 0; Mismatches 24; Indels 4; Gaps 4;

QY 849 CCCCTGCCGATGAGGAGGAGCTTTGGCATGACCCCGGCGGCTTGTGACCTGATC 908

Db 1 CCCCTGCCGATGAGGAGGAGCTTTGGCATGACCCCGGCGGCTTGTGACCTGATC 60

QY 909 ACCTGAGGCTAAGCTGATGAGAGCTTGGACCGATGCCCTTGTGCGAGTGCCTCTC 968

Db 61 ACCTGAGGCTAAGCTGATGAGAGCTTGGACCGATGCCCTTGTGCGAGTGCCTCTC 120

QY 969 TGCCAGCCCCCAGCCAGGCTGTGTATGTGTGCAAGCCGACCTTGTGGGAGGCGCT 1028

Db 121 TGCCAGCCCCCAGCCAGGCTGTGTATGTGTGCAAGCCGACCTTGTGGGAGGCGCT 180

QY 1029 GACCAAGATGGGAGATCTGCTGCCAGAGAGGTCCCGCATGATGATGAATTTGGCAGC 1088

Db 181 GACCAAGATGGGAGATCTGCTGCCAGAGAGGTCCCGCATGATGATGAATTTGGCAGC 240

QY 1089 TTCAATGAGAGAGTGTGCGCCAGAGAGCTGAGAGAGCTGAGAGAGCTGATGAAGATG 1148

Db 241 TTCAATGAGAGAGTGTGCGCCAGAGAGCTGAGAGAGCTGAGAGAGCTGATGAAGATG 300

QY 1149 GCGCTGGGGGAGCCTGCGGCTGCGCGGCTGCACTGCTGGAGGGGAGAGATTTAGATC 1208

Db 301 GCGCTGGGGGAGCCTGCGGCTGCGCGGCTGCACTGCTGGAGGGGAGAGATTTAGATC 360

QY 1209 TGAACCAAGCTGTGGGATGATGTGCAATGAAATGCTAATTTATTTCCCAAGGTGTG 1268

Db 361 TGAACCAAGCTGTGGGATGATGTGCAATGAAATGCTAATTTATTTCCCAAGGTGTG 420

QY 1269 CTTAGAGGCTGGGCTGACCAAGGCTTCTTCCCTACATCTTCTTCCAGTAAATTTCCCTCT 1328

Db 421 CTTAGAGGCTGGGCTGACCAAGGCTTCTTCCCTACATCTTCTTCCAGTAAATTTCCCTCT 480

QY 1329 GACTTGAACATGATGATGTGTGCAATTTGTTCACTTCCCTCCAGGCTGTCTCAAGCTT 1388

Db 481 GACTTGAACATGATGATGTGTGCAATTTGTTCACTTCCCTCCAGGCTGTCTCAAGCTT 540

QY 1389 CACAGTGTGGCTTGGGAGAGTGAAGAGGTTAACTGAGAGATAGTTTGGCAAGCTT 1448

Db 541 CACAGTGTGGCTTGGGAGAGTGAAGAGGTTAACTGAGAGATAGTTTGGCAAGCTT 600

QY 1449 TGTCAGATTAATGTGCTGCTTGTGCTTACCAAGTGCAGACGCTTGTGTTACATG 1508

Db 601 TGTCAGATTAATGTGCTGCTTGTGCTTACCAAGTGCAGACGCTTGTGTTACATG 660

QY 1509 GCTTGAATTAATTTTGGGAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1568

Db 661 GCTTGAATTAATTTTGGGAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 720

QY 1569 TTTGGGAAATGTGAGAGAGTGCCTGCTTGGCAACATCAACCTGGCAAAATGCAA 1628

Db 721 TTTGGGAAATGTGAGAGAGTGCCTGCTTGGCAACATCAACCTGGCAAAATGCAA 779

QY 1629 CAATGAATTTTCCAGCAGATCTTTCATGAGGAGTGAAGTGAAGTGAAGTGAAGT 1688

Db 780 CAATGAATTTT-CACGAGATCTTTCATGAGGAGTGAAGTGAAGTGAAGTGAAGT 838

QY 1689 GCAGTGAATGTTCTGTTCACTGATTAATGATGTTT-ATTCAATCAGCAGTGTGC 1747

Db 839 GCAGTGAATGTTCTGTTCACTGATTAATGATGTTT-ATTCAATCAGCAGTGTGC 898

QY 1748 TC-AGTCTCACTGCTGTGCGAGGAGCATTTT 1780

Db 899 TC-AGTCTCACTGCTGTGCGAGGAGCATTTT 932

RESULT 14

LOCUS B0890463 878 bp mRNA linear EST 16-AUG-2002

DEFINITION AGENCOURT\_8064243 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6207928

ACCESSION B0890463

VERSION B0890463

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
COMMENT

Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: c9abds-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM364 row: m column: 17  
High quality sequence stop: 677.  
Location/Qualifiers

FEATURES  
source

1..878  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6207928"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOT7; Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGACGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

BASE COUNT 175 a 218 c 264 g 219 t 2 others

ORIGIN

Query Match 32.4%; Score 837.2; DB 13; Length 878;  
Best Local Similarity 99.2%; Pred. No. 2,6e-100;  
Matches 872; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

849 CCCCTGCGCTGAGGCGAGCTTTGGCATGACCCCGCAGCGGCTTTCGACCTCARTC 908  
1 CCCCTGCGCTGAGGCGAGCTTTGGCATGACCCCGCAGCGGCTTTCGACCTCARTC 60  
909 ACCGTGGAGCTAGAGCCTGTATGAGCCTTGACCGATGCCCTTGTGCAGTGGCCTCCTC 968  
61 ACCGTGGAGCTAGAGCCTGTATGAGCCTTGACCGATGCCCTTGTGCAGTGGCCTCCTC 120  
969 TGGCAGCCCCCAGCAGCAGCCTGTATGTGTGCAAGCCGACCTTCGTGGGAGCCGT 1028  
121 TGGCAGCCCCCAGCAGCAGCCTGTATGTGTGCAAGCCGACCTTCGTGGGAGCCGT 180  
1029 GACCAAGATGGGAGATCTCTGCTCCAGAGAGTCCCGATAGATATGAAATTTGGCAGC 1088  
181 GACCAAGATGGGAGATCTCTGCTCCAGAGAGTCCCGATAGATATGAAATTTGGCAGC 240  
1089 TTCAATGAGAGAGTGCCCGCAGAGCTGTGAGACCTGTGAGAGAGCCTGACTGAGAGATG 1148  
241 TTCAATGAGAGAGTGCCCGCAGAGCTGTGAGACCTGTGAGAGAGCCTGACTGAGAGATG 300  
1149 GCGGTGGGAGAGCTGTGCGCTGCGCGCTGTCACTGTGGAGGGAGAGATTTAGATC 1208  
301 GCGGTGGGAGAGCTGTGCGCTGCGCGCTGTCACTGTGGAGGGAGAGATTTAGATC 360  
1209 TGGACCAAGCTGTGGTATGATGATAGATAAGTAAATTTATTTCCCAAGTGTG 1268  
361 TGGACCAAGCTGTGGTATGATGATAGATAAGTAAATTTATTTCCCAAGTGTG 420  
1269 CTTTAGGCGTGGGCTGACCAAGCTTTCTTCTACATCTTTCCCAAGTAAATTTCCCTCT 1328  
421 CTTTAGGCGTGGGCTGACCAAGCTTTCTTCTACATCTTTCCCAAGTAAATTTCCCTCT 480  
1329 GCGTTGACAGATAGAGTGTGATTTGTTCAGTCCCGCAGAGCTGTCTCCAGGCTT 1388  
481 GCGTTGACAGATAGAGTGTGATTTGTTCAGTCCCGCAGAGCTGTCTCCAGGCTT 540  
1389 CACAGTGTGCTGTGGAGAGTCAAGGAGGTTAAATCTGAGAGAGCATTTGGCACACCC 1448

Db 541 CACAGTGTGCTGTGGAGAGTCAAGGAGGTTAAATCTGAGAGAGCATTTGGCACACCC 600  
QY 1449 TGTCCAGATTAATTTGAGCTGCTTTGCTTACCTACAGTGGCAGACAGCCGTTTGTCTACATG 1508  
Db 601 TGTCCAGATTAATTTGAGCTGCTTTGCTTACCTACAGTGGCAGACAGCCGTTTGTCTACATG 660  
QY 1509 GCTTGTATTAATTTGTTGAGGGAGAGATGAAACATATGTGAAGTCTTCCCTGTGATTTG 1568  
Db 661 GCTTGTATTAATTTGTTGAGGGAGAGATGAAACATATGTGAAGTCTTCCCTGTGATTTG 720  
QY 1569 TTTGGGGAATATGTGAGAGAGATGCGCTTGTGAACATCAACCTTGGCAAAATATGCA 1628  
Db 721 TTTGGGGAATATGTGAGAGAGATGCGCTTGTGAACATCAACCTTGGCAAAATATGCA 778  
QY 1629 CAATGAATTTTCCACGAGTCTTTCCATGGGAGATGATGAGTGTGCC-TTCAGCTGT 1687  
Db 779 CAATGAATTTTCCACGAGTCTTTCCATGGGAGATGATGAGTGTGCC-TTCAGCTGT 838  
QY 1688 TGCAGATGAATATGTTCTGTCAACCTTGATTAACATTTGT 1726  
Db 839 TGCAGATGAATATGTTCTGTCAACCTTGATTAACATTTGT 877

RESULT 15  
BX391733/c  
BX391733 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
LOCUS CS0010361N1.3-PRIME, mRNA sequence.  
DEFINITION BX391733.1 GI:30611681  
ACCESSION BX391733  
VERSION BX391733.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Unpublished  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 6027.r For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0BA1021ZG05\_CS01959\_1&cluster=6027.r.  
Contact: Feng Liang Email: fliang@lifetech.com URL:  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID: CS0BA1021ZG05\_CS01959\_1.

FEATURES  
source

1..922  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0010361N1"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo (dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 245 a 261 c 213 g 192 t 11 others

ORIGIN

Query Match 32.2%; Score 833; DB 13; Length 922;  
Best Local Similarity 97.4%; Pred. No. 9e-100;  
Matches 894; Conservative 0; Mismatches 19; Indels 5; Gaps 5;  
QY 919 TAGACCTGATGAGACCTTTGACC-GATGCCCTTGTGCGAGTGGCCTCTGCGCAGCC 977

D	b		920	TAGAGCTTGAATGAAAGCCCTTGACCGNAGTGNCTTGTGGCAGATGGCTTTCTTNTGCAGAAGCCC	861
Q	y		978	CACAGCC-AACAAGCTGTGNGTATGTGTGTAACC-C-ACCTTGTGTGGAGAGCCGTGACCAAG	1035
D	b		860	CACAGCCNAAGCATGTGTGTATGTGTGAAGCCAACTTGTGTGGAGCCCGTAGCCAAG	801
Q	y		1036	ATGGGAGAGATCCTCTGTGCCAGAGAGGTCCCCGATGAGTATGAATTGGCAGCTTCATGG	1089
D	b		800	ATGGGAGAGATCCTGTGTGCCA-AGAAGGTGNCGATGAGTATGAAGTTGNCAGCTTCATGN	742
Q	y		1096	AGAGAGTGTCCGAGAGAGTGSAGAGACCTGAGAGAGAGCTTACTGAAAGATGGCGCTGG	1155
D	b		741	AGNAGTGTGGCGCAANAGCTGNAGGACTTGAGAGAGAGGCTGACCTGMAAGATGGCGCTGG	682
Q	y		1156	GGAAGCTGCGCGCTGCCCGCGCTGCACTGTGGGAGGGGAGAGATTAGATCTGAAACA	1215
D	b		681	GGAGAGCTGGCGCTGCCCGCGCTGCACTGTGGGAGGGGAGAGATTAGATCTGAAACA	622
Q	y		1216	GGCTGTGGGTATGATGTGCATAAGAAATNGTAAATTAATTAATTTCCCAAGTGTGTCTTAAG	1275
D	b		621	GGCTGTGGGTATGATGTGCATAAGAAATNGTAAATTAATTAATTTCCCAAGTGTGTCTTAAG	562
Q	y		1276	CGTGGGCTGACACAGGCTTCTCCATCATCTTCTCCGATAGTATTCCTGCTGGCTTGA	1335
D	b		561	CGTGGGCTGACACAGGCTTCTCTTCACTTCTTCCGATAGTATTCCTGCTGGCTTGA	502
Q	y		1336	CAGCATGAGGTGTGTGTGCATTTGTTCAAGCTCCCCAGGCTGTCTTCAGAGCTTCAAGTC	1395
D	b		501	CAGCATGAGGTGTGTGTGCATTTGTTCAAGCTCCCCAGGCTGTCTTCAGAGCTTCAAGTC	442
Q	y		1396	TGGTGCTTGGGAGAGTCAAGGAGTTAACTGAGAGAGAGTTGGCACCCGCTGCCAG	1455
D	b		441	TGGTGCTTGGGAGAGTCAAGGAGTTAACTGAGAGAGAGTTGGCACCCGCTGCCAG	382
Q	y		1456	ATTATTTGGCTGCTTGTGCTCTTACCAAGTGTGGAGACAGCGCTGTGTTCTACAGGCTTGA	1515
D	b		381	ATTATTTGGCTGCTTGTGCTCTTACCAAGTGTGGAGACAGCGCTGTGTTCTACAGGCTTGA	322
Q	y		1516	TAATTTGTTTGGGAGAGAGATGGAACAATGTGAGTCTCCCTGTGATTTGGTTTTGGGG	1575
D	b		321	TAATTTGTTTGGGAGAGAGATGGAACAATGTGAGTCTCCCTGTGATTTGGTTTTGGGG	262
Q	y		1576	AAATGTGAGAGAGTGGCTGCTTGCAGAACATCAACCTGGCAAAAATGACAACAATGA	1635
D	b		261	AAATGTGAGAGAGTGGCTGCTTGCAGAACATCAACCTGGCAAAAATGACAACAATGA	202
Q	y		1636	ATTTTCCACGAGTCTTTCCATGAGGCAATGAGTAAGCTGTGCTTCAAGCTGTTCAGATG	1695
D	b		201	ATTTTCCACGAGTCTTTCCATGAGGCAATGAGTAAGCTGTGCTTCAAGCTGTTCAGATG	142
Q	y		1696	AAATGTTCTGTTCACCTCGCATTAATGAGTTATTCANCCAGCAGTGTGTCAGCTCC	1755
D	b		141	AAATGTTCTGTTCACCTCGCATTAATGAGTTATTCANCCAGCAGTGTGTCAGCTCC	82
Q	y		1756	TACCTGTGTGCAAGGAGCAGATTTTCATATCCAGATCAATTCCTCTCTGACACAGCC	1815
D	b		81	TACCTGTGTGCAAGGAGCAGATTTTCATATCCAGATCAATTCCTCTCTGACACAG-C	23
Q	y		1816	TGGGAGGGGGGTCATTTT	1833
D	b		22	TGGGAGGGGGGTCATTTT	5

RESULT 16	
BO722575	
LOCUS	
DEFINITION	BO722575 .931 bp mRNA
	AGENCOURT_8304969 lupski_sympathetic_trunk Homo sapiens cDNA clone
	IMAGE:0193228 5', mRNA sequence.
ACCESSION	BO722575
VERSION	BO722575.1 GI:21861472
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE  
AUTHORS Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthalia; Primates; Carnivora; Homnidae; Homo.  
1 (bases 1 to 931)  
NID-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapds-remail.nih.gov](mailto:cgapds-remail.nih.gov)  
Tissue Procurement: Dr. James R. Lupski  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINTL at:  
<http://image.llnl.gov>  
plate: LRAM1356 row: 1 column: 05  
High quality sequence stop: 642.

FEATURES  
SOURCE

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6193228"
/sex="male"
/issue_type="sympathetic trunk"
/dev_stage="adult" 16 yr"
/lab_host="DH10B"
/clone_lbp="lupski: sympathetic trunk"
/notes="vector: pCMVSPORTS (Life Technologies); Site_1:
NotI, Site_2: SalI, cDNA made by oligo-dT priming:
Directionally cloned using the following adaptors:
5'-TCGACCACGCGATCCG-3' and
5'-GACATGTTAGATCGGAGCGGCCGCC(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."

```

BASE COUNT  
ORIGIN

Query Match	32.1%;	Score 829;	DB 13;	Length 931;
Best Local Similarity	96.7%;	Pred. No. 3e-99;	25;	
Matches 500;	Conservative	0;	Mismatches	6;
			Indels	5

QY	142	GCACAGCGGAGATGCAGCGGCTTTGGGGCAACCTCTGTGCTGTGCTGTGCGCGCGCG	201
Db	1	GCAGAGCGGAGATGCAGCGGCTTTGGGGCAACCTGTGCTGTGCTGTGCGCGCGCG	60
QY	202	TCGCCACGGCCCCCGCGCGCTCCGAGGGAGACTCTGGCTTCAGTCAAAGCCCGGCCGG	261
Db	61	TCGCCACGGCCCCCGCGCGCTCCGAGGGAGACTCTGGCTTCAGTCAAAGCCCGGCCGG	120
QY	262	CTCTCAGCTACCCGCAGGAGGAGCGCACTCAATGAGATGTTCCGCAGGTTTGAAGAAC	321
Db	121	CTCTCAGCTACCCGCAGGAGGAGCGCACTCAATGAGATGTTCCGCAGGTTTGAAGAAC	180
QY	322	TGATGGAGGACACGCGAGCAAAATTGGCGACGCGGTGGAGAGATGGAGGCGAAAGAG	381
Db	181	TGATGGAGGACACGCGAGCAAAATTGGCGACGCGGTGGAGAGATGGAGGCGAAAGAG	240
QY	382	CTGCTGCTAAAGCATCATCAGAGTGAACCTGGCGAAACTTACCTCCAGCTTTCACAAATG	441
Db	241	CTGCTGCTAAAGCATCATCAGAGTGAACCTGGCGAAACTTACCTCCAGCTTTCACAAATG	300
QY	442	AGACCAACACAGACACGAGGTTGGAAATAATACCATCATGTGACCCGAGAAATTACA	501
Db	301	AGACCAACACAGACACGAGGTTGGAAATAATACCATCATGTGACCCGAGAAATTACA	360
QY	502	AGATTAACCAACAACAGCTGAGCAAAATGACTTTTCAGAGACGTTTATCATCTGTGG	561
Db	361	AGATTAACCAACAACAGCTGAGCAAAATGACTTTTCAGAGACGTTTATCATCTGTGG	420

QY		562	GAGACGAAAGAAGCGAAGAAGAGCCACAGAGTCATCATCTGAAGAAGACTGTGGGCCACGCA	621
Db		421	GAGCAGAAAGAAGCGAAGAAGAGCCACAGAGTCATCATCTGAAGAAGACTGTGGGCCACGCA	480
QY		622	TGTACTGCAGATTGTGGCAGCTTCCAGTGACACTGTGCAGACCCTGCGGGGCCAGAGATGC	681
Db		481	TGTACTGCAGATTGTGGCAGCTTCCAGTGACACTGTGCAGACCCTGCGGGGCCAGAGATGC	540
QY		682	TTGSCACCCCGGGAAGATGAAGTCGTGTGAAGACAGAGCTGTGTGTCTGGGGTCACTGCACA	741
Db		541	TTGSCACCCCGGGAAGATGAAGTCGTGTGAAGACAGAGCTGTGTGTCTGGGGTCACTGCACA	600
QY		742	AAATGGCCACAGGGGCGACGAATGGGACATCTGTGACAAACAGAGGACTGCAGGCCG	801
Db		601	AAATGGCCACAGGGGCGACGAATGGGACATCTGTGACAAACAGAGGACTGCAGGCCG	660
QY		802	GGCTGTGTGTGTGCTTCCAGAGAGGCTGTGTCTCTGTGTGACACCTCTGCCC-GTG	860
Db		661	GGCTGTGTGTGTGCTTCCAGAGAGGCTGTGTCTCTGTGTGACACCTCTGCCC-GTG	720
QY		861	GAGGGCGACGCTTGTGCATGACCCCGCCA-GCGGGCTTGTGACCTCATCACCTGGAGACT	919
Db		721	GAGGGCGACGCTTGTGCATGACCCCGCCA-GCGGGCTTGTGACCTCATCACCTGGAGACT	780
QY		920	AGAGCTGTATGAGGCTTGTGACCCAGATGCTCTGTGACAGTGGCTCTCTGCCCCA	979
Db		781	AGAGCTGTATGAGGCTTGTGACCCAGATGCTCTGTGACAGTGGCTCTCTGCCCCA	840
QY		980	CAGCCACAGCCT-GGTGTATGTGTGACAGCCG-ACCTCTGTGGGAGCCGTGAGC--TAG	1035
Db		841	CAGCCACAGCCTGGGGGTATGTGTGGCAACTGTGCAACTTTCGTGTAAACGTGACCCAAA	900
QY		1036	ATGGGAGAGTCTGTGTGCCAGAGAGTGTCC	1066
Db		901	AGGGGGAATCCGCTGTGCCAAAAAGTGTCC	931
RESULT 17				
LOCUS	AL534481			
DEFINITION	AL534481 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone			
ACCESSION	AL534481			
VERSION	AL534481.2			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	Ll,w.B., Gruber,C., Jeessee,J. and Polayes,D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished			
COMMENT	On Feb 13, 2001 this sequence version replaced gi:12797974. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6027.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgl-bin/cluster.cgi?seq=CSDF004AD01QPLcluster=6027.r. Contact : Feng Liang Email : fliang@lifetech.com URL : Corporation 1600 Parade Avenue Genoscope sequence ID : CSDF004AD01QPL. Location/Qualifiers 1..906 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSDF004YG01" /feature="FETAL BRAIN"			
FEATURES	source			

Query Match	31.9%	Score 825.4	DB 9	Length 906
Best Local Similarity	98.7%	Pred. No. 8,9e-99		
Matches 848	Conservative 4	Mismatches 5	Indels 2	Gaps 2
ORIGIN	209 a	266 c	274 g	153 t 4 others
Query Match	31.9% <td>Score 825.4 <td>DB 9 <td>Length 906 </td></td></td>	Score 825.4 <td>DB 9 <td>Length 906 </td></td>	DB 9 <td>Length 906 </td>	Length 906
Best Local Similarity	98.7% <td>Pred. No. 8,9e-99</td> <td></td> <td></td>	Pred. No. 8,9e-99		
Matches 848	Conservative 4	Mismatches 5	Indels 2	Gaps 2
ORIGIN	209 a	266 c	274 g	153 t 4 others

RESULT 18  
 BU190800  
 LOCUS  
 DEFINITION BU190800 1007 bp mRNA linear EST 04-SHP-2002  
 AGENCOURT 8073522 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6083260  
 5', mRNA sequence.  
 BU190800  
 ACCESSION BU190800.1 GI:22704784  
 VERSION  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 1007)  
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: sgabds-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LICM2313 row: c column: 05  
 High quality sequence stop: 575.  
 Location/Qualifiers  
 1..1007  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6083260"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_1lb="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI;  
 Site\_2: EcoRI; CDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: This is a NIH\_MGC Library."

BASE COUNT 199 a 261 c 297 g 250 t  
 ORIGIN

Query Match 31.9%; Score 825.2; DB 13; Length 1007;  
 Best Local Similarity 95.0%; Pred. No. 9e-99;  
 Matches 939; Conservative 0; Mismatches 38; Indels 11; Gaps 8;

QY 849 CCCTGCGCGTGGAGGGGCGAGCTTTGGCATGACCCGCGCGCTTGTGACCTCAGC 908  
 DB 1 CCCTGCGCGTGGAGGGGCGAGCTTTGGCATGACCCGCGCGCTTGTGACCTCAGC 60  
 QY 909 ACCTGGAGCTAGAGCTGATGAGAGCTTGGACCGATGACCTTGTGCAAGTGGCCTCC 968  
 DB 61 ACCTGGAGCTAGAGCTGATGAGAGCTTGGACCGATGACCTTGTGCAAGTGGCCTCC 120  
 QY 969 TGCCAGCCCAACAGCCAGCTGTGTATGTGTGTGCAAGCCGACCTTGTGTGGAGCCGT 1028  
 DB 121 TGCCAGCCCAACAGCCAGCTGTGTATGTGTGTGCAAGCCGACCTTGTGTGGAGCCGT 180  
 QY 1029 GACCAAGATGGGGAGATCTGCTGCGCCAGAGAGTCCCGGATAGTATGAAGTTGACAGC 1088  
 DB 181 GACCAAGATGGGGAGATCTGCTGCGCCAGAGAGTCCCGGATAGTATGAAGTTGACAGC 240  
 QY 1089 TTCAATGAGAGAGTGCAGCAGAGCTTGAGAGAGCTTGAGAGAGAGCTGACTGAAGAGATG 1148  
 DB 241 TTCAATGAGAGAGTGCAGCAGAGCTTGAGAGAGAGCTTGAGAGAGAGCTGACTGAAGAGATG 300

QY 1149 GCGCTGGGGAGAGCCTGCGGCTGCCGCCGCTGCATCTGCTGGGAGGGGAGAGATTATGATC 1208  
 DB 301 GCGCTGGAGAGAGCCTGCGGCTGCCGCCGCTGCATCTGCTGGGAGGGGAGAGATTATGATC 360  
 QY 1209 TGACACAGAGCTGTGGGTATAGATGTCATAGAAATAGCTAAATTATTTATCCAGAGTGTGTG 1268  
 DB 361 TGACACAGAGCTGTGGGTATAGATGTCATAGAAATAGCTAAATTATTTATCCAGAGTGTGTG 420  
 QY 1269 CTTTAAAGGCTGGGCTGACACAGGCTTTCTTCCATCACTCTTCTTCCAGTAAGTTTCCCTCT 1328  
 DB 421 CTTTAAAGGCTGGGCTGACACAGGCTTTCTTCCATCACTCTTCTTCCAGTAAGTTTCCCTCT 480  
 QY 1329 GCGCTGACAGCATAGAGGTGTGTGCATTTGTTCAGCTCCGCCAGGCTGTCTCCAGGCTT 1388  
 DB 481 GCGCTGACAGCATAGAGGTGTGTGCATTTGTTCAGCTCCGCCAGGCTGTCTCCAGGCTT 540  
 QY 1389 CACAGCTGTGTGCTTTGGAGAGAGTCAAGGAGGGTTAACTGAGAGAGCAATTGGCACCCC 1448  
 DB 541 CACAGCTGTGTGCTTTGGAGAGAGTCAAGGAGGGTTAACTGAGAGAGCAATTGGCACCCC 600  
 QY 1449 TGTCAGATTAATTGCTGCTTGTGCTCTCAACAGTTGGCAGACAGCGTTTGTCTACATG 1508  
 DB 601 TGTCAGATTAATTGCTGCTTGTGCTCTCAACAGTTGGCAGACAGCGTTTGTCTACATG 660  
 QY 1509 GCTTTGATTAATTGTTTGAAGGAGAGAGATGGAACAATGTGAGTCTTCCCTGATTTGCT 1568  
 DB 661 GCTTTGATTAATTGTTTGAAGGAGAGAGATGGAACAATGTGAGTCTTCCCTGATTTGCT 719  
 QY 1569 TTTGGGGGAAATGTGGAGAGAGTCCCTGCTTTCACAAACATCACTGGGCAAAATGCA 1628  
 DB 720 TTTGGGGGAAATGTGGAGAGAGTCCCTGCTTTCACAAACATCACTGGGCAAAATGCA 779  
 QY 1629 CAATGAATTTTCCACAGCAGTCTTTCATATGAGGAT-AGTAACTGTG-CTTCACTG 1686  
 DB 780 CAATGAATTTTCCACAGTCTTTCATATGAGGAT-AGTAACTGTG-CTTCACTG 839  
 QY 1687 TTGAGAGTAAT-GTCTGTTCACCCGCAATTA--CATGCTTATTCATCCAGCAGTG 1743  
 DB 840 TTGAGAGTAATGTGTTGTTCCCTGCAATTAACATGAGGTTTATCATCCAGCAGG 899  
 QY 1744 TTGCT-CAGCTCTCACTCTGTGTCAGAGGAGCATTTTCAATA--TCCAGATCAAT-C 1798  
 DB 900 TTGCTCAAGTCTCACTCTGTGTCAGAGGAGCATTTTCAATAATTCAGATCAATTC 959  
 QY 1799 CTTCTTCAAGCAGAGCTTGGGAGAGGG 1826  
 DB 960 CCGCTCTCAACAAAGCCGTGGGAGAGG 987

RESULT 19  
 AK004853  
 LOCUS AK004853 3357 bp mRNA linear HTC 05-DEC-2002  
 DEFINITION Mus musculus adult male liver cDNA, RIKEN full-length enriched  
 library, clone:1300002107 product:dictkopf homolog 3 (Xenopus  
 laevis), full insert sequence.  
 ACCESSION AK004853  
 VERSION AK004853.1 GI:12836349  
 KEYWORDS HTC; CAP trapper;  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1  
 REFERENCE Carninci, P. and Hayashizaki, Y.  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99379253  
 PUBMED 10349636  
 REFERENCE  
 AUTHORS  
 TITLE  
 Prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL  
MEDICAL  
PUBMED  
REFERENCES  
AUTHORS

Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
11042159

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,



[illegible]

FEATURES	source
<p> <b>AUTHORS</b> NT-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a>  <b>TITLE</b> National Institutes of Health, Mammalian Gene Collection (MGC)  <b>JOURNAL</b> Unpublished  <b>COMMENT</b> Contact: Robert Strausberg, Ph.D.  Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a>  Tissue Procurement: ATCC  cDNA Library Preparation: Rubin Laboratory  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  DNA Sequencing by: Agencourt Bioscience Corporation  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  <a href="http://image.lnl.gov">http://image.lnl.gov</a>  Plate: LNCM368 row: a column: 11  High quality sequence stop: 584.  Location/Qualifiers  1. 858  /mol_type="mRNA"  /db_xref="taxon:9606"  /clone="IMAGE:6209170"  /tissue_type="ductal carcinoma, cell line"  /lab_host="DH10B (phage-resistant)"  /clone_lib="NIH_MGC_110"  /notes="Organ: pancreas; Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."  </p>	<p> <b>BASE COUNT</b> 170 a 212 c 263 g 212 t 1 others  <b>ORIGIN</b>  Query Match 31.7%; Score 819; DB 13; Length 858;  Best Local Similarity 99.1%; Pred. 6.3e-98;  Matches 844; Conservative 0; Mismatches 6; Indels 2; Gaps 2;  </p>
<p> 849 CCCCTGCCCTGGAGGGCGAGCTTTGGCATGACCCCGCAGCCGGCTTGTGACCTTCATC 908  1 CCCCTGCCCTGGAGGGCGAGCTTTGGCATGACCCCGCAGCCGGCTTGTGACCTTCATC 60  </p>	<p> 909 ACCCTGGAGAGCTAGAGCTGATGAGAGCTTGGACCGAGTCCCTGTGTGCACTGGAGCTTCCTC 968  61 ACCCTGGAGAGCTAGAGCTGATGAGAGCTTGGACCGAGTCCCTGTGTGCACTGGAGCTTCCTC 120  </p>
<p> 969 TGCCAGCCCCCAGACCCAGAGCTTGATATGTGTGCAAGCCGACTTTGTGGGAGAGCCGT 1028  121 TGCCAGCCCCCAGACCCAGAGCTTGATATGTGTGCAAGCCGACTTTGTGGGAGAGCCGT 180  </p>	<p> 1029 GACCAAGATGGGGAGATCCTGCTGCCAGAGAGAGTCCCGCATGATGAAAGTTGGCAGC 1088  181 GACCAAGATGGGGAGATCCTGCTGCCAGAGAGTCCCGCATGATGAAAGTTGGCAGC 240  </p>
<p> 1089 TTCAATGAGAGAGGTGGCCAGAGAGCTGAGAGAGCTTGGAGAGAGAGCTTGAAGAGATG 1148  241 TTCAATGAGAGAGGTGGCCAGAGAGCTGAGAGAGCTTGGAGAGAGAGCTTGAAGAGATG 300  </p>	<p> 1149 GCGCTGGGGAGAGCTGGAGCTGGCCGCGAGCTTGCACTGTGTGGAGAGGGGAAAGATTAGATC 1208  301 GCGCTGGGGAGAGCTGGAGCTGGCCGCGAGCTTGCACTGTGTGGAGAGGGGAAAGATTAGATC 360  </p>
<p> 1209 TGGACAGAGCTGTGGGTGATGTGCAATAGAAATAGCTAATTTATTTCCCGAGGTGTGTG 1268  361 TGGACAGAGCTGTGGGTGATGTGCAATAGAAATAGCTAATTTATTTCCCGAGGTGTGTG 420  </p>	<p> 1269 CTTAAGAGCTGTGGGTGATGTGCAATAGAAATAGCTAATTTATTTCCCGAGGTGTGTG 1328  421 CTTAAGAGCTGTGGGTGATGTGCAATAGAAATAGCTAATTTATTTCCCGAGGTGTGTG 480  </p>
<p> 1329 GAGCTGACAGATGAGGTGTGTGTGCAATTTGTCAAGCTCCCCAGAGGTGTTCACAGGCTT 1388  481 GAGCTGACAGATGAGGTGTGTGTGCAATTTGTCAAGCTCCCCAGAGGTGTTCACAGGCTT 540  </p>	

QY 1389 CACAGTCTGCTGCTTGGAGAGTACGACAGGCTTAACTGACAGAGATTTGCCCC 1448  
 Db 541 CACAGTCTGCTGCTTGGAGAGTACGACAGGCTTAACTGACAGAGATTTGCCCC 600  
 QY 1449 TGTCCAGATTATTTGGCTGCTTGGCTTACCACTTGGCAGACAGCCCTTTGTTCAATG 1508  
 Db 601 TGTCCAGATTATTTGGCTGCTTGGCTTACCACTTGGCAGACAGCCCTTTGTTCAATG 660  
 QY 1509 GCTTTGATTAATTTGTTGAGGAGAGAGATGAAACAATGTGAGTCTCCCTTGATTTGGT 1568  
 Db 661 GCTTTGATTAATTTGTTGAGGAGAGAGATGAAACAATGTGAGTCTCCCTTGATTTGGT 1720  
 QY 1569 TTTGGGGAATTTGGAGAGAGAGTGCCTGCTTCAACATCAACCTGGCAAAATGCAA 1628  
 Db 721 TTTGGGGAATTTGGAGAGAGAGTGCCTGCTTCAACATCAACCTGGCAAAATGCAA 1780  
 QY 1629 CAAATGAATTTTCCACGAGCTTCTTTCATGAGGAGT-AGGTAACTGTGCC-TTCACTG 1686  
 Db 781 CAAATGAATTTTCCACGAGCTTCTTTCATGAGGAGTAAAGTGTGCTTTCAGCTG 840  
 QY 1687 TTGAGATGAAA 1698  
 Db 841 TTGAGATGAAA 852

RESULT 21  
 AL565532/c 896 bp mRNA linear EST 12-MAY-2003  
 LOCUS CS0DF004YG01 3-PRIME, mRNA sequence.  
 DEFINITION AL565532 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
 ACCESSION AL565532  
 VERSION AL565532.2 GI:30549640  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 896)  
 Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished  
 On Feb 16, 2001 this sequence version replaced gi:12917002.  
 CONTACT: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6027.r For more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0DF004AD01NP1;cluster=6027.r. Contact :  
 Feng Liang Email: fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0DF004AD01NP1.

## FEATURES

Location/Qualifiers  
 1..896

1..896  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DF004YG01"  
 /tissue\_type="FETAL BRAIN"  
 /dev\_stage="fetal"  
 /clone\_lib="Homo sapiens FETAL BRAIN"  
 /note="Organ: brain; Vector: PCWSPORT 6; 1st strand cDNA was primed with a Not-I-oligo(OT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCWSPORT 6 vector. Library was not normalized."  
 BASE COUNT 234 a 189 c 207 g 250 t 16 others  
 ORIGIN

Query Match 31.6%, Score 817.2; DB 9; Length 896;

Best Local Similarity 96.6%; Pred. No. 1..1e-97;  
 Matches 845; Conservative 9; Mismatches 18; Indels 3; Gaps 2;  
 QY 1647 AGTTCTTTCATGGGAGATAGTAACTGCTTCACTGTTGCAGATGAATGTTCTGT 1706  
 Db 896 AGTTCTTTCATGGGAGATAGTAACTGCTTCACTGTTGCAGATGAATGTTCTGT 837  
 QY 1707 TCACCTGATTAATGTTGTTTATTCATCCAGCAATGTTGCTCAGCTCTACCTGTGCG 1766  
 Db 836 TCACCTGATTAATGTTGTTTATTCATCCAGCAATGTTGCTCAGCTCTACCTGTGCG 777  
 QY 1767 CAGGAGAGATTTTATATTCAGATCAATTCCTCTCTCAAGCAAGCTGGAGAGGGG 1826  
 Db 776 CAGGAGAGATTTTATATTCAGATCAATTCCTCTCTCAAGCAAGCTGGAGAGGGG 717  
 QY 1827 TCATTTGTTCTCTGCTGCTATCCAGGATCTCAGAGGCTCAGAGACTGCAAGCTGTGCC 1886  
 Db 716 TCATTTGTTCTCTGCTGCTATCCAGGATCTCAGAGGCTCAGAGACTGCAAGCTGTGCC 657  
 QY 1887 AAGTCAACAGCTAGTGAAGAACAAGAGAGATTTCTATCTGTTGACTCTAAGCTCAATG 1946  
 Db 656 AAGTCAACAGCTAGTGAAGAACAAGAGAGATTTCTATCTGTTGACTCTAAGCTCAATG 597  
 QY 1947 CTCTCTCACTACCCCAACAAGCTTGTGTCACAAAAGTGTCTCCCAAAAAGAGAGA 2006  
 Db 596 CTCTCTCACTACCCCAACAAGCTTGTGTCACAAAAGTGTCTCCCAAAAAGAGAGA 537  
 QY 2007 GAATGGAGATTTTTC--TTGAGGAGTGAACATCTGGAATTAAGTCAAACTAATTCACA 2064  
 Db 536 GAATGGAGATTTTCTTTGAGGAGTGAACATCTGGAATTAAGTCAAACTAATTCACA 477  
 QY 2065 TCCCTCTAAAGTAACTAATCTGTTAGAAACAGAGCTGTTCTCAAGTGTGGAGACCGCT 2124  
 Db 476 TCCCTCTAAAGTAACTAATCTGTTAGAAACAGAGCTGTTCTCAAGTGTGGAGACCGCT 417  
 QY 2125 CCTTCTAATGAAGAAATGATTTGACACTGTCCTCTTGGCAGTGTGATTAAGTACT 2184  
 Db 416 CCTTCTAATGAAGAAATGATTTGACACTGTCCTCTTGGCAGTGTGATTAAGTACT 357  
 QY 2185 TGAAGATTAATGACTGAGCGTACATAGTAACTGCGAAGAGTAACTTAAGTAA 2244  
 Db 356 TGAAGATTAATGACTGAGCGTACATAGTAACTGCGAAGAGTAACTTAAGTAA 297  
 QY 2245 TTGTAGGCGGAGATTTAATGAATTTTGCAATTCATTAGCAGCACTGAAGACAT 2304  
 Db 296 TTGTAGGCGGAGATTTAATGAATTTTGCAATTCATTAGCAGCACTGAAGACAT 237  
 QY 2305 TATCAACCAAGTGAAGAAATCAAAACGAGAGGCTGTGTAACATGTTGTAATG 2364  
 Db 236 TATCAACCAAGTGAAGAAATCAAAACGAGAGGCTGTGTAACATGTTGTAATG 177  
 QY 2365 CAGCTGCGAAGCTGAATCTTAGCCACTCCCAAAATGATTTTCAAGTGTGCAAGT 2424  
 Db 176 CAGCTGCGAAGCTGAATCTTAGCCACTCCCAAAATGATTTTCAAGTGTGCAAGT 117  
 QY 2425 GTTGGCAACATGATTTCACTCCAGATCTTAAAGTTAAAGTTGACATGATTAAG 2484  
 Db 116 GTTGGCAACATGATTTCACTCCAGATCTTAAAGTTAAAGTTGACATGATTAAG 58  
 QY 2485 CATGCTTCTTTGAGCTTTAAATTAATTAATTAACA 2519  
 Db 57 CATGCTTCTTTGAGCTTTAAATTAATTAATTAACA 23  
 RESULT 22  
 LOCUS BQ878479 871 bp mRNA linear EST 16-AUG-2002  
 DEFINITION AGENCOURT 8064671 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6206301  
 5', mRNA sequence.  
 ACCESSION BQ878479  
 VERSION BQ878479.1 GI:22270487  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 871)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LCM2360 row: 1 column: 22  
 High quality sequence stop: 686.  
 Location/Qualifiers  
 1. 871  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6206301"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 110"  
 /note="Organ: pancreas; Vector: pORF7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAAGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH MGC Library." 1 others

BASE COUNT 173 a 219 c 262 g 216 t

Query Match 31.5%; Score 815.2; DB 13; Length 871;  
 Best Local Similarity 99.5%; Pred. No. 2e-97;  
 Matches 828; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 849 CCCTGCGGCTGAGGCGGAGCTTTGCGCATGACCCGCGCGGCTTGTGAGCCCTC 908  
 Db 1 CCGCTGCGGCTGAGGCGGAGCTTTGCGCATGACCCGCGCGGCTTGTGAGCCCTC 60

QY 909 ACCTGGAGGTAGAGCTTGAAGCCTTGAACCGATGCTTGTGCAAGTGGCTCTTC 968  
 Db 61 ACCTGGAGGTAGAGCTTGAAGCCTTGAACCGATGCTTGTGCAAGTGGCTCTTC 120

QY 969 TGGCAGCCCAAGCCCAAGCCTTGTGATGTGCAAGCCGACCTTGTGAGGAGCCCT 1028  
 Db 121 TGGCAGCCCAAGCCCAAGCCTTGTGATGTGCAAGCCGACCTTGTGAGGAGCCCT 180

QY 1029 GACCAAGATGGGAGATCTGCTGCGCCAGAGAGGTCGCCGATGATGAAGTTGCA 1088  
 Db 181 GACCAAGATGGGAGATCTGCTGCGCCAGAGAGGTCGCCGATGATGAAGTTGCA 240

QY 1089 TTCTATGAGAGAGTGGCCCGCAGAGCTTGAAGCCTTGAAGAGCCTGACTGAAGAG 1148  
 Db 241 TTCTATGAGAGAGTGGCCCGCAGAGCTTGAAGCCTTGAAGAGCCTGACTGAAGAG 300

QY 1149 GCGCTGGGAGAGCTTGGGCTGCGCGCGCTGCACTGCTGGGAGGAGAGATTAGATC 1208  
 Db 301 GCGCTGGGAGAGCTTGGGCTGCGCGCGCTGCACTGCTGGGAGGAGAGATTAGATC 360

QY 1209 TGGACCAAGGCTGTGGGTAGATGTGCATAGAATAAGTATTATTTCCCAAGTGTG 1268  
 Db 361 TGGACCAAGGCTGTGGGTAGATGTGCATAGAATAAGTATTATTTCCCAAGTGTG 420

QY 1269 CTTTAGGCGTGGGCTGACCAAGGCTTCTTCTACATCTTCTCCAGTAAGTTCCCTCT 1328  
 Db 421 CTTTAGGCGTGGGCTGACCAAGGCTTCTTCTACATCTTCTCCAGTAAGTTCCCTCT 480

QY 1329 GGCTTGCAGAGATGAGTGTGTGCAATTTGTGAGCTCCCGCAGGCTGTCTCAGGCTT 1388  
 Db 481 GGCTTGCAGAGATGAGTGTGTGCAATTTGTGAGCTCCCGCAGGCTGTCTCAGGCTT 540

QY 1389 CACAGCTGTGGGCTTGGGAGAGTGCAGAGGTTAACTGACAGAGAGTTGGCAACCC 1448  
 Db 541 CACAGCTGTGGGCTTGGGAGAGTGCAGAGGTTAACTGACAGAGAGTTGGCAACCC 600

QY 1449 TGTCAGATTATTTGCTGCTTGTGCTTACAGTGGCAGACAGCCGTTGTTCTACATG 1508  
 Db 601 TGTCAGATTATTTGCTGCTTGTGCTTACAGTGGCAGACAGCCGTTGTTCTACATG 660

QY 1509 GCTTTGATATTTGTTTGAAGGAGAGATGGAACAATGTGAGTCCCTGATTTGT 1568  
 Db 661 GCTTTGATATTTGTTTGAAGGAGAGATGGAACAATGTGAGTCCCTGATTTGT 720

QY 1569 TTTGGGGAATGTGAGAGAGTGCCTGCTTTCACAAATCAACCTGGCAAAATGCAA 1628  
 Db 721 TTTGGGGAATGTGAGAGTGCCTGCTTTCACAAATCAACCTGGCAAAATGCAA 779

QY 1629 CAATGAAATTTCCAGCAGCTTCTTCATGAGGATAGTAACTGTGCTT 1680  
 Db 780 CAATGAAATTTCCAGCAGCTTCTTCATGAGGATAGTAACTGTGCTT 831

RESULT 23  
 BU196879 985 bp mRNA linear EST 04-SEP-2002  
 AGENCOURT 8076102 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6084691  
 LOCUS 5', mRNA sequence.  
 DEFINITION BU196879  
 ACCESSION BU196879  
 VERSION BU196879.1 GI:22710863  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 985)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LCM2317 row: 9 column: 04  
 High quality sequence stop: 644.  
 Location/Qualifiers  
 1. 985  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6084691"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 110"  
 /note="Organ: pancreas; Vector: pORF7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAAGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH MGC Library." 1 others

BASE COUNT 199 a 256 c 282 g 248 t



Db 361 CAATGGAGCAATCTGTGACCAACGAGGAGCTCCAGCCGGGCTGTGTGCTTCCA 420  
QY 821 GAGAGCCCTGCTGTTCCCTGTGTGACACCCCTGCGGTGAGGGGAGCTTGGCATGA 880  
Db 421 GAGAGCCCTGCTGTTCCCTGTGTGACACCCCTGCGGTGAGGGGAGCTTGGCATGA 480  
QY 881 CCCCCGACGCGGCTTGTGAGCTCATCACTGGAGGAGCTGATGAGCTTGA 940  
Db 481 CCCCCGACGCGGCTTGTGAGCTCATCACTGGAGGAGCTGATGAGCTTGA 540  
QY 941 CGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1000  
Db 541 CGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
QY 1001 GTGCAAGCCGACCTTGTGAGGAGCGGTGACCAAGATGGGAGATCTGCTCCAGAG 1060  
Db 601 GTGCAAGCCGACCTTGTGAGGAGCGGTGACCAAGATGGGAGATCTGCTCCAGAG 660  
QY 1061 GGTCCCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1120  
Db 661 GGTCCCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
QY 1121 CCTGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1179  
Db 721 CCTGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
QY 1180 CACTGC-TGGGAGGAGGAGATTTAGATCTGAGACGAGCTGT-GGTTAGATGTCGA-T 1236  
Db 781 CACTGCTTGGAGGAGGAGATTTAGATCTGAGACGAGCTGTGGGTTAAATGTCGA-TT 840  
QY 1237 AGAATAGCTAAATTTA-TTCCCGAGGTGTGTGCTTGTAGCGTGGGCTGACGAGCTTCT 1295  
Db 841 AGAATAGCTAAATTTA-TTCCCGAGGTGTGTGCTTGTAGCGGCTTGTAGCGGAGGTTGACAGGCT 900  
QY 1296 TCTTACAT 1303  
Db 901 TCTTCTCT 908

RESULT 25  
AL519269 901 bp mRNA linear EST 12-MAY-2003  
LOCUS AL519269  
DEFINITION CS0DA012YB24 5-PRIME, mRNA sequence.  
ACCESSION AL519269  
VERSION AL519269.2 GI:30538385  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 901)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT On Feb 13, 2001 this sequence version replaced gi:12782762.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 6027.r. For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DA012DA12QPLcluster=6027.r. Contact :  
Feng Liang, Email: fliang@life.techn.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID: CS0DA012DA12QPL.  
Location/Qualifiers  
1..901  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"

/clone="CS0DA012YB24"  
/tissue\_type="NEUROBLASTOMA"  
/clone\_lib="Homo sapiens NEUROBLASTOMA"  
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."  
BASE COUNT 212 a 266 c 259 g 153 t 11 others  
ORIGIN

Query Match 31.3%; Score 810; DB 9; Length 901;  
Best Local Similarity 97.8%; Pred. No. 9.2e-97;  
Matches 829; Conservative 11; Mismatches 6; Indels 2; Gaps 2;  
128 CGGCGGCTGGCGGCGGAGAGAGATGACGCGCTTGGGAGCACCCTGCTGCTGCT 187  
Db 56 CCGGAGATTGGCGGCGGAGAGAGATGACGCGCTTGGGAGCACCCTGCTGCTGCT 115  
QY 188 GCTGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247  
Db 116 GCTGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 175  
QY 248 CAAGCCCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 307  
Db 176 CAAGCCCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 234  
QY 308 CGAGTTGAGGAATCTATGAGAGACAGCAGCAAAATTCGAGCGGCTGGAAGAT 367  
Db 235 CGAGTTGAGGAATCTATGAGAGACAGCAGCAAAATTCGCA-CGGGTGGAAGAT 293  
QY 368 GAGAGCGAGGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 427  
Db 294 GAGAGCGAGGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 353  
QY 428 CAGCTATCAATGAGACCAACACAGACAGAGGTTGGAATTAATCAATCATGCTGCA 487  
Db 354 CAGCTATCAATGAGACCAACACAGACAGAGGTTGGAATTAATCAATCATGCTGCA 413  
QY 488 CCGAGAAATTCACAGATTAACCAACACAGCTGCAAAATGCTTTTCAAGACAGT 547  
Db 414 CCGAGAAATTCACAGATTAACCAACACAGCTGCAAAATGCTTTTCAAGACAGT 473  
QY 548 TATCACTCTGTGGAGACGAAGAGGAGAGGACAGAGTGCATCATGACAGAGA 607  
Db 474 TATCACTCTGTGGAGACGAAGAGGAGAGGACAGAGTGCATCATGACAGAGA 533  
QY 608 CTGTGGGCGCAGCATGATCTGCCAGTTTGGCAGCTTCAAGTACACCTGCGAGCATGCG 667  
Db 534 CTGTGGGCGCAGCATGATCTGCCAGTTTGGCAGCTTCAAGTACACCTGCGAGCATGCG 593  
QY 668 GGGCGAGAGATGCTGTGCAACCCGGGACAGTAGTGTGTGAGACAGCTGTGTCTG 727  
Db 594 GGGCGAGAGATGCTGTGCAACCCGGGACAGTAGTGTGTGAGACAGCTGTGTCTG 653  
QY 728 GGGTCACTGACCAAAATGAGCAGAGGAGCAGCAATGGGACCATGCTGTGACACAGAG 787  
Db 654 GGGTCACTGACCAAAATGAGCAGAGGAGCAGCAATGGGACCATGCTGTGACACAGAG 713  
QY 788 GAGATGCAACCCGGGCTGTGTGCTGCTTCCAGAGAGCTGTGCTTCCCTGTGTGAC 847  
Db 714 GAGATGCAACCCGGGCTGTGTGCTGCTTCCAGAGAGCTGTGCTTCCCTGTGTGAC 773  
QY 848 ACCGCTGCGGCTGAGAGGAGGCTTTGGCATGACCCCGGACGCGGCTTGTGACCTCAT 907  
Db 774 ACCGCTGCGGCTGAGAGGAGGCTTTGGCATGACCCCGGACGCGGCTTGTGACCTCAT 853  
QY 908 CACCTGGAAGTATGAGCTGATGAGAGCTTGAACCATGCTGTGTGCAAGTGGCTCTCT 967  
Db 834 CACCTGGAAGTATGAGCTGATGAGAGCTTGAACCATGCTGTGTGCAAGTGGCTCTCT 893  
QY 968 CTGCGAGC 975

Db 894 CTGCCAAC 901

RESULT 26  
BO897122 906 bp mRNA linear EST 16-AUG-2002  
LOCUS AGENCOURT 8074293 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6085612  
DEFINITION 5', mRNA sequence.

ACCESSION  
BO897122  
VERSION BO897122.1 GI:22289136  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: L1CM2319 row: e column: 05  
High quality sequence stop: 607.

FEATURES  
source  
1..906  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6085612"  
/issue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOT87; Site: 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dt priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

BASE COUNT 183 a 227 c 271 g 225 t  
ORIGIN

Query Match 31.2%; Score 807.4; DB 13; Length 906;  
Best Local Similarity 97.9%; Pred. No. 2e-96; Indels 8; Gaps 5;  
Matches 872; Conservative 0; Mismatches 11;

849 CCCCTGCCCGTGGAGGCGAGCTTTGGCATGACCCCGCAGCCGCTTCTGACCTTCATC 908  
1 CCCCTGCCCGTGGAGGCGAGCTTTGGCATGACCCCGCAGCCGCTTCTGACCTTCATC 60

909 ACCCTGGAGCTAGAGGCTGATGAGGCTTTGACCGATGCCCTTGTGCAATGGCTTCTC 968  
61 ACCCTGGAGCTAGAGGCTGATGAGGCTTTGACCGATGCCCTTGTGCAATGGCTTCTC 120

969 TGGCAGCCCCACACACACAGCCTGCTGTATATGTGTCAAGCCGACCTTGTGGGAGCCGT 1028  
121 TGGCAGCCCCACACACAGCCTGCTGTATATGTGTCAAGCCGACCTTGTGGGAGCCGT 180

1029 GACCAAGATGGGGAGATCTCTGCTGCTCCAGAGAGGTCCCGATGATGTGAAGTTGGAGC 1088  
181 GACCAAGATGGGGAGATCTCTGCTGCTCCAGAGAGGTCCCGATGATGTGAAGTTGGAGC 240

1089 TTCAATGAGAGGTGGCGCAGAGCTGAGAGACTTGAGAGAGAGCTGATGAAGAGATG 1148  
241 TTCAATGAGAGGTGGCGCAGAGCTGAGAGACTTGAGAGAGAGCTGATGAAGAGATG 300

QY 1149 GCGCTGGGGAGAGCTTGGGCGCTGCGCGCGCTGCATCTGCTGGAGAGGAGAGATTAGATC 1208  
Db 301 GCGCTGAGAGAGAGCTTGGGCGCTGCGCGCGCTGCATCTGCTGGAGAGGAGAGATTAGATC 360

QY 1209 TGAACAGAGCTGTGGGTAGATGTCATAGAAATAGCTAAATTTATTTCCAGAGGTGTG 1268  
Db 361 TGAACAGAGCTGTGGGTAGATGTCATAGAAATAGCTAAATTTATTTCCAGAGGTGTG 420

QY 1269 CTTTAGGGGTGGGCTGACAGAGCTTTCTTCCACATCTTTCTCCAGTAAGTTTCCCTCT 1328  
Db 421 CTTTAGGGGTGGGCTGACAGAGCTTTCTTCCACATCTTTCTCCAGTAAGTTTCCCTCT 480

QY 1329 GCGTTGACAGATAGAGGTGTTGTCATTTGTTACAGTCCGCCAGAGCTTCTCCAGGCTT 1388  
Db 481 GCGTTGACAGATAGAGGTGTTGTCATTTGTTACAGTCCGCCAGAGCTTCTCCAGGCTT 540

QY 1389 CACAGCTGTGTGCTTGGAGAGGTCAAGCAGAGGTAAACTGACAGAGCAAGTTGCCACCC 1448  
Db 541 CACAGCTGTGTGCTTGGAGAGGTCAAGCAGAGGTAAACTGACAGAGCAAGTTGCCACCC 600

QY 1449 TGTCCAGATTATTTGGCTGCTTGGCTCTTACAGTTGGACAGACAGCCGTTTGTCTACATG 1508  
Db 601 TGTCCAGATTATTTGGCTGCTTGGCTCTTACAGTTGGACAGACAGCCGTTTGTCTACATG 660

QY 1509 GCTTTGATTAATTTGTTGAGGGAGAGATGGAACAATGTGAGTCTTCTGTGATTGGT 1568  
Db 661 GCTTTGATTAATTTGTTGAGGGAGAGATGGAACAATGTGAGTCTTCTGTGATTGGT 720

QY 1569 TTTGGGGAAATGTGG-AGAGAGTGCCTGCTTGGCAACATCAACCTGGCAAAATGCA 1627  
Db 721 TTTGGGGAAATGTGGAAAGAGTGCCTGCTTGGCAACATCAACCTGGCAAAATGCA 780

QY 1628 ACAATGAAATTTTCCACGCA-GTTCTTTCATGGGC--ATAGTAAGCTGTGCTTACG 1684  
Db 781 ACAATGAAATTTTCCACGCAAGTCTTTCATGGGCATTAAGTAAGCTGTGCTTACG 840

QY 1685 TGTGTG--CAGATGAAATGTTCTGTTCAACC--TGATTAACATGTGTTATT 1731  
Db 841 TGTGTGCAAAATGAAATGTTCTGTTCAACCCTGGCATTAACCTGGGTTTAA 891

RESULT 27  
BO687864 898 bp mRNA linear EST 15-JUL-2002  
LOCUS AGENCOURT 8346023 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6250987  
DEFINITION 5', mRNA sequence.

ACCESSION  
BO687864  
VERSION BO687864.1 GI:21813180  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: L1CM2319 row: o column: 20  
High quality sequence stop: 650.

FEATURES  
source  
1..898  
/organism="Homo sapiens"  
/mol\_type="mRNA"



/db\_xref="taxon:9606"  
 /clone="IMAGE:6250987"  
 /issue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_11b="NIH MG\_C 110"  
 /note="Organ: pancreas; Vector: pOT37; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAAGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH MG\_C library."

BASE COUNT 181 a 222 c 267 g 227 t 1 others  
 ORIGIN

Query Match 31.2%; Score 806.8; DB 13; Length 898;  
 Best Local Similarity 99.5%; Pred. No. 2,4e-96;  
 Matches 830; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

849 CCCCTGCCGCTGAGAGGGGAGAGCTTGGCAGTACCCCGGAGCGGGCTTGGAGCTTCATC 908  
 1 CCCCCTGCCGCTGAGAGGGGAGAGCTTGGCAGTACCCCGGAGCGGGCTTGGAGCTTCATC 60  
 909 ACCCTGGAGCTAGAGCCTGATGAGACCTTGGACCGATGCCCTTGTGCCAGTGGCTCTTC 968  
 61 ACCCTGGAGCTAGAGCCTGATGAGACCTTGGACCGATGCCCTTGTGCCAGTGGCTCTTC 120  
 969 TGGCAGGCCCCAGAGCCAGCCTGCTGTATGTGTGAGAGCCGACCTTCGTGGGAGACCGCT 1028  
 121 TGGCAGGCCCCAGAGCCAGCCTGCTGTATGTGTGAGAGCCGACCTTCGTGGGAGACCGCT 180  
 1029 GACCAAGATGGGAGAGATCTCTGCTCCAGAGAGGATCCCGCATGATGAAGTTGGCAGC 1088  
 181 GACCAAGATGGGAGAGATCTCTGCTCCAGAGAGGATCCCGCATGATGAAGTTGGCAGC 240  
 1089 TTCAATGAGAGAGTGGCCGAGAGCTTGAAGAGCCTTGAAGAGAGCTTGAAGAGAGT 1148  
 241 TTCAATGAGAGAGTGGCCGAGAGCTTGAAGAGCCTTGAAGAGAGCTTGAAGAGAGT 300  
 1149 GCGCTGGGGAGAGCTGGGGAGCTGGCGCGTGCATGCTGGGAGGGGAGAGATTAGATC 1208  
 301 GCGCTGGGGAGAGCTGGGGAGCTGGCGCGTGCATGCTGGGAGGGGAGAGATTAGATC 360  
 1209 TGAACCAAGCTGTGGGTGATGATGCAATGAAATAGCTAATTTATTTCCCAAGTGTG 1268  
 361 TGAACCAAGCTGTGGGTGATGATGCAATGAAATAGCTAATTTATTTCCCAAGTGTG 420  
 1269 CTTAGAGCGTGGGTGAGACAGGCTTCTTCCATCATCTTCTTCCAGTAAGTTCCCTCT 1328  
 421 CTTAGAGCGTGGGTGAGACAGGCTTCTTCCATCATCTTCTTCCAGTAAGTTCCCTCT 480  
 1329 GCGTTGACAGATAGAGTGTGTGATGATTTGTCAGCTTCCCGCAGGCTGTCTCCAGGCTT 1388  
 481 GCGTTGACAGATAGAGTGTGTGATGATTTGTCAGCTTCCCGCAGGCTGTCTCCAGGCTT 540  
 1389 CACAGCTGTGCTGGAGAGTGAAGGAGGCTTAACACTGAGAGAGAGTTCGCAAGCC 1448  
 541 CACAGCTGTGCTGGAGAGTGAAGGAGGCTTAACACTGAGAGAGAGTTCGCAAGCC 600  
 1449 TGTCAGATTAATTTGAGCTTGTGCTTCAACAGTTGGAGAGACGCTTTGTTCAATG 1508  
 601 TGTCAGATTAATTTGAGCTTGTGCTTCAACAGTTGGAGAGACGCTTTGTTCAATG 660  
 1509 GCTTGAATTAATTTGAGAGGAGAGATGGAACATGAGAGTTCCTCCCTGATTTGCT 1568  
 661 GCTTGAATTAATTTGAGAGGAGAGATGGAACATGAGAGTTCCTCCCTGATTTGCT 720  
 1569 TTTGGGGGAA-ATGTGAGAGAGAGTCCCTGCTTTCGCAACATCAACCTGGCAAAATGCA 1627  
 721 TTTGGGGGAAATGTGAGAGAGAGTCCCTGCTTTCGCAACATCAACCTGGCAAAATGCA 780  
 1628 ACAATGATTTTCCAGCAGCTTC-TTTCATGGGCAATGAGTAAGTGTGCTT 1680

Db

781 ACAATGATTTTCCAGCAGCTTCTTTCATGAGGCAATGATAGCTGTGCTT 834

RESULT 28  
 AKO13622  
 LOCUS  
 DEFINITION

AKO13622 2123 bp mRNA linear HTC 05-DEC-2002  
 Mus musculus adult male hippocampus cDNA, RIKEN full-length  
 enriched library, clone:250036K07 product:diclkopf homolog 3  
 (Xenopus laevis), full insert sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

AKO13622  
 AKO13622.1 GI:12851055  
 HTC; CAP trapper.  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 Carninci, P. and Hayashizaki, Y.

AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED

High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
 99279253  
 10349636

REFERENCE

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.

AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED

Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 20499374  
 11042159

REFERENCE

3 Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P.,  
 Kono, H., Akiyama, J., Nishi, K., Kitsumaru, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED

RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multiplexed sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 20530913  
 11076861

TITLE

4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,  
 Aikawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S.,  
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I.,  
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,  
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,  
 Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,  
 Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, T., Pesole, G.,  
 Quackenbush, J., Schriml, L. M., Stanbly, P., Suzuki, R., Tomita, M.,  
 Wagner, L., Washio, T., Sakai, K., Okido, I., Furuno, M., Aono, H.,  
 Baldairelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, A. N.,  
 Carninci, P., de Bonaldo, M. F., Brownstein, M. J., But, C.,  
 Fletcher, C., Fujita, M., Gariboldi, M., Gustinich, S., Hill, D.,  
 Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,  
 Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,  
 Ring, B., Ringwald, M., Rodriguez, I., Sakumoto, N., Sasaki, H.,  
 Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,  
 Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Williams, J.,  
 Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kontuski, S.  
 and Hayashizaki, Y.

REFERENCE

Functional annotation of a full-length mouse cDNA collection  
 Nature 409 (6821), 685-690 (2001)  
 21085660  
 11217851

TITLE

5 The PANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs



RESULT 29  
LOCUS B0686410 879 bp mRNA linear EST 15-JUL-2002  
DEFINITION AGENCOURT\_8046835 NIH\_MGC\_110 Homo sapiens CDNA clone IMAGE:6209080  
5', mRNA sequence.  
ACCESSION B0686410  
VERSION B0686410.1 GI:21811726  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 879)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LNCM2367 row: m column: 17  
High quality sequence stop: 614.  
Location/Qualifiers  
1..879  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6209080"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 110"  
/note="Organ: pancreas; Vector: pORF7; Site: 1: XhoI;  
Site: 2: EcoRI; CDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-CDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC library." 1 others

BASE COUNT 174 a 219 c 262 g 223 t  
ORIGIN

Query Match 30.9%; Score 799.6; DB 13; Length 879;  
Best Local Similarity 99.2%; Pred. No. 2.1e-95;  
Matches 835; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

QY 849 CCCCTGCCCTGGAGGGGCGAGCTTTGGCCATGACCCCGGCGGTTTGTGACCTTCATC 908  
DB 1 CCCCTGCCCTGGAGGGGCGAGCTTTGGCCATGACCCCGGCGGTTTGTGACCTTCATC 60

QY 909 ACCTGGAGCTAGAGCTGATGAGCTTGCACGACGATGCTTGTGCGAGTGCCTCTC 968  
DB 61 ACCTGGAGCTAGAGCTGATGAGCTTGCACGACGATGCTTGTGCGAGTGCCTCTC 120

QY 969 TGGCAGGCCCAACGACGACCTTGTGTATGTGTGCAAGCCGACCTTGTGGGAGCCGT 1028  
DB 121 TGGCAGGCCCAACGACGACCTTGTGTATGTGTGCAAGCCGACCTTGTGGGAGCCGT 180

QY 1029 GACCAAGATGGGAGATCTGCTGTCGACAGAGAGTCCCGATGATGATGATGAGTGCAGC 1088  
DB 181 GACCAAGATGGGAGATCTGCTGTCGACAGAGAGTCCCGATGATGATGATGAGTGCAGC 240

QY 1089 TTATGAGAGAGGTGGCCAGAGAGCTGAGAGAGCTTGAAGAGAGCTTGAAGAGATG 1148  
DB 241 TTATGAGAGAGGTGGCCAGAGAGCTGAGAGAGCTTGAAGAGAGCTTGAAGAGATG 300

QY 1149 GCGCTGGGAGAGCTGCGGCTGCGCGCTGCACTGCTGGAGAGGGAAGATTGATTC 1208

DB 301 CGCGTAGAGGAGCCTGGCGCTGCCCGCTGCACCTGCTGGAGGGAGAGATTGATGATC 360

QY 1209 TGAACCAAGCTGTGGGTAGATGTGCATATAGAAAATAGCTAATTATTTTCCAGAGTGTG 1268  
DB 361 TGAACCAAGCTGTGGGTAGATGTGCATATAGAAAATAGCTAATTATTTTCCAGAGTGTG 420

QY 1269 CTTTAGCGTGGGCTACACAGGCTTCTCTACATCTTCTCCAGTAAGTTTCCCTCT 1328  
DB 421 CTTTAGCGTGGGCTACACAGGCTTCTCTACATCTTCTCCAGTAAGTTTCCCTCT 480

QY 1329 GCGTTGACAGATGAGGTGTGTGATTTGTTCAGCTCCCGCAGGCTGTTCAGGCTT 1388  
DB 481 GCGTTGACAGATGAGGTGTGTGATTTGTTCAGCTCCCGCAGGCTGTTCAGGCTT 540

QY 1389 CACAGCTGTGGCTTGGAGAGATGACAGAGGTTAAATGACAGAGAGTTGACAGCC 1448  
DB 541 CACAGCTGTGGCTTGGAGAGATGACAGAGGTTAAATGACAGAGAGTTGACAGCC 600

QY 1449 TGTCAGATTAATTTGGCTGCTTTGCTTACAGTTGACAGAGCGGTTTGTTCATG 1508  
DB 601 TGTCAGATTAATTTGGCTGCTTTGCTTACAGTTGACAGAGCGGTTTGTTCATG 660

QY 1509 GCTTTGATTAATTTGTTTGAAGGAGAGAGTGAAGAAATGTGAGTCTCCCTGATGT 1568  
DB 661 GCTTTGATTAATTTGTTTGAAGGAGAGAGTGAAGAAATGTGAGTCTCCCTGATGT 720

QY 1569 TTTGGGAAATTTGTGAGAGAGATGCTCCTGTTGCAACATCAACCTGGCAAAATGCA 1628  
DB 721 TTTGGGAAATTTGTGAGAGAGATGCTCCTGTTGCAACATCAACCTGGCAAAATGCA 779

QY 1629 CAATGATTTTTCACAGCAGTCTT CCAATGGCAATGATGATGT GCTTCAGCTG 1686  
DB 780 CAATGATTTTTCACAGCAGTCTTCCATGGCAATGATGATGTGCTTCAGCTG 839

QY 1687 TT 1688  
DB 840 TT 841

RESULT 30  
LOCUS B0688783 940 bp mRNA linear EST 15-JUL-2002  
DEFINITION AGENCOURT\_834454 NIH\_MGC\_110 Homo sapiens CDNA clone IMAGE:6251276  
5', mRNA sequence.  
ACCESSION B0688783  
VERSION B0688783.1 GI:21814099  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 940)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LNCM2395 row: k column: 21  
High quality sequence stop: 684.  
Location/Qualifiers  
1..940  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6251276"

/tissue type="ductal carcinoma, cell line"  
/lab host="DH10B (phage-resistant)"  
/clone 11b="N1H\_MGC\_110"  
/note="Organ: pancreas; Vector: pCRB7; Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-RT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGAG(5). Library constructed by  
ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a N1H\_MGC library." 2 others

BASE COUNT 188 a 235 c 276 g 239 t  
ORIGIN

Query Match 30.9%; Score 798.8; DB 13; Length 940;  
Best Local Similarity 98.9%; Pred. No. 2.6e-95;  
Matches 814; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 849 CCCCTGCGGTGGAGGGCGGAGCTTTGCAATGACCCCGCAGCCGGCTTTGGACCTCATC 908  
D 1 CCCCTGCGGTGGAGGGCGGAGCTTTGCAATGACCCCGCAGCCGGCTTTGGACCTCATC 60  
QY 909 ACCTGGAGCTAGAGCTGATGGAGCTTGGACCGATGCTTGTGCGCAGTGGACCTCTC 968  
D 61 ACCTGGAGCTAGAGCTGATGGAGCTTGGACCGATGCTTGTGCGCAGTGGACCTCTC 120  
QY 969 TGGCAGCCCCCAGCCAGCCAGCTGTGTATGTGTGCGAGCCGACTTGTGGGGAGCCGT 1028  
D 121 TGGCAGCCCCCAGCCAGCCAGCTGTGTATGTGTGCGAGCCGACTTGTGGGGAGCCGT 180  
QY 1029 GACCAAGATGGGGAGATCCCTGCTGCCAGAGAGTCCCGATGAGATGATAGTGGAGC 1088  
D 181 GACCAAGATGGGGAGATCCCTGCTGCCAGAGAGTCCCGATGAGATGATAGTGGAGC 240  
QY 1089 TTGATGAGAGAGTGGCCAGAGCTGTGAGAGAGCTTGGAGAGAGCTGACTGAAGAAGATG 1148  
D 241 TTGATGAGAGAGTGGCCAGAGCTGTGAGAGAGCTTGGAGAGAGCTGACTGAAGAAGATG 300  
QY 1149 GCGCTGGGGAGCGCTGCGCTGCCCGCGCTGCACTGCTGGAGGGAGAGATTTAGATC 1208  
D 301 GCGCTGGGGAGCGCTGCGCTGCCCGCGCTGCACTGCTGGAGGGAGAGATTTAGATC 360  
QY 1209 TGGACAGAGCTGTGGGTAGATGTGCAATAGAAATAGTATTTATTTCCCAAGTGTGTG 1268  
D 361 TGGACAGAGCTGTGGGTAGATGTGCAATAGAAATAGTATTTATTTCCCAAGTGTGTG 420  
QY 1269 CTTTGGAGCGTGGCTGACAGAGCTTCTTCTTACATCTTCTCCAGTAAAGTTCCCTCT 1328  
D 421 CTTTGGAGCGTGGCTGACAGAGCTTCTTCTTACATCTTCTCCAGTAAAGTTCCCTCT 480  
QY 1329 GCGTTGACAGCATGAGGTGTGTGCAATTTGTTGAGCTTCCCGCAGGTGTCTTCCAGAGCTT 1388  
D 481 GCGTTGACAGCATGAGGTGTGTGCAATTTGTTGAGCTTCCCGCAGGTGTCTTCCAGAGCTT 540  
QY 1389 CACAGCTGTGTCTTGGAGAGTGTGAGGAGGTTAAATCTGACAGAGAGCTTTGCCACCCC 1448  
D 541 CACAGCTGTGTCTTGGAGAGTGTGAGGAGGTTAAATCTGACAGAGAGCTTTGCCACCCC 600  
QY 1449 TGTCCAGATTTATGGGCTGTGGCTCTTACCACTTGGAGAGAGCGGTTGTCTCATG 1508  
D 601 TGTCCAGATTTATGGGCTGTGGCTCTTACCACTTGGAGAGAGCGGTTGTCTCATG 660  
QY 1509 GCTTTGATAATTTTGGAGGAGAGATGGAACAATGTGAGTGTCCCTGTGATGTGT 1568  
D 661 GCTTTGATAATTTTGGAGGAGAGATGGAACAATGTGAGTGTCCCTGTGATGTGT 720  
QY 1569 TTTGGGGAATTTGGGGAAGAGTGCCTGCTTGCACCAATCAACT-66CAAAATGGA 1627  
D 721 TTTGGGGAATTTGGGGAAGAGTGCCTGCTTGCACCAATCAACTGGGCAAAATGGA 780  
QY 1628 ACAATGAAATTTTCCAGCAGTCTTTTCCATGGGCAATAGTTAA 1670  
D 781 ACAATGAAATTTTCCAGCAGTCTTTTCCATGGGCAATAGTTAA 823

RESULT 31  
AK013054  
LOCUS  
DEFINITION  
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length  
enriched library, clone:2810409E22 product:dictkopf homolog 3  
(Xenopus laevis), full insert sequence.  
AK013054  
AK013054.2 GI:26105950  
HTC; CAP trapper.  
Mus musculus (house mouse)  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
KEYWORDS  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
KEYWORDS  
REFERENCE  
AUTHORS

1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
11042159  
2  
3

Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,  
Kono, H., Akiyama, J., Nishi, K., Kikuma, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, K., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Onari, E., Watanaka, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

4  
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,  
Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Aichi, J., Fukuda, S.,  
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,  
Saito, T., Okazaki, Y., Gotohori, T., Boni, H., Kasukawa, T., Saito, R.,  
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,  
Fleischmann, W., Gaasterland, T., Glisi, C., King, B., Kochiwa, H.,  
Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,  
Quackenbush, J., Schriml, L.M., Staudl, F., Suzuki, R., Tomita, M.,  
Wagner, L., Washio, T., Sakai, K., Okido, T., Furum, M., Aono, H.,  
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,  
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bull, C.,  
Pletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,  
Hofmann, M., Hume, D.A., Kamilya, M., Lee, N.H., Lyons, P.,  
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,  
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,  
Sato, K., Schombach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,  
Toyo-Oka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L.,  
Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S.,  
and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)  
21085660  
11217851

5  
The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 2303)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
KEYWORDS  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
KEYWORDS  
REFERENCE  
AUTHORS



DEFINITION AGNCOURT 8343875 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6248433  
5', mRNA sequence.  
ACCESSION BQ689483  
VERSION BQ689483.1 GI:21814799  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.  
1 (bases 1 to 867)  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabds@mail.nih.gov](mailto:cgabds@mail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>  
Plate: LILCM2388 row: e column: 10  
High quality sequence stop: 689.  
Location/Qualifiers  
1. 867  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6248433"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 110"  
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

BASE COUNT 173 a 218 c 261 g 215 t  
ORIGIN

Query Match 30.7%; Score 794.6; DB 13; Length 867;  
Best Local Similarity 98.0%; Pired. No. 9.7e-95;  
Matches 836; Conservative 0; Mismatches 14; Indels 3; Gaps 3;

QY 849 CCCCTCCCGTGGAGGGCGAGCTTTGCCATGACCCCGCAGCGCGCTTCTGGACCTCATC 908  
Db 1 CCCCTCCCGTGGAGGGCGAGCTTTGCCATGACCCCGCAGCGCGCTTCTGGACCTCATC 60

QY 909 ACCTGGAGCTAGAGCCTGATGGAGCCTTGACCCGATGCCCTTGTGCCAGTGGCCTCTC 968  
Db 61 ACCTGGAGCTAGAGCCTGATGGAGCCTTGACCCGATGCCCTTGTGCCAGTGGCCTCTC 120

QY 969 TGGCAGCCCGCAGCGCAGACGCTTGATGTGTGCAAGCCGACCTTCTGGAGGAGCGCT 1028  
Db 121 TGGCAGCCCGCAGCGCAGACGCTTGATGTGTGCAAGCCGACCTTCTGGAGGAGCGCT 180

QY 1029 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGATAGATGAGATTGGCAGC 1088  
Db 181 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGATAGATGAGATTGGCAGC 240

QY 1089 TTATATGAGAGAGTGGCGCCAGAGCTGTGAGAGACCTTGAGAGAGAGCCTGATGAAGATG 1148  
Db 241 TTATATGAGAGAGTGGCGCCAGAGCTGTGAGAGACCTTGAGAGAGAGCCTGATGAAGATG 300

QY 1149 GCGCTGGGGAGAGCTGGCGCTGCGCGCTGCACTCTGGAGAGGAGAGATTAGATC 1208  
Db 301 GCGCTGGGGAGAGCTGGCGCTGCGCGCTGCACTCTGGAGAGGAGAGATTAGATC 360

QY 1209 TGAACCAAGGCTGTGGGTAGATGTGCATTAGAAATAGCTAATTTATTTCCCGCAGGTGTG 1268

Db 361 TGAACCAAGGCTGTGGGTAGATGTGCATTAGAAATAGCTAATTTATTTCCCGCAGGTGTG 420

QY 1269 CTTTAGGCGTGGGCTGACACAGAGCTTCTTCCATCATCTTCTCCAGTAGATTCCCTCT 1328  
Db 421 CTTTAGGCGTGGGCTGACACAGAGCTTCTTCCATCATCTTCTCCAGTAGATTCCCTCT 480

QY 1329 GCGTTGACAGATGAGAGTGTGTCATTTTGTCACTCCCGCAGGCTGTCTCCAGGCTT 1388  
Db 481 GCGTTGACAGATGAGAGTGTGTCATTTTGTCACTCCCGCAGGCTGTCTCCAGGCTT 540

QY 1389 CACAGCTGTGCTTGGAGAGACAGCAGGCTTAACTCAGAGAGAGTTTGCACCCC 1448  
Db 541 CACAGCTGTGCTTGGAGAGACAGCAGGCTTAACTCAGAGAGAGTTTGCACCCC 600

QY 1449 TGTCCAGATTATTGCGTCTTTGCTTACCAAGTTGGCAGACAGCGCTTGTCTCATG 1508  
Db 601 TGTCCAGATTATTGCGTCTTTGCTTACCAAGTTGGCAGACAGCGCTTGTCTCATG 660

QY 1509 GCTTGAATTAATTTTGGAGGAGAGAGATGAGAAATGTGAGAGTCTCCCTGATTTGT 1568  
Db 661 GCTTGAATTAATTTTGGAGGAGAGAGATGAGAAATGTGAGAGTCTCCCTGATTTGT 720

QY 1569 TTTGGGAGAAATGTGAGAGAGTGCCTGCTTGGCAATCAATCAACTGGCAAAAATGCA 1628  
Db 721 TTTGGGAGAAATGTGAGAGAGTGCCTGCTTGGCAATCAATCAACTGGCAAAAATGCA 780

QY 1629 CAATGAA-TTTTCCAGCAGGCTTCTTCCATGAG-CATAGTAAAGCTGTG-CCTTCAGCT 1685  
Db 781 CAATGAA-TTTTCCAGCAGGCTTCTTCCATGAG-CATAGTAAAGCTGTG-CCTTCAGCT 840

QY 1686 GTTCAGATGAAA 1698  
Db 841 GTTCAGATGAAA 853

RESULT 33  
LOCUS AL547689 1182 bp mRNA linear EST 31-MAY-2003  
DEFINITION AL547689 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CSOD1008YN07 5-PRIME, mRNA sequence.  
AL547689  
VERSION AL547689.2 GI:31269518  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 1182)  
AUTHORS L4 M.B., Gruber, C., Jesse, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT On Feb 15, 2001 this sequence version replaced gi:12881985.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: [seq@genoscope.cns.fr](mailto:seq@genoscope.cns.fr), Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6027.r For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSOD1008CG04QP1&cluster=6027.r>. Contact: Feng Liang Email: [liang@lifetech.com](mailto:liang@lifetech.com) URL: <http://fulllength.invitrogen.com/InvitrogenCorporation1600>  
Faraday Avenue Genoscope sequence ID: CSOD1008CG04QP1.

FEATURES  
Location/Qualifiers  
1..1182  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSOD1008YN07"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"





```

QY 1149 GCGCTGGGGAGAGCTGGCGCTGCCGCCGCTGCACTGCTGGAGAGGAGATTAGATC 1208
Db 301 GCGCTGGAGGAGAGCTGGCGCTGCCGCCGCTGCACTGCTGGAGAGGAGATTAGATC 360
QY 1209 TGGACCAAGCTGGTGGGTAGATGTGCATATAGAAATAGCTAATTTATTTCCCAAGTGTGTG 1268
Db 361 TGGACCAAGCTGGTGGGTAGATGTGCATATAGAAATAGCTAATTTATTTCCCAAGTGTGTG 420
QY 1269 CTTAGAGCTGGGCTGACCAAGGCTTCTCTACATCTTCTCCAGTAAGTTCCCTCT 1328
Db 421 CTTAGAGCTGGGCTGACCAAGGCTTCTCTACATCTTCTCCAGTAAGTTCCCTCT 480
QY 1329 GCGTTGACAGCATAGAGGTGTGTGCATTTGTTCAGCTCCCAAGGCTGTCTCCAGGCTT 1388
Db 481 GCGTTGACAGCATAGAGGTGTGTGCATTTGTTCAGCTCCCAAGGCTGTCTCCAGGCTT 540
QY 1389 CACAGTGTGGTGTGGAGAGTGCAGGAGGTTAACTGCAGAGAGCTTTGCCACCCC 1448
Db 541 CACAGTGTGGTGTGGAGAGTGCAGGAGGTTAACTGCAGAGAGCTTTGCCACCCC 600
QY 1449 TGTCCAGATTATTTGGCTGCTTGTGCTCTACAGATTGGCAGACAGCCGTTGTCTACATG 1508
Db 601 TGTCCAGATTATTTGGCTGCTTGTGCTCTACAGATTGGCAGACAGCCGTTGTCTACATG 660
QY 1509 GCTTTGATTAATTTGTTTGGAGGAGAGATGGAACAATGTGAGTCTCCCTCTGATTTGCT 1568
Db 661 GCTTTGATTAATTTGTTTGGAGGAGAGATGGAACAATGTGAGTCTCCCTCTGATTTGCT 720
QY 1569 TTTGGGAAATGTGAGAGAGTGCCTGCTTTGCAACATCAA-CCTGGCAAAAATGCA 1627
Db 721 TTTGGGAAATGTGAGAGAGTGCCTGCTTTGCAACATCAA-CCTGGCAAAAATGCA 780
QY 1628 ACAATGAAATTTTCCAGCCAG-TTCTTTCCATGGGCAT-AGTAACTGTGCTT 1680
Db 781 ACAATGAAATTTTCCAGCCAGTTCCTTCATGGGCATTAAGTAACTGTGCTT 835

RESULT 35
LOCUS B0897670 877 bp mRNA linear EST 16-ANG-2002
DEFINITION AGENCOURT_8074427 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5085740
5', mRNA sequence.
ACCESSION B0897670
VERSION B0897670.1 GI:22289684
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 877)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: gsp@ds-mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LCM2319 row: 3 column: 13
High quality sequence stop: 576.
Location/Qualifiers
1..877
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5085740"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"

```

```

/clone.lib="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOT87; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 177 a 220 c 263 g 217 t
ORIGIN
Query Match 30.6%; Score 792.4; DB 13; Length 877;
Best Local Similarity 97.5%; Pred. No. 1.9e-94;
Matches 848; Conservative 0; Mismatches 16; Indels 6; Gaps 4;
QY 849 CCCCTGCCCGTGGAGGAGGAGCTTTGACATGACCCCGCAGCCGCTTCTGGACCTCATC 908
Db 1 CCCCTGCCCGTGGAGGAGGAGCTTTGACATGACCCCGCAGCCGCTTCTGGACCTCATC 60
QY 909 ACTGGAGCTTAGAGCTGTATGAGCCTTGGACCGATGCCCTTGTGCAATGAGCTGCTCTC 968
Db 61 ACTGGAGCTTAGAGCCTGTATGAGCCTTGGACCGATGCCCTTGTGCAATGAGCTGCTCTC 120
QY 969 TGCCAGCCCCACAGCACAAGCCTGTGTATGTGTGCAAGCCGACCTTGTTGGGAGAGCCGT 1028
Db 121 TGCCAGCCCCACAGCACAAGCCTGTGTATGTGTGCAAGCCGACCTTGTTGGGAGAGCCGT 180
QY 1029 GACCAAGATGGGGAGATCTCTGCTGCCAGAGAGGTCCCGATGTAGTAAAGTTGGCAGC 1088
Db 181 GACCAAGATGGGGAGATCTCTGCTGCCAGAGAGGTCCCGATGTAGTAAAGTTGGCAGC 240
QY 1089 TTCTATGAGAGAGGTGCCAGAGCTGTGAGAGACCTGTGAGAGAGACCTGTACTGAAGATG 1148
Db 241 TTCTATGAGAGAGGTGCCAGAGCTGTGAGAGACCTGTGAGAGAGACCTGTACTGAAGATG 300
QY 1149 GCGCTGGGGAGAGCTGCGGCTGCGCGCTGCACTGTGAGAGGAGGAGAAATTTAGATC 1208
Db 301 GCGCTGGAGGAGAGCTGCGGCTGCGCGCTGCACTGTGAGAGGAGGAGAAATTTAGATC 360
QY 1209 TGGACCAAGCTGTGGGTAGATGTGCATATAGAAATAGCTAATTTATTTCCCAAGTGTGTG 1268
Db 361 TGGACCAAGCTGTGGGTAGATGTGCATATAGAAATAGCTAATTTATTTCCCAAGTGTGTG 420
QY 1269 CTTTGGAGGTGGGCTGACCAAGCTTCTCTACATCTTCTTCCAGTAAGTTCCCTCT 1328
Db 421 CTTTGGAGGTGGGCTGACCAAGCTTCTCTACATCTTCTTCCAGTAAGTTCCCTCT 480
QY 1329 GCGTTGACAGCATAGAGGTGTGTGCATTTGTTCAGCTCCCAAGGCTGTCTCCAGGCTT 1388
Db 481 GCGTTGACAGCATAGAGGTGTGTGCATTTGTTCAGCTCCCAAGGCTGTCTCCAGGCTT 540
QY 1389 CACAGTGTGGTGTGGAGAGTGCAGGAGGTTAACTGCAGAGAGCAGTTGGCAACCCC 1448
Db 541 CACAGTGTGGTGTGGAGAGTGCAGGAGGTTAACTGCAGAGAGCAGTTGGCAACCCC 600
QY 1449 TGTCCAGATTATTTGGCTGCTTGTGCTCTACAGATTGGCAGACAGCCGTTGTCTACATG 1508
Db 601 TGTCCAGATTATTTGGCTGCTTGTGCTCTACAGATTGGCAGACAGCCGTTGTCTACATG 660
QY 1509 GCTTTGATTAATTTGTTTGGAGGAGAGATGGAACAATGTGAGTCTCCCTCTGATTTGCT 1568
Db 661 GCTTTGATTAATTTGTTTGGAGGAGAGATGGAACAATGTGAGTCTCCCTCTGATTTGCT 720
QY 1569 TTTGGGAAATGTGAGAGAGTGCCTGCTTTGCAACATCAA-CCTGGCAAAAATGCA 1628
Db 721 TTTGGGAAATGTGAGAGAGTGCCTGCTTTGCAACATCAA-CCTGGCAAAAATGCA 780
QY 1629 C-AAATGAAATTTTCCAGCAGTCTTT---CCATGGGAGATGAGTAAGTGTG-CCTTAG 1683
Db 781 CAAATGAAATTTTCCCGCAGTCTTTTTCATGGGAGATAGAGTAAGTGTGCTGCTTCCAG 840
QY 1684 CTGTGAG-ATGAATGTCTGTTCACCC 1712

```

Db 841 CTCCTGCAGAAATGAATCTTCTTCAACC 870

RESULT 36  
LOCUS BQ897953  
DEFINITION AGENCOURT 8061767 NIH\_MGC\_110 Homo sapiens CDNA clone IMAGE:6208520  
5', mRNA Sequence.  
ACCESSION BQ897953  
VERSION BQ897953.1 GI:22289967  
SOURCE EST.  
KEYWORDS Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
1 (bases 1 to 883)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLCM2366 row: f column: 09  
High quality sequence stop: 684.  
Location/Qualifiers  
1..883  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6208520"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="PHIOB (phage-resistant)"  
/clone\_11b="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; CDNA made by oligo-RT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACTGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

BASE COUNT 178 a 220 c 263 g 222 t

ORIGIN

Query Match 30.6%; Score 791.2; DB 13; Length 883;  
Best Local Similarity 99.3%; Pred. No. 2.7e-94;  
Matches 816; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

QY 849 CCCCTGCCCTGGAGGGCGCAAGCTTTGCCATGACCCGCCAGCGCGCTTGTGACCTCATC 908  
DB 1 CCCCTGCCCTGGAGGGCGCAAGCTTTGCCATGACCCGCCAGCGCGCTTGTGACCTCATC 60

QY 909 ACCTGGAGAGCTGAGAGCTGATGAGAGCTTGGACCGATGCGCTTGTGACAGTGGCTCTGC 968  
DB 61 ACTGGGAGAGCTGAGAGCTGATGAGAGCTTGGACCGATGCGCTTGTGACAGTGGCTCTGC 120

QY 969 TGGCAGCCCAAGCAGCAGCAGCTGTGTATGTGTGTGCAAGCCGACCTTGTGTGGAGCCGT 1028  
DB 121 TGGCAGCCCAAGCAGCAGCAGCTGTGTATGTGTGTGCAAGCCGACCTTGTGTGGAGCCGT 180

QY 1029 GACCAAGATGGGGAGATCTGTGCTGCCAGAGAGTCCCGATGAGATGAATTTGGCAGC 1088  
DB 181 GACCAAGATGGGGAGATCTGTGCTGCCAGAGAGTCCCGATGAGATGAATTTGGCAGC 240

QY 1089 TTTCATGAGAGAGGTGGCCAGGAGCTGTGAGAGACTGTGAGAGAGGCTGTGCTGAGAGATG 1148

Db 241 TTTCATGAGAGAGGTGGCCAGGAGCTGTGAGAGACTGTGAGAGAGGCTGTGAGAGATG 300

QY 1149 GCGCTGGGGAGAGCTGTGGGCTGCCCGCGCTGCACTGCTGGGAGGGGAGAGATTTGATC 1208

Db 301 GCGCTGGGGAGAGCTGTGGGCTGCCCGCGCTGCACTGCTGGGAGGGGAGAGATTTGATC 360

QY 1209 TGGACAGGCTGTGGGAGATGTGCATATAGATTAATTAATTTCCACAGGTGTG 1268

Db 361 TGGACAGGCTGTGGGAGATGTGCATATAGATTAATTAATTTCCACAGGTGTG 420

QY 1269 CTTTAGCGGTGGGCTGACAGCGCTTCTCTCAATCTTCTTCCAGTAAGTTCCCTCT 1328

Db 421 CTTTAGCGGTGGGCTGACAGCGCTTCTCTCAATCTTCTTCCAGTAAGTTCCCTCT 480

QY 1329 GCGCTTGACAGATAGAGGTGTGTGCAATTTTTCAGCTCCCGAGGCTGTTCAGAGCTT 1388

Db 481 GCGCTTGACAGATAGAGGTGTGTGCAATTTTTCAGCTCCCGAGGCTGTTCAGAGCTT 540

QY 1389 CACAGTCTGTGCTTGGAGAGTCAAGGCTTAACTGACAGAGCAGTTTCCACCCC 1448

Db 541 CACAGTCTGTGCTTGGAGAGTCAAGGCTTAACTGACAGAGCAGTTTCCACCCC 600

QY 1449 TGTCCAGATTAATTTGGCTTGGCTTGCCTTCACTGAGTGGCAGACGCGTTGTTCTCATG 1508

Db 601 TGTCCAGATTAATTTGGCTTGGCTTGCCTTCACTGAGTGGCAGACGCGTTGTTCTCATG 660

QY 1509 GCTTTGATTAATTTTGAAGGAGAGAGATGAAACAATGTGAGTCTCCCTGATTTGGT 1568

Db 661 GCTTTGATTAATTTTGAAGGAGAGAGATGAAACAATGTGAGTCTCCCTGATTTGGT 720

QY 1569 TTGGGGGAATGTGGAGAGAGTCCCTGCTTGGCAACATGCA-CCTGGCAAAATATGCA 1627

Db 721 TTGGGGGAATGTGGAGAGAGTCCCTGCTTGGCAACATGCA-CCTGGCAAAATATGCA 780

QY 1628 ACAATGAATTTTCCACGAGCTT-CCTTCCATGGGCATAGG 1667

Db 781 ACAATGAATTTTCCACGAGCTTCTTTTCCATGGGCATAGG 822

RESULT 37  
LOCUS BQ889489  
DEFINITION AGENCOURT 8061866 NIH\_MGC\_110 Homo sapiens CDNA clone IMAGE:6208646  
5', mRNA Sequence.  
ACCESSION BQ889489  
VERSION BQ889489.1 GI:22281503  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
1 (bases 1 to 892)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLCM2366 row: k column: 15  
High quality sequence stop: 680.  
Location/Qualifiers  
1..892  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6208646"  
/tissue\_type="ductal carcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"  
 /clone\_id="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pORF7; Site: 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dt priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC library."

BASE COUNT 179 a 223 c 269 g 221 t

ORIGIN

Query Match 30.6%; Score 790.8; DB 13; Length 892;  
 Best Local Similarity 99.0%; Pred. No. 36-94;  
 Matches 806; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

849 CCCCTGCCGTGGAGGCGAGCTTTCATGACCCCGCAGCGGCTTCTGACCTCATC 908  
 1 CCCCTGCCGTGGAGGCGAGCTTTCATGACCCCGCAGCGGCTTCTGACCTCATC 60

909 ACCGTGGAGCTAAGCTGATGAGAGCTTGGACCAATGCTTGTGCGAGTGGCTCTC 968  
 61 ACCGTGGAGCTAAGCTGATGAGAGCTTGGACCAATGCTTGTGCGAGTGGCTCTC 120

969 TGCCAGCCCGACACGACAGCTGTGTATGTGTGCAAGCCGCTTGTGGGAGACCT 1028  
 121 TGCCAGCCCGACACGACAGCTGTGTATGTGTGCAAGCCGCTTGTGGGAGACCT 180

1029 GACCAAGATGGGAGATCCTGCTGCCAGAGAGTCCCGATGATGATGATGAGTTGGCAGC 1088  
 181 GACCAAGATGGGAGATCCTGCTGCCAGAGAGTCCCGATGATGATGATGATGAGTTGGCAGC 240

1089 TTCTATGAGAGAGGTGGGCGCAGAGCTGAGGACCTGAGAGAGAGCTGAGTGAAGATG 1148  
 241 TTCTATGAGAGAGGTGGGCGCAGAGCTGAGGACCTGAGAGAGAGCTGAGTGAAGATG 300

1149 GCGCTGGGGAGGCTGCGGCTGCGGCTGCGA CTGCTGCGAGGGAGAGATTTAGATC 1208  
 301 GCGCTGGGGAGGCTGCGGCTGCGGCTGCGA CTGCTGCGAGGGAGAGATTTAGATC 360

1209 TGAGACAGGCTGTGGGTAGATGTGCAATGAAATAGCTAATTTATTTCCCGAGGTGTG 1268  
 361 TGAGACAGGCTGTGGGTAGATGTGCAATGAAATAGCTAATTTATTTCCCGAGGTGTG 420

1269 CTTTAGGCGTGGGCTGACAGAGCTTCTCTACATCTTCTCCAGTAAATTTCCCTCT 1328  
 421 CTTTAGGCGTGGGCTGACAGAGCTTCTCTACATCTTCTCCAGTAAATTTCCCTCT 480

1329 GCGTTGACAGCAAGAGGTGTGTGCAATTTGTCAGTCTCCCGAGGTGTGTCGAGGCTT 1388  
 481 GCGTTGACAGCAAGAGGTGTGTGCAATTTGTCAGTCTCCCGAGGTGTGTCGAGGCTT 540

1389 CACAGCTGTGTGCTTGGAGAGTCAAGAGGTTAACTGACAGAGCACTTTGCCACCC 1448  
 541 CACAGCTGTGTGCTTGGAGAGTCAAGAGGTTAACTGACAGAGCACTTTGCCACCC 600

1449 TGTCGAGATTTATGCTGCTTTGCTCTACAGTGTGGCAAGAGGCTTTGTTTACATG 1508  
 601 TGTCGAGATTTATGCTGCTTTGCTCTACAGTGTGGCAAGAGGCTTTGTTTACATG 660

1509 GCTTTGATATTTGTTGAGGGAGAGATGAGAAACAATGTGAGTCTCCCTGATGAGT 1568  
 661 GCTTTGATATTTGTTGAGGGAGAGATGAGAAACAATGTGAGTCTCCCTGATGAGT 720

1569 TTTGGGGAATGTGGAGAGAGTCCCTGCTTTGCAACATCACTGTGCAAAAATGCA 1628  
 721 TTTGGGGAATGTGGAGAGAGTCCCTGCTTTGCAACATCACTGTGCAAAAATGCA 780

1629 CAATGATATTTT-CCAGCAGTCTTTCCATGG 1661  
 781 CAATGATATTTTCCAGCAGTCTTTCCATGG 814

RESULT 38

BUI74805

LOCUS

DEFINITION

AGNCOURT 7974830 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6082014

5' mRNA sequence.

BUI74805

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapds-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: LICM2309 row: c column: 07

High quality sequence stop: 649.

Location/Qualifiers

1. 841

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/mol\_type="mRNA"

/clone="IMAGE:6082014"

/issue\_type="ductal carcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_id="NIH\_MGC\_110"

/note="Organ: pancreas; Vector: pORF7; Site: 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dt priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC library."

BASE COUNT 168 a 210 c 254 g 209 t

ORIGIN

Query Match 30.5%; Score 789.4; DB 13; Length 841;  
 Best Local Similarity 98.9%; Pred. No. 4,76-94;  
 Matches 826; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

849 CCCCTGCCGTGGAGGCGAGCTTGGCATGACCCCGCAGCGGCTTCTGACCTCATC 908  
 1 CCCCTGCCGTGGAGGCGAGCTTGGCATGACCCCGCAGCGGCTTCTGACCTCATC 60

909 ACTGGAGAGCTAAGCTGATGAGAGCTTGGACCAATGCTTGTGCGAGTGGCTCTC 968  
 61 ACTGGAGAGCTAAGCTGATGAGAGCTTGGACCAATGCTTGTGCGAGTGGCTCTC 120

969 TGCCAGCCCGACACGACAGCTGTGTATGTGTGCAAGCGGACCTTGTGGGAGACCT 1028  
 121 TGCCAGCCCGACACGACAGCTGTGTATGTGTGCAAGCGGACCTTGTGGGAGACCT 180

1029 GACCAAGATGGGAGATCTGCTGCGCAGAGAGTCCCGATGATGATGAGTTGGCAGC 1088  
 181 GACCAAGATGGGAGATCTGCTGCGCAGAGAGTCCCGATGATGATGAGTTGGCAGC 240

1089 TTCTATGAGAGAGGTGGGCGCAGAGCTGAGAGACCTGAGAGAGAGCTGAGTGAAGATG 1148  
 241 TTCTATGAGAGAGGTGGGCGCAGAGCTGAGAGACCTGAGAGAGAGCTGAGTGAAGATG 300

1149 GCGCTGGGGAGGCTGCGGCTGCGGCTGCGA CTGCTGCGAGGGAGAGATTTAGATC 1208

[illegible]

RESULT 39	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	JOURNAL	COMMENT
BO686534	BO686534	AGENCOURT 8034689 NIH_MGC_110 Homo sapiens cDNA IMAGE:6207165	BO686534	BO686534	BO686534.1 GI:21811850	EST.	Homo sapiens (human)	877 bp	MRNA	linear	EST 15-JUL-2002
		5', mRNA sequence.					Homo sapiens				
							Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
							1 (bases 1 to 877)				
							NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
							National Institutes of Health, Mammalian Gene Collection (MGC)				
							Unpublished				
							Contact: Robert Strausberg, Ph.D.				
							Email: <a href="mailto:cgabbs-r@mail.nih.gov">cgabbs-r@mail.nih.gov</a>				
							Tissue Procurement: ATCC				
							CDNA Library Preparation: Rubin Laboratory				
							CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)				
							DNA Sequencing by: Agencourt Bioscience Corporation				
							clone distribution: MGC clone distribution information can be				
							found through the I.M.A.G.E. Consortium/LNL at:				
							<a href="http://image.lnl.gov">http://image.lnl.gov</a>				
							Place: LNCM2352 row: n column: 02				
							High quality sequence stop:692.				

FEATURES  
source

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6207169"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH_MGC_110"
/organ="Pancreas"; Vector: pOTB7; Site_1:
XhoI;

```

Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MCC library."

BASE COUNT	179	a	213	c	265	g	219	t	1	others
------------	-----	---	-----	---	-----	---	-----	---	---	--------

Query Match	30.5%	Score 788.2	DB 13	Length 877
Best Local Similarity	99.1%	Pred. No. 6.6e-94		
Matches 814	Conservative 0	Mismatches 3	Indels 4	Gaps 2
QY 849	CCCTGCCCCGTGAGGGCGAGCTTTGCGCATGACCCCGCAGCCGGCTTTGAGACTATC	908		
Db 1	CCCTGCCCCGTGAGGGCGAGCTTTGCGCATGACCCCGCAGCCGGCTTTGAGACTATC	60		
QY 909	ACCTGGAGAGCTAGAGCCTGATGAGACCTTGGACCGATGACCTTTGTCAGTGGCCTCTC	968		
Db 61	ACCTGGAGAGCTAGAGCCTGATGAGACCTTGGACCGATGACCTTTGTCAGTGGCCTCTC	120		
QY 969	TGCCAGCCCCCAGCCACAGCCTGCTGTATGTGTGCAAGCCGACCTTCTGTGGAGCCGT	1028		
Db 121	TGCCAGCCCCCAGCCACAGCCTGCTGTATGTGTGCAAGCCGACCTTCTGTGGAGCCGT	180		
QY 1029	GACCAAGATGGGGAGATCTGCTGCCCCAGAGAGGTCCCCGATGATGATGAGTTGGACGC	1088		
Db 181	GACCAAGATGGGGAGATCTGCTGCCCCAGAGAGGTCCCCGATGATGATGAGTTGGACGC	240		
QY 1089	TTCAATGAGAGAGTGTGCGCCAGAGACCTGAGAGCCTTGAAGAGAGCCTGACTGAAGATG	1148		
Db 241	TTCAATGAGAGAGTGTGCGCCAGAGACCTGAGAGCCTTGAAGAGAGCCTGACTGAAGATG	300		
QY 1149	GCCTTGGGGAGCCTGTGGCTGCGCCGCTGCTCATCTGCTGGAGGGGAGAGATTTAGATC	1208		
Db 301	GCCTTGGGGAGCCTGTGGCTGCGCCGCTGCTCATCTGCTGGAGGGGAGAGATTTAGATC	360		
QY 1209	TGACACAGAGCTGTGGAGATGTGTCAATAGAAATAGCTAATTTATTTCCCGAGTGTGTG	1268		
Db 361	TGACACAGAGCTGTGGAGATGTGTCAATAGAAATAGCTAATTTATTTCCCGAGTGTGTG	420		
QY 1269	CTTTAGGCGTGGAGTACCAAGCCTTTCTTCTCAACTTTCTTCCAGTAAAGTTTCCCTCT	1328		
Db 421	CTTTAGGCGTGGAGTACCAAGCCTTTCTTCTCAACTTTCTTCCAGTAAAGTTTCCCTCT	480		
QY 1329	GGCTTGAACAGATAGAGTGTGTGCATTTGTTCAGCTGCCCGAGAGCTTCTCAGAGCTT	1388		
Db 481	GGCTTGAACAGATAGAGTGTGTGTGCATTTGTTCAGCTGCCCGAGAGCTTCTCAGAGCTT	540		
QY 1389	CACAGTCTGTGCTTGGAGAGTCAAGCAGAGGTTAACTGACAGAGACAGTTTGCACCCC	1448		
Db 541	CACAGTCTGTGCTTGGAGAGTCAAGCAGAGGTTAACTGACAGAGACAGTTTGCACCCC	600		
QY 1449	TGTCAGATTAATGGCGCTTTTGCTCTCAACAGTTGGACAGACCGCTTGTCTCAATG	1508		
Db 601	TGTCAGATTAATGGCGCTTTTGCTCTCAACAGTTGGACAGACCGCTTGTCTCAATG	660		
QY 1509	GCCTTGAATATTTTGAAGGAGAGATGAAACAAATGTGAGTCTCCCTCTGATTTGGT	1568		
Db 661	GCCTTGAATATTTTGAAGGAGAGATGAAACAAATGTGAGTCTCCCTCTGATTTGGT	720		
QY 1569	TTTGGGAAATGCT-GAGAAAGATGCCCTGCTTTGGAAACATCAACCTGGGAAATATGCA	1628		
Db 721	TTTGGGAAATGCTGGGAAAGATGCCCTGCTTTGGAAACATCAACCTGGGAAATATGCA	780		
QY 1628	ACAATATGATTTT--CCACGACAGTTCTTTCCATGGGCATA 1665			
Db 781	ACAATATGATTTTTCACGACAGTTCTTTCCATGGGGAAT 821			

LOCUS B0689208 870 bp mRNA linear EST 15-JUL-2002  
 DEFINITION AGENCOURT 806399 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6207819  
 5', mRNA sequence.  
 ACCESSION B0689208  
 VERSION B0689208.1 GI:21814524  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 870)  
 NIH-MGC http://mgs.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgapds-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LNCM364 row: 1 column: 04  
 High quality sequence stop: 691.  
 Location/Qualifiers  
 1..870  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6207819"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAAGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."  
 BASE COUNT 170 a 217 c 267 g 216 t  
 ORIGIN  
 Query Match 30.5%; Score 788; DB 13; Length 870;  
 Best Local Similarity 99.4%; Pred. No. 7e-94; 5; Indels 0; Gaps 0;  
 Matches 791; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 849 CCCCCTGCCGCTGAGGGCGAGCTTGGCCATGAGCCGCCAGCCGGCTTGTGAGACTTCATC 908  
 Db 1 CCCCCTGCCGCTGAGGGCGAGCTTGGCCATGAGCCGCCAGCCGGCTTGTGAGACTTCATC 60  
 QY 909 ACCGCGAGGCTAGAGGCTGATGAGGCTTGGAGCCGATGAGCCCTTGTGAGGCTTCCTC 988  
 Db 61 ACCGCGAGGCTAGAGGCTTGTGAGGCTTGGAGCCGATGAGCCCTTGTGAGGCTTCCTC 120  
 QY 969 TGCAGCCCCCAGCCAGCCAGCTGTGTATGTGTGCAAGCCGACCTTCGTGGGAGCCGT 1028  
 Db 121 TGCAGCCCCCAGCCAGCCAGCTGTGTATGTGTGCAAGCCGACCTTCGTGGGAGCCGT 180  
 QY 1029 GACCAAGATGGGAGGATCTCTGCTGCCAGAGAGTCCCGCATGATGTGAAGTTGGAGC 1088  
 Db 181 GACCAAGATGGGAGGATCTCTGCTGCCAGAGAGTCCCGCATGATGTGAAGTTGGAGC 240  
 QY 1089 TTCTATGAGAGAGTGTGCGCCAGAGAGCTGGAGAGCTTGAAGAGAGCTGATGAAGATG 1148  
 Db 241 TTCTATGAGAGAGTGTGCGCCAGAGAGCTTGAAGAGAGCTTGAAGAGATG 300  
 QY 1149 GCGGTGGGAGGCTTGGGCTGCGCGCTGCTGCACTGTCTGGAGAGGGAAGATTATATC 1208  
 Db 301 GCGGTGGGAGGCTTGGGCTGCGCGCTGCTGCACTGTCTGGAGAGGGAAGATTATATC 360

QY 1209 TGGACAGGCTGTGGTNGATGTGCAATAGAAATAGTAATTTATTTCCAGGTGTG 1268  
 Db 361 TGGACAGGCTGTGGTNGATGTGCAATAGAAATAGTAATTTATTTCCAGGTGTG 420  
 QY 1269 CTTTATGAGGCTGTGGGCTGACAGGCTTCTCCATACATCTTCCAGTATGTTCCCTCT 1328  
 Db 421 CTTTATGAGGCTGTGGGCTGACAGGCTTCTTCTACATCTTCTCCAGTATGTTCCCTCT 480  
 QY 1329 GCGTTGACAGCATGAGTGTGTTGATTTGTTCAAGTCTCCAGGCTTCTCCAGGCTT 1388  
 Db 481 GCGTTGACAGCATGAGTGTGTTGATTTGTTCAAGTCTCCAGGCTTCTCCAGGCTT 540  
 QY 1389 CACAGTCTGTGCTTGGAGAGTCAAGAGAGGTTAAATGAGAGAGAGTTCACAGCC 1448  
 Db 541 CACAGTCTGTGCTTGGAGAGTCAAGAGAGGTTAAATGAGAGAGAGTTCACAGCC 600  
 QY 1449 TGTCCAGATTATGAGCTGCTTGTGCTTACAGATGGAGAGAGCCGTTGTCTACATG 1508  
 Db 601 TGTCCAGATTATGAGCTGCTTGTGCTTACAGATGGAGAGAGCCGTTGTCTACATG 660  
 QY 1509 GCTTTGATTAATTTGTTGAGGAGAGATGGAACAAATGTGAGCTTCTCATTTGCT 1568  
 Db 661 GCTTTGATTAATTTGTTGAGGAGAGATGGAACAAATGTGAGCTTCTCATTTGCT 720  
 QY 1569 TTTGGGAAATGTGAGAGAGTGCCTGCTTGTGCAACATCAACTGGCAAAATGCA 1628  
 Db 721 TTTGGGAAATGTGAGAGAGTGCCTGCTTGTGCAACATCAACTGGCAAAATGCA 780  
 QY 1629 CAATATGATTTTCCAC 1644  
 Db 781 CAATATGATTTTCCC 796  
 RESULT 41  
 LOCUS B0688234 883 bp mRNA linear EST 15-JUL-2002  
 DEFINITION AGENCOURT 8063962 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6207793  
 5', mRNA sequence.  
 ACCESSION B0688234  
 VERSION B0688234.1 GI:21813550  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 883)  
 NIH-MGC http://mgs.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgapds-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LNCM364 row: h column: 02  
 High quality sequence stop: 680.  
 Location/Qualifiers  
 1..883  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6207793"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAAGAG(G). Library constructed by



ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

BASE COUNT 175 a 223 c 263 g 221 t 1 others

Query Match 30.3%; Score 783.4; DB 13; Length 887;  
Best Local Similarity 98.4%; Pred. No. 2.8e-93;  
Matches 801; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

849 CCCCTCCCGTGGAGGCGAGCTTTGCAATGACCCCGCCAGCGGCTTGGACCTCATC 908  
1 CCCCTCCCGTGGAGGCGAGCTTTGCAATGACCCCGCCAGCGGCTTGGACCTCATC 60  
909 ACCCTGGAGCTAGAGCTTGAAGCTTGAACCCATGCTTGTGCTGCTGCTCTCTC 968  
61 ACCCTGGAGCTAGAGCTTGAAGCTTGAACCCATGCTTGTGCTGCTGCTCTCTC 120  
969 TGGCAGCCCAACAGCAGCTGTGTATGTGTGCAAGCCGACCTTCTGTGGAGCCGT 1028  
121 TGGCAGCCCAACAGCAGCTGTGTATGTGTGCAAGCCGACCTTCTGTGGAGCCGT 180  
1029 GACCAAGATGGAGATCTCTGCTGCGCAAGAGCTCCCGATGATGATGAATTGGCAGC 1088  
181 GACCAAGATGGAGATCTCTGCTGCGCAAGAGCTCCCGATGATGATGAATTGGCAGC 240  
1089 TTGATGAGAGAGGTGGCGCCAGAGCTGAGAGACCTGAGAGAGGCTGACTGAAGAGATG 1148  
241 TTGATGAGAGAGGTGGCGCCAGAGCTGAGAGACCTGAGAGAGGCTGACTGAAGAGATG 300  
1149 GCGCTGGGAGAGCTCTGCGCTGCGCGCTGCACTGTCTGGAGAGGAGAGATTGATC 1208  
301 GCGCTGGGAGAGCTCTGCGCTGCGCGCTGCACTGTCTGGAGAGGAGAGATTGATC 360  
1209 TGGACAGAGCTGTGGAGATGTGCAATGAAATAGCTAATTATTTCCCGAGGTGTG 1268  
361 TGGACAGAGCTGTGGAGATGTGCAATGAAATAGCTAATTATTTCCCGAGGTGTG 420  
1269 CTTTGGCGGTGGGCTGACAGAGCTTCTTCCATGCTTCTCCAGTAAATTTCCCTCT 1328  
421 CTTTGGCGGTGGGCTGACAGAGCTTCTTCCATGCTTCTCCAGTAAATTTCCCTCT 480  
1329 GCGTTCACAGATGAGGTGTGTGCAATTTGATGCTTCCCGCAGGCTTTCCTCCAGGCT 1388  
481 GCGTTCACAGATGAGGTGTGTGCAATTTGATGCTTCCCGCAGGCTTTCCTCCAGGCT 540  
1389 CACAGTCTGTGCTTGGAGAGTCAAGCAGGCTTAAATGTCAGAGAGAGTTCACACCC 1448  
541 CACAGTCTGTGCTTGGAGAGTCAAGCAGGCTTAAATGTCAGAGAGAGTTCACACCC 600  
1449 TGTCCAGATTAATTTGCTGCTTGTGCTTACCAATGTCAGAGAGCCGTTTGTCTACAG 1508  
601 TGTCCAGATTAATTTGCTGCTTGTGCTTACCAATGTCAGAGAGCCGTTTGTCTACAG 660  
1509 GCTTGAATTAATTTGTCAGAGAGAGATGGAACAATGAGTGTGCTTCTGATTTGAT 1568  
661 GCTTGAATTAATTTGTCAGAGAGAGATGGAACAATGAGTGTGCTTCTGATTTGAT 720  
1569 TTTGGGGAATTTGTCAGAGAGAGTGTGCTTGTGCAATCAACTGCGCAAAAATGCA 1628  
721 TTTGGGGAATTTGTCAGAGAGAGTGTGCTTGTGCAATCAACTGCGCAAAAATGCA 780  
1629 CAATGAA-TTTTCAGCAGAGTCTTTCATGAG 1661  
781 CAATGAA-TTTTCAGCAGAGTCTTTCATGAG 814

RESULT 42  
BUI91090 887 bp mRNA linear EST 04-SEP-2002  
LOCUS AGENCOURT 8074903 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6086034  
DEFINITION 5', mRNA sequence.

ACCESSION BUI91090  
VERSION BUI91090.1 GI:22705074  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 887)  
NIH-MGC <http://mgc.ncl.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LCM2320 row: F column: 19  
High quality sequence stop: 592.

FEATURES  
source  
1..887  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6086034"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOT7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT 179 a 223 c 269 g 216 t

Query Match 30.3%; Score 783.4; DB 13; Length 887;  
Best Local Similarity 97.3%; Pred. No. 2.8e-93;  
Matches 807; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

849 CCCCTGCCCGTGGAGGCGAGCTTTGCCATGACCCCGCCAGCGGCTTGGACCTCATC 908  
1 CCCCTGCCCGTGGAGGCGAGCTTTGCCATGACCCCGCCAGCGGCTTGGACCTCATC 60  
909 ACCCTGGAGCTAGAGCTTGAAGCTTGAACCCATGCTTGTGCTGCTGCTCTCTC 968  
61 ACCCTGGAGCTAGAGCTTGAAGCTTGAACCCATGCTTGTGCTGCTGCTCTCTC 120  
969 TGGCAGCCCAACAGCAGCTGTGTATGTGTGCAAGCCGACCTTCTGTGGAGCCGT 1028  
121 TGGCAGCCCAACAGCAGCTGTGTATGTGTGCAAGCCGACCTTCTGTGGAGCCGT 180  
1029 GACCAAGATGGAGATCTCTGCTGCGCAAGAGCTCCCGATGATGATGAATTGGCAGC 1088  
181 GACCAAGATGGAGATCTCTGCTGCGCAAGAGCTCCCGATGATGATGAATTGGCAGC 240  
1089 TTGATGAGAGAGGTGGCGCCAGAGCTGAGAGACCTGAGAGAGGCTGACTGAAGAGATG 1148  
241 TTGATGAGAGAGGTGGCGCCAGAGCTGAGAGACCTGAGAGAGGCTGACTGAAGAGATG 300  
1149 GCGCTGGGAGAGCTCTGCGCTGCGCGCTGCACTGTCTGGAGAGGAGAGATTGATC 1208  
301 GCGCTGGGAGAGCTCTGCGCTGCGCGCTGCACTGTCTGGAGAGGAGAGATTGATC 360  
1209 TGGACAGAGCTGTGGAGATGTGCAATGAAATAGCTAATTATTTCCCGAGGTGTG 1268  
361 TGGACAGAGCTGTGGAGATGTGCAATGAAATAGCTAATTATTTCCCGAGGTGTG 420

QY 1269 CTTTAAAGCGTGGGCTGACCAAGGCTTCTTCTCAATCTTCTTCCAGTAAGTTCCCTCT 1328  
DB 421 CTTTAAAGCGTGGGCTGACCAAGGCTTCTTCTCAATCTTCTTCCAGTAAGTTCCCTCT 480  
QY 1329 GCGTTGACAGCATGAGAGTGTGTGATTTGTTGACAGTCCCGAGGCTGTTCCAGAGCTT 1388  
DB 481 GCGTTGACAGCATGAGAGTGTGTGATTTGTTGACAGTCCCGAGGCTGTTCCAGAGCTT 540  
QY 1389 CACAGTCTGGTGTGGAGAGTCAAGGAGGTTAACTGCAAGAGCAAGTTGCCACCC 1448  
DB 541 CACAGTCTGGTGTGGAGAGTCAAGGAGGTTAACTGCAAGAGCAAGTTGCCACCC 600  
QY 1449 TGTCCAGATTAATGAGTGTGGTGTGCTTCAAGTGGAGAGGCTTGTCTTCAATG 1508  
DB 601 TGTCCAGATTAATGAGTGTGGTGTGCTTCAAGTGGAGAGGCTTGTCTTCAATG 660  
QY 1509 GCTTTGATTAATGTTGAGGGAGAGATGAAACAAATGTGAGTCTCCCTGATGGT 1568  
DB 661 GCTTTGATTAATGTTGAGGGAGAGATGAAACAAATGTGAGTCTCCCTGATGGT 720  
QY 1569 TTTGGGAAATGTGAGAGAGTCCCTGCTTTCGAAACATCAACCTGGCAAAATGCA 1628  
DB 721 TTTGGGAAATGTGAGAGAGTCCCTGCTTTCGAAACATCAACCTGGCAAAATGCA 780  
QY 1629 CAATG-AAATTTCCAGCAGTCTTCCATGGGCATAGTAAGTGTG 1676  
DB 781 CAATGAAATTTCCCGAGTCTTTCAGAGGGCTTTAGTAACCTTG 829

RESULT 43  
BU196397 1043 bp mRNA linear EST 04-SEP-2002  
LOCUS AGENCOURT 6910865 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:5952243  
DEFINITION 5', mRNA sequence.  
ACCESSION BU196397  
VERSION BU196397.1 GI:22710381  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1043)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strauberg, Ph.D.  
Email: gsaubs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubi Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LICM2139 row: P column: 04  
High quality sequence stop: 599.  
Location/Qualifiers  
1..1043  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5952243"  
/issue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1lb="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOT87; Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Library constructed  
by Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 207 a 264 c 308 g 263 t 1 others  
ORIGIN  
Query Match 30.3%; Score 783.4; DB 13; Length 1043;  
Best Local Similarity 96.8%; Pred. No. 2,6e-93;  
Matches 842; Conservative 0; Mismatches 22; Indels 6; Gaps 4;  
QY 849 CCCCCTGCGGTGAGAGGCGAGCTTTGTCATGACCCCGAGCGGCTTGTGACCTATC 908  
DB 1 CCCCCTGCGGTGAGAGGCGAGCTTTGTCATGACCCCGAGCGGCTTGTGACCTATC 60  
QY 909 ACCTGGAGCTTGAAGCTGTATGAGACCTTGAACCAATGCCCTTGTGCACTGCTCTC 968  
DB 61 ACCTGGAGCTTGAAGCTGTATGAGACCTTGAACCAATGCCCTTGTGCACTGCTCTC 120  
QY 969 TGCAGGCCCAACAGCCCAAGCTGTGTATGTGTGCAAGCGGACCTTGTGAGGAGCGT 1028  
DB 121 TGCAGGCCCAACAGCCCAAGCTGTGTATGTGTGCAAGCGGACCTTGTGAGGAGCGT 180  
QY 1029 GACCAAGATGGGAGATCTGCTGCTGCCAGAGAGTCCCGATGATGATGAAGTTGCGAGC 1088  
DB 181 GACCAAGATGGGAGATCTGCTGCTGCCAGAGAGTCCCGATGATGATGAAGTTGCGAGC 240  
QY 1089 TTCAATGAGAGAGTGTGCGCCAGAGAGCTGAGAGACTGTGAGAGAGCTTGAATGAAGATG 1148  
DB 241 TTCAATGAGAGAGTGTGCGCCAGAGAGCTGAGAGACTGTGAGAGAGCTTGAATGAAGATG 300  
QY 1149 GCGCTGGGGAGAGCTGTGGGCTGCCCGCTGCACTGTGAGAGAGGAGAAATTAATGATC 1208  
DB 301 GCGCTGGGGAGAGCTGTGGGCTGCCCGCTGCACTGTGAGAGAGGAGAAATTAATGATC 360  
QY 1209 TGAACACAGCTGTGTGGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1268  
DB 361 TGAACACAGCTGTGTGGTATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
QY 1269 CTTTAAAGCGTGGGCTGACCAAGGCTTCTTCTCAATCTTCTTCCAGTAAGTTCCCTCT 1328  
DB 421 CTTTAAAGCGTGGGCTGACCAAGGCTTCTTCTCAATCTTCTTCCAGTAAGTTCCCTCT 480  
QY 1329 GCGTTGACAGCATGAGAGTGTGTGATTTGTTGACAGTCCCGAGGCTGTTCCAGAGCTT 1388  
DB 481 GCGTTGACAGCATGAGAGTGTGTGATTTGTTGACAGTCCCGAGGCTGTTCCAGAGCTT 540  
QY 1389 CACAGTCTGGTGTGGAGAGTCAAGGAGGTTAACTGCAAGAGCAAGTTGCCACCC 1448  
DB 541 CACAGTCTGGTGTGGAGAGTCAAGGAGGTTAACTGCAAGAGCAAGTTGCCACCC 600  
QY 1449 TGTCCAGATTAATGAGTGTGGTGTGCTTCAAGTGGAGAGGCTTGTCTTCAATG 1508  
DB 601 TGTCCAGATTAATGAGTGTGGTGTGCTTCAAGTGGAGAGGCTTGTCTTCAATG 660  
QY 1509 GCTTTGATTAATGTTGAGGGAGAGATGAAACAAATGTGAGTCTCCCTGATGGT 1567  
DB 661 GCTTTGATTAATGTTGAGGGAGAGATGAAACAAATGTGAGTCTCCCTGATGGT 720  
QY 1569 TTTGGGAAATGTGAGAGAGTCCCTGCTTTCGAAACATCAACCTGGCAAAATGCA 1627  
DB 721 TTTGGGAAATGTGAGAGAGTCCCTGCTTTCGAAACATCAACCTGGCAAAATGCA 780  
QY 1628 AC-AAATGAATTTTCCAGCAGTCTTTCATGAGGATAGGTAAAGTGTG--CCTTGA 1683  
DB 781 AC-AAATGAATTTTCCCGAGGCTTTCATGAGGATAGGTAAAGTGTG--CCTTGA 840  
QY 1684 CTG-TTGCAGATGAATGTTCTGTGACCC 1712  
DB 841 CTGTTTGCAGATGAATGTTCTGTGACCC 870

RESULT 44  
BX440690 1201 bp mRNA linear EST 15-MAY-2003  
LOCUS BX440690  
DEFINITION BX440690 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone

Accession	Version	KeyWords	Source	Organism	Reference Authors Title Journal	Comment
CS0DF010YE05	5-PRIME, mRNA sequence.					
BX440690	EST.					
BX440690.1	GI:30771871					
Homo sapiens (human)						
Homo sapiens						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.						
1 (bases 1 to 1201)						
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.						
Full-length cDNA libraries and normalization						
Unpublished						
Contact: Genoscope						
Genoscope - Centre National de Séquencage						
Bp 191 91006 EVRY cedex - France						
Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr						
Library was constructed by Life Technologies, a division of						
Invitrogen. This sequence belongs to sequence cluster 6027.r For						
more information about this cluster, see						
http://www.genoscope.cns.fr/						
cgi-bin/cluster.cgi?seq=CS0DF010AC030P1&cluster=6027.r. Contact :						
Feng Liang Email : fliang@lifetech.com URL :						
http://fulllength.invitrogen.com/invitrogen Corporation 1600						
Faraday Avenue Genoscope sequence ID : CS0DF010AC030P1.						
Location/Qualifiers						
1..1201						
/organism="Homo sapiens"						
/mol_type="mRNA"						
/db_xref="taxon:9606"						
/clone="CS0DF010YE05"						
/tissue_type="FETAL BRAIN"						
/dev_stage="fetal"						
/clone_1ib="Homo sapiens FETAL BRAIN"						
/note="Torgan: brain; Vector: pGMSPORT_6; 1st strand cDNA						
was primed with a NotI-Oligo(dT) primer. Five prime end						
enriched, double-strand cDNA was digested with Not I and						
cloned into the Not I and EcoRI sites of the pGMSPORT 6						
vector. Library was not normalized."						
BASE COUNT	248 a	340 c	367 g	198 t	48 others	
ORIGIN						
Query Match	30.2%;	Score 781.4;	DB 13;	Length 1201;		
Best Local Similarity	96.4%;	Fred. No. 4.4e-93;				
Matches 836;	Conservative	6;	Mismatches 17;	Indels 8;	Gaps 4	
1	CGCGCGGCTCCGACACCGCGGCCGCCACCGCGCGCTCCGCATCTGCACCCGACG	60				
136	CGCGCGGCTCCGACACCGCGGCCGCCACCGCGCGCTCCGCATCTGCACCCGACG	195				
61	CGCGCGGCTCCGCGCGGAGCGAGCATTCAGTCCGGCCCGAGCGCACTCGGTCA	120				
196	CGCGCGGCTCCGCGCGGAGCGAGCAATTCAGTCCGGCCCGAGCGCACTCGGTCA	255				
121	GTCGCGGCGCGGCTCCGCGGCGCAGAGCGAGATTCAGCGGCTTGGGAGCACTCTGT	180				
256	GTCGCGGCGCGGCTCCGCGGCGCAGAGCGAGATTCAGCGGCTTGGGAGCACTCTGT	315				
181	GCTGTGCTGTGCGCGCGGCTCCCGAGCGGCCCGCGGCTCCGAGCGACCTCGG	240				
316	GCTGTGCTGTGCGCGCGGCTCCCGAGCGGCCCGCGGCTCCGAGCGACCTCGG	375				
241	CTCCAGTCAAGCCCGGCGCGGCTTCAGGTACCCGACAGAGAGGACCTCAATGAGA	300				
376	CTCCAGTCAAGCCCGGCGCGGCTTCAGGTACCCGACAGAGAGGACCTCAATGAGA	435				
301	TGTTCCGCGAGGTTGAGAACTGATGAGAGACGACCAATTGGCGAGCGCGGTGG	360				
436	TGTTCCGCGAGGTTGAGAACTGATGAGAGACGACCAAAATTTCGGA-58CGGTGG	494				
361	AAGAGATGAGAGGAGAAAGCTGCTGCTAAAGCATCATCGAAGTGAACCTGGCAAAC	420				
495	AAGAGATGAGAGGAGAAAGCTGCTGCTAAAGCATCATCGAAGTGAACCTGGCAAAC	554				

QY	421	TACCTCCACACTATCAACAATGAGACCAACAACAAGATTGGAAATATACATCC	480
Db	555	TACCTCCACACTATCAACAATGAGACCAACAACAAGATTGGAAATATATCATCC	614
QY	481	ATGTGCACCGAGAAATTCACAAGATATCAACAACCACTGAGCAATGTCTTTTCAG	540
Db	615	ATGTGCACCGAGAAATTCACAAGATATCAACAACCACTGAGCAATATGTCTTTTCAG	674
QY	541	AGACAGTTATCACATCTGTGGAGAGCAAGAAAGGACAAAGACCAAGTGCATCTCG	600
Db	675	AGACAGTTATCACATCTGTGGAGAGCAAGAAAGGACAAAGACCAAGTGCATCTCG	734
QY	601	ACGAGGACTGTGGGCCCCAGCATGTACTGTCAGATTTCAGCTTCAGTAACCTGCCAGC	660
Db	735	ACGAGGACTGTGGGCCCCAGCATGTACTGTCAGATTTCAGTAACCTGCCAGC	794
QY	661	CATGCCGGGGGCCAGAGGATGCTCTGCACCCGGGCAAGTGAAGTGTGTGAGAACCAAGCTGT	720
Db	795	CATGCCGGGGGCCAGAGGATGCTCTGCACCCGGGCAAGTGAAGTGTGTGAGAACCAAGCTGT	854
QY	721	GTTGCTTGGGGTCACTGTCACCAAAATGAGCCACAGGGGCAAGCAATGGGACCATCTGTGACA	780
Db	855	GTTGCTTGGGGTCACTGTCACCAAAATGAGCCACAGGGGCAAGCAATGGGACCATCTGTGAGC	913
QY	781	ACCAAGAGGACTGTCCAAACCCGGGGCTGTGTGTGTGCTTCCAGAAGAGGCTGTGTTCCTCG	840
Db	914	ACCAAGAGGACTGTCCAAACCCGGGGCTGTGTGTGTGCTTCCAGAAGAGGCTGTGTTCCTCG	967
QY	841	TGTGCACACCCCTGACCCGTTGAGAGGGCG	867
Db	968	TGTGTSAACCTCTCCGCTGAGGGGAG	994

```

RESULT 45
B0686811
LOCUS
DEFINITION B0686811 915 bp mRNA linear EST 15-JUL-2002
ACCESSION AGNCNCURT_9345155 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250117
VERSION 5, mRNA sequence.
KEYWORDS B0686811
SOURCE B0686811.1 GI:21812127
ORGANISM EST.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 915)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strauberg, Ph.D.
Email: rgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: L16CM2392 row: k column: 14
High quality sequence stop: 688.
location/Qualifiers
1. 915
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6250117"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1b="NIH MGC 110"
/notes="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by

```



QY 1269 CTTTAAAGGCGTGGAGTCCAGCAGGCTTCTTCCATCTTCTTCCAGTAAGTTCCCTCT 1328  
DB 421 CTTTAAAGGCGTGGAGTCCAGCAGGCTTCTTCCATCTTCTTCCAGTAAGTTCCCTCT 480  
QY 1329 GCGTTGACAGCATGAGGTTGTGTGATTTGTTCAGCTCCCGAGGCTGTTCACAGGCTT 1388  
DB 481 GCGTTGACAGCATGAGGTTGTGTGATTTGTTCAGCTCCCGAGGCTGTTCACAGGCTT 540  
QY 1389 CACAGCTGCTGCTTGGAGAGTCCAGCAGGCTTAACTGACAGGACAGTTGCCACCC 1448  
DB 541 CACAGCTGCTGCTTGGAGAGTCCAGCAGGCTTAACTGACAGGACAGTTGCCACCC 600  
QY 1449 TGTCCAGATTAATGAGTGTGCTTGTCTTACAGATTCAGCAGAGCGCTTTGTCTACATG 1508  
DB 601 TGTCCAGATTAATGAGTGTGCTTGTCTTACAGATTCAGCAGAGCGCTTTGTCTACATG 660  
QY 1509 GCGTTGATTAATGTTTGGAGGAGAGATGAAACAATGTGAGATCTCCCTGTGATTTGGT 1568  
DB 661 GCGTTGATTAATGTTTGGAGGAGAGATGAAACAATGTGAGATCTCCCTGTGATTTGGT 720  
QY 1569 TTTGGGGAATGTGAGAGAGATG-CCCTGCTTTGCAAACTCACTGACAAATGCA 1627  
DB 721 TTTGGGGAATGTGAGAGAGATG-CCCTGCTTTGCAAACTCACTGACAAATGCA 780  
QY 1628 ACAATGAA-TTTTCCACGACGATCTTTCCATGGG 1661  
DB 781 ACAATGAAATTTTCCACGACGATCTTTCCATGGG 816

RESULT 47  
LOCUS BUI49760 921 bp mRNA linear EST 03-SEP-2002  
DEFINITION AGENCOURT\_8074878 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6086248  
5', mRNA sequence.  
ACCESSION BUI49760  
VERSION BUI49760.1 GI:22663292  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LHCW2320 row: 0 column: 17  
High quality sequence stop: 647.  
Location/Qualifiers  
1. 921  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6086248"  
/issue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGACGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

FEATURES  
source

BASE COUNT 183 a 231 c 278 g 229 t  
ORIGIN  
Query Match 30.1%; Score 778.2; DB 13; Length 921;  
Best Local Similarity 98.8%; Pred. No. 1.3e-92;  
Matches 805; Conservative 0; Mismatches 8; Indels 2; Gaps 2;  
Note: this is a NIH\_MGC Library."

QY 849 CCCCTGCGGTGAGAGGCGAGCTTTGCGATGACCCCGCAGCGGCTTGTGACCTCATC 908  
DB 1 CCCCTGCGGTGAGAGGCGAGCTTTGCGATGACCCCGCAGCGGCTTGTGACCTCATC 60  
QY 909 ACCGTGAGCTAAGAGCTGTATGAGAGCTTGTGACCGATGCTTTGTGCGAGCTCTC 968  
DB 61 ACCGTGAGCTAAGAGCTGTATGAGAGCTTGTGACCGATGCTTTGTGCGAGCTCTC 120  
QY 969 TGCAGGCCCAAGCCCAAGCCAGCTGTATGATGTGAGAGCCAGCTTGTGAGAGCCGT 1028  
DB 121 TGCAGGCCCAAGCCCAAGCCAGCTGTATGATGTGAGAGCCAGCTTGTGAGAGCCGT 180  
QY 1029 GACCAAGATGAGAGATCTCTGCTGCCAGAGAGTCCCGATGATGAAATGTGACAG 1088  
DB 181 GACCAAGATGAGAGATCTCTGCTGCCAGAGAGTCCCGATGATGAAATGTGACAG 240  
QY 1089 TTTATGAGAGAGTGTGCGCCAGAGCTGTGAGAGACTGTGAGAGAGCTGTGAGAGATG 1148  
DB 241 TTTATGAGAGAGTGTGCGCCAGAGCTGTGAGAGACTGTGAGAGAGCTGTGAGAGATG 300  
QY 1149 GCGCTGAGAGAGCTGTGCGAGCTGTGCGCGCTGTGACCTGTGAGAGAGAGATTTAGATC 1208  
DB 301 GCGCTGAGAGAGCTGTGCGAGCTGTGCGCGCTGTGACCTGTGAGAGAGAGATTTAGATC 360  
QY 1209 TGAACACAGCTGTGAGAGATGTGCAATGAAATAGCTAATTTATTTCCCGAGCTGTG 1268  
DB 361 TGAACACAGCTGTGAGAGATGTGCAATGAAATAGCTAATTTATTTCCCGAGCTGTG 420  
QY 1269 CTTTAAAGGCGTGGAGTCCAGCAGGCTTCTTCCATCTTCTTCCAGTAAGTTCCCTCT 1328  
DB 421 CTTTAAAGGCGTGGAGTCCAGCAGGCTTCTTCCATCTTCTTCCAGTAAGTTCCCTCT 480  
QY 1329 GCGTTGACAGCATGAGGTTGTGTGATTTGTTCAGCTCCCGAGGCTGTTCACAGGCTT 1388  
DB 481 GCGTTGACAGCATGAGGTTGTGTGATTTGTTCAGCTCCCGAGGCTGTTCACAGGCTT 540  
QY 1389 CACAGCTGCTGCTTGGAGAGTCCAGCAGGCTTAACTGACAGGACAGTTGCCACCC 1448  
DB 541 CACAGCTGCTGCTTGGAGAGTCCAGCAGGCTTAACTGACAGGACAGTTGCCACCC 600  
QY 1449 TGTCCAGATTAATGAGTGTGCTTGTCTTACAGATTCAGCAGAGCGCTTTGTCTACATG 1508  
DB 601 TGTCCAGATTAATGAGTGTGCTTGTCTTACAGATTCAGCAGAGCGCTTTGTCTACATG 660  
QY 1509 GCGTTGATTAATGTTTGGAGGAGAGATGAAACAATGTGAGATCTCCCTGTGATTTGGT 1568  
DB 661 GCGTTGATTAATGTTTGGAGGAGAGATGAAACAATGTGAGATCTCCCTGTGATTTGGT 720  
QY 1569 TTTGGGGAATGTGAGAGAGATG-CCCTGCTTTGCAAACTCACTGACAAATGCA 1626  
DB 721 TTTGGGGAATGTGAGAGAGATG-CCCTGCTTTGCAAACTCACTGACAAATGCA 780  
QY 1627 AACCAATGAAATTTTCCACGAGATCTTTCCATGGG 1661  
DB 781 AACCAATGAAATTTTCCACGAGATCTTTCCATGGG 815

RESULT 48  
LOCUS B0685185 879 bp mRNA linear EST 15-JUL-2002  
DEFINITION AGENCOURT\_8343820 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6248669  
5', mRNA sequence.  
ACCESSION B0685185  
VERSION B0685185.1 GI:21810501  
KEYWORDS EST.

Db	Accession	Source	Organism	Reference	Authors	Title	Journal	Comment
Db	421	CTTAAAGCGCGGTACACAGAGCTTCTTCTCATATCTTCTCCAGTAAGTTCCCTCT	480					
Qy	1329	GGCTTGAACAGCATGAGGTGTGTGCAATTTGTTCAAGTCTCCCGAGGCTTTCTCAGGCTT	1388					
Db	481	GGCTTAAACAGCATGAGGTGTGTGCAATTTGTTCAAGTCTCCCGAGGCTTTCTCAGGCTT	540					
Qy	1389	CACAGTCTGGTGTGTGTGAGAGTCAAGGAGGTTAACTGACAGAGCAGTTTGGCCACCCC	1448					
Db	541	CACAGTCTGGTGTGTGTGAGAGTCAAGGAGGTTAACTGACAGAGCAGTTTGGCCACCCC	600					
Qy	1449	TGTCCAGATTATTTGGCTGTCTTGGCTTCCCTCTACCAATTTGGAGACAGCCGTTTGTCTAATG	1508					
Db	601	TGTCCAGATTATTTGGCTGTCTTGGCTTCCCTCTACCAATTTGGAGACAGCCGTTTGTCTAATG	660					
Qy	1509	GCTTTATATAATGTTTGA-GGGAGAGAGATGAGAAACATGTGAGTCTCCCTGTGATTGG	1567					
Db	661	GCTTTATATAATGTTTGA-GGGAGAGAGATGAGAAACATGTGAGTCTCCCTGTGATTGG	720					
Qy	1568	TTTTGGGGAAT-GTGAGAAAGAGTCCCTGCTTTGGCAATCAACCTGGCAAAAATGC	1626					
Db	721	TTTTGGGGAATGTGTGAGAAAGTCCCTGCTTTGGCAATCAACCTGGCAAAAATGC	780					
Qy	1627	AACAAATGA-ATTTCACGCAATCTTTTCCATG	1660					
Db	781	AACAAATGATTTTTCACGCAATCTTTTCCATG	815					
RESULT 49								
LOCUS	BU196968							
DEFINITION	AGENCOURT 7974356 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6082897							
ACCESSION	BU196968							
VERSION	5, mRNA sequence.							
KEYWORDS	EST.							
SOURCE	BU196968.1 GI:22710952							
ORGANISM	Homo sapiens (human)							
REFERENCE	Homo sapiens							
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
JOURNAL	1 (bases 1 to 905)							
COMMENT	NIH-MGC http://imgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Strausberg, Ph.D. Email: cgaps-femail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LHC#312 row: d column: 02 High quality sequence, stop: 571. Location/Qualifiers 1. 305 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6082897" /issue_type="ductal carcinoma, cell line" /lab_host="DH10B (phage-resistant)" /clone_id="NIH_MGC_110" /note="Organ: pancreas; Vector: pOT7; Site:1: XhoI; Site:2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: This is a NIH_MGC Library."							
BASE COUNT	189 a	223 c	271 g	222 t				



Query Match 30.0%; Score 774.6; DB 13; Length 905;  
 Best Local Similarity 97.8%; Pred. No. 3.9e-92;  
 Matches 807; Conservative 0; Mismatches 14; Indels 4; Gaps 2;

849 CCCCTGCGGTGGAGGCGAGCTTTGTCATGACCCCGCAGCCGCTTTGGACCTCATC  
 1 CCCCTGCGGTGGAGGCGAGCTTTGTCATGACCCCGCAGCCGCTTTGGACCTCATC 60

909 ACCCTGGAGACTAGAGCTTATGAGAGCTTTGACCAATGCTCTTGTGCAAGTCTCTC  
 61 ACCCTGGAGACTAGAGCTTATGAGAGCTTTGACCAATGCTCTTGTGCAAGTCTCTC 120

969 TGGCAGCCCGCAGCAGCAGCTTGTATGTATGTGCAAGCCGCTGTGAGGAGCCGT  
 121 TGGCAGCCCGCAGCAGCAGCTTGTATGTATGTGCAAGCCGCTGTGAGGAGCCGT 180

1029 GACCAAGATGGGAGATCTCTGCTGCCAAGAGGTCCCGATGATGAAATTTGGCAGC  
 181 GACCAAGATGGGAGATCTCTGCTGCCAAGAGGTCCCGATGATGAAATTTGGCAGC 240

1089 TTTCATGAGAGAGGTGGCCAGAGAGCTGAGAGACCTGAGAGAGCCTGACCTGAAGATG  
 241 TTTCATGAGAGAGGTGGCCAGAGAGCTGAGAGACCTGAGAGAGCCTGACCTGAAGATG 300

1149 GCGCTGGGAGAGCTTGGCGCTGCGCGCTGCACTGTGAGAGGAGAGAGATTTAGATC  
 301 GCGCTGGGAGAGCTTGGCGCTGCGCGCTGCACTGTGAGAGGAGAGATTTAGATC 360

1209 TGGACCAAGGTGGGTAGATGTGCAATGAAATAGCTAATTTATTTCCCGAGGTGTG  
 361 TGGACCAAGGTGGGTAGATGTGCAATGAAATAGCTAATTTATTTCCCGAGGTGTG 420

1269 CTTTAAAGCGTGGCTGACCAAGCTTTCTTCCATCTTCTCCAGTAAAGTTCCCTCT  
 421 CTTTAAAGCGTGGCTGACCAAGCTTTCTTCCATCTTCTCCAGTAAAGTTCCCTCT 480

1329 GCGTTACAGAGAGAGGTGTGCAATTTGTTGAGTCTCCCGAGGTGTGTTCCAGGCT  
 481 GCGTTACAGAGAGAGGTGTGCAATTTGTTGAGTCTCCCGAGGTGTGTTCCAGGCT 540

1389 CACAGTCTGGTGTGGAGAGTCAAGAGAGTTAACTGACAGAGCAGTTTGCACCC  
 541 CACAGTCTGGTGTGGAGAGTCAAGAGAGTTAACTGACAGAGCAGTTTGCACCC 600

1449 TGTCCAGATTTATGCTGCTTGTGCTTACCAATTTGGCAGAGCCGTTTGTTCATG  
 601 TGTCCAGATTTATGCTGCTTGTGCTTACCAATTTGGCAGAGCCGTTTGTTCATG 660

1509 GCTTATATATTTGTTGAGGAGAGAGATGAAACATGATGAGTCTCCTCTGATGAT  
 661 GCTTATATATTTGTTGAGGAGAGAGATGAAACATGATGAGTCTCCTCTGATGATG 719

1569 TTTGGGAGAAATGTGAGAGAGTCCCTGTTTGGCAATCACTGCGCAAAATGCA  
 720 TTTGGGAGAAATGTGAGAGAGTCCCTGTTTGGCAATCACTGCGCAAAATGCA 779

1629 CAATGAAATTTTCCAGC--AGTTCTTCCATGGCATAGTAA 1670  
 780 CAATGAAATTTTCCAGCAGGTTCTTCCATGGCATAGGAA 824

RESULT 50  
 B0230977/c 853 bp mRNA linear EST 02-MAY-2002  
 LOCUS AGENCYCOURT 7546543 NIH\_MGC\_70 Homo sapiens cDNA clone IMAGE:6025929  
 DEFINITION 5', mRNA Sequence.  
 ACCESSION B0230977.1 GI:20412377  
 VERSION B0230977.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 853)  
 AUTHORS NIH-MGC. <http://mgi.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strauberg, Ph.D.  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:  
<http://image.llnl.gov>  
 Plate: LIML3238 row: n column: 10  
 High quality sequence stop: 658.

FEATURES  
 Source  
 Location/Qualifiers  
 1..853  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6025929"  
 /tissue\_type="epithelioid carcinoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_id="NIH\_MGC\_70"  
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.1 kb. Library constructed by Life Technologies."

BASE COUNT 226 a 179 c 188 g 260 t  
 ORIGIN

Query Match 29.98%; Score 772.6; DB 13; Length 853;  
 Best Local Similarity 99.1%; Pred. No. 7.3e-92;  
 Matches 806; Conservative 0; Mismatches 3; Indels 4; Gaps 3;

1769 GGGCAGATTTTCAATATCC-AAGTCAATCCCTC-TCTCAGCAGACCTGGGAGGAG  
 837 GGGCAGATTTTCAATATCCAAAGATCAATTCCTCTTCTCAGCAGACCTGGGAGGAG 778

1827 TCATTTGTTCTCTGTCATCAAGGATCTCAGAGCTCAGAGCTGCAAGCTGCTTGC  
 777 TCATTTGTTCTCTGTCATCAAGGATCTCAGAGCTCAGAGCTGCAAGCTGCTTGC 718

1887 AAGTCACAGCTAGTAAAGACCAAGCAGTTTCACTGCTGTTGACTTAAGTCACTG  
 717 AAGTCACAGCTAGTAAAGACCAAGCAGTTTCACTGCTGTTGACTTAAGTCACTG 658

1947 CTCTCTCACTACCCACACACAGCTTGTGTCACCAAAAGTCTCTCCCAAAAGAGGA  
 657 CTCTCTCACTACCCACACACAGCTTGTGTCACCAAAAGTCTCTCCCAAAAGAGGA 598

2007 GAATGGAGATTTTC--TTGAGGACATGACATCTGAATTAAGTCAACATTTCTACA  
 597 GAATGGAGATTTTC--TTGAGGACATGACATCTGAATTAAGTCAACATTTCTACA 538

2065 TCCCTCTAAAGTAACTACTGTTAGGACAGAGTCTTCTCAAGTGTGGGCAAGCGT  
 537 TCCCTCTAAAGTAACTACTGTTAGGACAGAGTCTTCTCAAGTGTGGGCAAGCGT 478

2125 CCTCTTAATGAAGCATGATTTGACACGTCCCTTTGGAGTGTGACTTAAGTAACTT  
 477 CCTCTTAATGAAGCATGATTTGACACGTCCCTTTGGAGTGTGACTTAAGTAACTT 418

2185 TGAAGGATATATGACTAGGCTAGCATACAGTTAACTTCAGAGAAACGTAAGTAA  
 417 TGAAGGATATATGACTAGGCTAGCATACAGTTAACTTCAGAGAAACGTAAGTAA 358

2245 TTGTAGGCGCAGAGTTTAAATGAAATTTGCAAAATCACTTACAGAGAACTGAAGCAAT  
 357 TTGTAGGCGCAGAGTTTAAATGAAATTTGCAAAATCACTTACAGAGAACTGAAGCAAT 298

2305 TATCAACACAGCTGAGAAATCAACCGACAGGCGTGTGTGAACATGTTTAATATG  
 2364

```
Db      297 TATCAACCACTGAGAAATCAACCGACAGGCTGTGAAACATGTTGTAATATG 238
QY      2365 CGACTGCGAACTGTAAGTCTAGCGCACTCCACAAATGATGTTTCAGGTGCATGACT 2424
Db      237 CGACTGCGAACTGTAAGTCTAGCGCACTCCACAAATGATGTTTCAGGTGCATGACT 178
QY      2425 GTTGCACCATGATTCATCCAGAGTTCTTAAGTTAAGTGCACATGTTGATAAG 2484
Db      177 GTTGCACCATGATTCATCCAGAGTTCTTAAGTTAAGTGCACATGTTGATAAG 118
QY      2485 CATGCTTCTTGTAGTTTAATTATGTAATAACATAGTGCATTTAGAAATCAAGCAT 2544
Db      117 CATGCTTCTTGTAGTTTAATTATGTAATAACATAGTGCATTTAGAAATCAAGCAT 58
QY      2545 AAATCACTTGAATGCAAAAAAAAAAAAAA 2577
Db      57 AAATCACTTGAATGCAAAAAAAAAAAAAA 25
```

Search completed: February 20, 2004, 01:31:06  
Job time : 5357 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2004, 18:12:56 ; Search time 156 Seconds  
(without alignments)  
7316.774 Million cell updates/sec

Title: US-10-063-671-7

Sequence: 1 CGCGCGCTCCCGCACC...AAAAAAAAAAAAAAAAAAAA 2586

Scoring table: IDENTITY NJC  
Gapop 10.0, Gapext 1.0

Searched: 56978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents NA:  
1: /cgn2\_6/prodata/2/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/prodata/2/ina/5A\_COMB.seq.\*  
4: /cgn2\_6/prodata/2/ina/5B\_COMB.seq.\*  
5: /cgn2\_6/prodata/2/ina/5C\_COMB.seq.\*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1053	40.7	1053	4 US-09-161-241-2	Sequence 2, Appl1
2	769.8	29.8	1050	4 US-09-161-241-1	Sequence 1, Appl1
3	693.8	26.8	1050	4 US-09-161-241-77	Sequence 77, Appl1
4	137	5.3	150	3 US-08-305-223-215	Sequence 215, App
5	52.4	2.0	7218	1 US-08-332-463-14	Sequence 14, Appl
6	51.6	2.0	882	4 US-09-461-325-118	Sequence 118, App
7	51.6	2.0	152331	3 US-09-128-153-16	Sequence 16, Appl
8	49	1.9	6803	3 US-08-665-259-19	Sequence 19, Appl
9	49	1.9	6803	3 US-08-762-500-19	Sequence 19, Appl
10	48.4	1.9	1026	3 US-07-751-891B-24	Sequence 24, Appl
11	48.4	1.9	5222	3 US-07-751-891B-23	Sequence 23, Appl
12	47.4	1.8	1269	4 US-09-252-991A-9441	Sequence 9441, Ap
13	47.4	1.8	1890	4 US-09-252-991A-9392	Sequence 9392, Ap
14	47	1.8	2003	1 US-08-469-526A-21	Sequence 21, Appl
15	47	1.8	2003	2 US-08-734-591A-21	Sequence 21, Appl
16	47	1.8	2003	3 US-08-341-018-71	Sequence 71, Appl
17	47	1.8	2003	3 US-08-470-335-21	Sequence 21, Appl
18	47	1.8	2003	3 US-08-735-021-21	Sequence 21, Appl
19	47	1.8	2003	3 US-08-734-664A-21	Sequence 21, Appl
20	47	1.8	2003	4 US-08-470-339-21	Sequence 21, Appl
21	47	1.8	2003	4 US-08-467-602-21	Sequence 21, Appl
22	47	1.8	7812	3 US-09-368-590-1	Sequence 1, Appl1
23	46.6	1.8	1453	3 US-09-305-640-1	Sequence 1, Appl1
24	46.4	1.8	1453	4 US-08-984-709A-52	Sequence 52, Appl
25	46.2	1.8	576	4 US-09-252-991A-7331	Sequence 7331, Ap
26	46.2	1.8	1302	4 US-09-252-991A-7221	Sequence 7221, Ap
27	46.2	1.8	1487	2 US-08-318-837-6	Sequence 6, Appl1

28	46.2	1.8	1551	4 US-09-252-991A-7473	Sequence 7473, Ap
29	46.2	1.8	1578	4 US-09-252-991A-7410	Sequence 7410, Ap
30	46.2	1.8	3232	4 US-09-177-650-1	Sequence 1, Appl1
31	46.2	1.8	3237	4 US-09-177-650-95	Sequence 95, Appl
32	46	1.8	16389	4 US-09-741-154-3	Sequence 3, Appl1
33	45.8	1.8	1203	3 US-09-086-010-1	Sequence 1, Appl1
34	45.4	1.8	745	1 US-08-036-555B-163	Sequence 163, App
35	45.4	1.8	745	1 US-08-469-569-163	Sequence 163, App
36	45.4	1.8	745	1 US-08-249-322A-163	Sequence 163, App
37	45.4	1.8	745	1 US-08-469-526A-163	Sequence 163, App
38	45.4	1.8	745	2 US-08-734-591A-163	Sequence 163, App
39	45.4	1.8	745	2 US-08-469-660-163	Sequence 163, App
40	45.4	1.8	745	3 US-08-341-018-51	Sequence 51, Appl
41	45.4	1.8	745	3 US-08-470-335-163	Sequence 163, App
42	45.4	1.8	745	3 US-08-735-021-163	Sequence 163, App
43	45.4	1.8	745	3 US-08-734-664A-163	Sequence 163, App
44	45.4	1.8	745	3 US-08-470-339-163	Sequence 163, App
45	45.4	1.8	745	4 US-08-467-602-163	Sequence 163, App

## ALIGNMENTS

```
RESULT 1
US-09-161-241-2
; Sequence 2, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daguang
; TITLE OF INVENTION: NOVEL DNR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1053
; TYPE: DNA
; ORGANISM: Human
US-09-161-241-2

Query Match      40.7%; Score 1053; DB 4; Length 1053;
Best Local Similarity 100.0%; Pred. No. 2.3e-243;
Matches 1053; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      153  ATGAGCGGCTTGAGGCGCACCCCTGCTGCTGCTGCGCGCGCGGTCGCCAGCGCC 212
DB      1  ATGAGCGGCTTGAGGCGCACCCCTGCTGCTGCTGCTGCGCGCGCGGTCGCCAGCGCC 60

QY      213  CCGCGCGCGCTCCGAGCGGCACTCGGCTCAAGTCAAGCCCGCGCGCTTCAAGTCA 272
DB      61  CCGCGCGCGCTCCGAGCGGCACTCGGCTCAAGTCAAGCCCGCGCGCTTCAAGTCA 120

QY      273  CCGCGAGAGAGCGCACCCCTCAATGAGTGTTCGCGAGGTTGAGAACTGATGAGAGAC 332
DB      121  CCGCGAGAGAGCGCACCCCTCAATGAGTGTTCGCGAGGTTGAGAACTGATGAGAGAC 180

QY      333  ACGCAGCAAAATTCGCGAGCGCGCTGAGAGATGAGAGCGCAAGAAAGTCTGCTTAA 392
DB      181  ACGCAGCAAAATTCGCGAGCGCGCTGAGAGATGAGAGCGCAAGAAAGTCTGCTTAA 240

QY      393  GCATCATGAGAGGAGACCTTGCAAACTTACCTCCAGCTTCAATGAGACCAACA 300
DB      241  GCATCATGAGAGGAGACCTTGCAAACTTACCTCCAGCTTCAATGAGACCAACA 300

QY      453  GACACGAAAGTTGAGAAATATACATCCATGTCACCGAGAAATTCACAGATACCAAC 512
DB      301  GACACGAAAGTTGAGAAATATACATCCATGTCACCGAGAAATTCACAGATACCAAC 360

QY      513  AACCAAGATGAGCAAAATGCTTTTCAGAGACATTTATCATCTGTGGAGAGAGAA 572
```

Db	361	AAACGAGCTGGACAAATAGTCTTTTCAGAGACGTTATCACTCTGTGGAGACGAGAA	420
Qy	573	GGCAGAGAGACCACGAGTGCATCATCGACGAGACTGTGGGCCCCAGATGTACTGCCAG	632
Db	421	GGCAGAAAGAGACCAGAGTGCATCATCGACGAGACTGTGGGCCCCAGATGTACTGCCAG	480
Qy	633	TTTGCAGACTTCAGTACACCTGGCAGCATGCCGGGCGCAGAGAGTCTGTGACCCGG	692
Db	481	TTTGCAGACTTCAGTACACCTGGCAGCATGCCGGGCGCAGAGAGTCTGTGACCCGG	540
Qy	693	GACAGTAGT	752
Db	541	GACAGTAGT	600
Qy	753	AGGGGACAGCAATGGGACCATCTGTGTACAACAGAGAGGACTCCAGCCGGGCTGTGTGT	812
Db	601	AGGGGACAGCAATGGGACCATCTGTGTACAACAGAGAGACTCCAGCCGGGCTGTGTGT	660
Qy	813	GCCTTTCCAGAGAGGCTGT	872
Db	661	GCCTTTCCAGAGAGGCTGT	720
Qy	873	TGCCATGACCCCGCAGCCGGCTTGTGACCTCATCACTCTGGAGACTAGACCTGATGGA	932
Db	721	TGCCATGACCCCGCAGCCGGCTTGTGACCTCATCACTCTGGAGACTAGACCTGATGGA	780
Qy	933	GCCTTTGGACCGATGCTGCTTGTGTGCCAGTGTGCTCTCTGCGACGCCACAGCCACGCTG	992
Db	781	GCCTTTGGACCGATGCTGCTTGTGTGCCAGTGTGCTCTCTGCGACGCCACAGCCACGCTG	840
Qy	993	GTTGATGTGTCAAGCCGACCTTCGTGTGGAGAGCCGTGACCAAGATGTGGAGATCTGTG	1052
Db	841	GTTGATGTGTCAAGCCGACCTTCGTGTGGAGAGCCGTGACCAAGATGTGGAGATCTGTG	900
Qy	1053	CCCAAGAGAGTTCCTCGATGATGTGAATTTGGCAGCTTCATGTGAGAGAGTGTGCCAAGAG	1112
Db	901	CCCAAGAGAGTTCCTCGATGATGTGAATTTGGCAGCTTCATGTGAGAGAGTGTGCCAAGAG	960
Qy	1113	CTGAGAGACTGTGAGAGAGGCTTGACTGAAGATGTGCGCTGTGGGAGACTGTGCGGCTGC	1172
Db	961	CTGAGAGACTGTGAGAGAGGCTTGACTGAAGATGTGCGCTGTGGGAGACTGTGCGGCTGC	1020
Qy	1173	GCCGCTGACCTGCTGGAGGGGAGAGATTTAG	1205
Db	1021	GCCGCTGACCTGCTGGAGGGGAGAGATTTAG	1053

```

RESULT 2
US-09-161-241-1
Sequence 1 Application US/09161241
Patent No. 6344641
GENERAL INFORMATION:
APPLICANT: Bass, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daguang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ. ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1050
TYPE: DNA
ORGANISM: Mouse
US-09-161-241-1

```

Query Match	29.8%	Score 769.8;	DB 4;	Length 1050;
Best Local Similarity	83.9%	Pred. No. 2.8e-175;		
Matches 883; Conservative	0;	Mismatches 167;	Indels 3;	Gaps 1;

OY	153	ATGAGAGGGCTTGGAGGCA	CCCTGCTGCTGCTGCTGGGCGGGGGGAGTCCCAAGCACC	212
Db	1	ATGAGAGGGCTCGAGGGGTATTTTCTCTGTACACTGCTGGCGGGGGGTGCCCACTGCT	60	
OY	213	CCGCGGCCCGCTCCGACGGCGCACTCGAGCTTCAGTCAAGCCCGGCTCTCAGCTAC	272	
Db	61	CCTCTCTCTTCCCGACGGTCACTTGGACCTCCGGAGCCGGGCGCAAGCTTCAATAC	120	
OY	273	CCGAGAGGAGGACACCCCTCAATGAGATGTTCCGCGAGGTTGAGAACTATGAGAGAC	332	
Db	121	CCTCAGAGGAGGAGCTTAGCTCAATGAGATGTTTGAGAGGTGGAGAGAGCTGATGGAAGAC	180	
OY	333	ACGCAACAATTTGCGAGCGCGGTGGAGAGATGAGAGCAAGAAAGCTGCTGTAA	392	
Db	181	ACTGAGCAAACTGCCACAGTGCCTGGAGAGATGAGAGGGGGAAGAAAGCTGCTAA	240	
OY	393	GCATCATGAAAGTGAACCTGGCAAACTTACCTCCAGCTATTCAAATGAGACCAACACA	452	
Db	241	ACGCTCTTGAGGTGAACCTGGCAAGCTTACCTCCCACTATCAATGAGACGACGACG	300	
OY	453	GACACGAAGTTGGAAATATATACCATCACTGTGACCGAGAAATTCACAGATTAACAAC	512	
Db	301	GAGACCGAGGTGGGAAATTAACAAGTCCATGTGACCAAGAAAGTTCAACAATTAACCAAC	360	
OY	513	AACACGACTGACAAATGATCTTTCAAGACAGTTATCAATCTGAGGAGAGGAAGAA	572	
Db	361	AACAGAGATGACAGGTGTCTTTCTGAGACAGTCACTAATCTGTGAGGGAGTGAAGAA	420	
OY	573	GGCAAGAGGACCAAGATGATATGACGAGGAGCTGTGGGCGCCAGCATTTACTGCCAG	632	
Db	421	GGCAAGAGGACCAAGATGATATGATGAAAGACTGTGGGCGCCACCAAGTACTGCCAG	480	
OY	633	TTTGCGAGCTTCCAGTCAACCTGGCAGCAATGCGGGGCGCAGAGATGCTCTGACCCGG	692	
Db	481	TTCTCCAGCTTCAAGTACACTGTGCACGCACGACCGGGACCAAGACAGATGCTATGACCCGA	540	
OY	693	GACAGTAGTGTCTGTGAGACCAAGCTGTGTCTGGGGTCACTGCAACAAATGGCCAC	752	
Db	541	GACAGTAGTGTCTGTGAGACCAAGCTGTGTCTGGGGTCACTGCAACCAAAAGGCCAC	600	
OY	753	AGGGGCAAGATGGAGCACTGTGACAAACAGAGGGAGCTGCAGCCGGGCTGTGCTGT	812	
Db	601	AAAGGTGCAATGGGACCATCTGTGACAAACAGAGGAGATGGCAGCTGTGTGTGT	660	
OY	813	GCCTTCCAGAGAGGCTGTGTGTCTGTGTGCAACCCCTGCCCCGTGGAGGGCGAGCTT	872	
Db	661	GCCTTCCAAAGAGGCTGTGTGTCTGTGTGCAACCCCTGCCCCGTGGAGGGAGAGCTT	720	
OY	873	TGCGATGACCCCGGCGAGCCGGCTCTGGAACCTCAACCTGGAGAGCTAGACCTGATGGA	932	
Db	721	TGCGATGACCCCGACAGCCAGCTGTGTGATTTCACTACTGGGAACGTGAGACTGGAAGA	780	
OY	933	GCCTTGGACCGGATCCCTTGTGCCAGTGGCTCTCTTGCACAGCCCCACAGCCACAGCTG	992	
Db	781	GCTTTGGACCATGACCTCTGTGCCAGTGGCTCTCTTATGCGCCACACAGCCACAGTGTG	840	
OY	993	GTTGATGTGTCAAGCGGACCTTGCTGTGGGGAGCGTGCACAAAGATGGGAGATCCTGTG	1052	
Db	841	GTTGATGTGTCAAGCGGACCTTGCTGTGGGGAGCCATGACCAATGAGAGAGCCAGCTG	900	
OY	1053	CCCAAGAGAGTCCCGATGAGTATGAATTTGCAAGCTTCATGAGAGAGTGGCCAGAG	1112	
Db	901	CCCAAGAGAGTCCCGATGAGTATGAAGATTTGTGGCTTCATAGGAGGAAGTGCACAGAG	960	
OY	1113	CTGAGAGAGCTGAGAGAGGAGCTGACATGAAAGATGAGGCTGGGGGAGAGCTGCAGCTGCC	1172	
Db	961	CTGAGAGAGCTGAGAGGAGAGCTGAGCCCAAGAGATGGCATTTGAGAGGGGCTGCCCT---	1017	
OY	1173	GCCGCTGACTGCTGGGAGGGGAAAGATTTAG	1205	
Db	1018	GTGAGATCACTAGCGGAGAGAGAGAGATTTAG	1050	

Db 1018 GTGAGTCACTAGCGGAGAGAGAGATTAG 1050



OTHER INFORMATION: region 36.167  
OTHER INFORMATION: id HUM137D01B  
FEATURE:  
NAME/KEY: other  
LOCATION: 12.142  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 99  
OTHER INFORMATION: region 143.273  
OTHER INFORMATION: id AA155928  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: 12.141  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 99  
OTHER INFORMATION: region 115.244  
OTHER INFORMATION: id W39572  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: complement(12.135)  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 95  
OTHER INFORMATION: region 1.124  
OTHER INFORMATION: id M78698  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: other  
LOCATION: complement(32.151)  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: identity 98  
OTHER INFORMATION: region 346.465  
OTHER INFORMATION: id H99266  
OTHER INFORMATION: est  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 67.114  
IDENTIFICATION METHOD: Von Heijne matrix  
OTHER INFORMATION: score 5.9  
OTHER INFORMATION: seq MULTISFSCIS/NF  
US-08-905-223-215  
Query Match  
Best Local Similarity 5.3%; Score 137; DB 3; Length 150;  
Matches 137; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
DB 2077 TAACTACTGTTAGGAACAGAGTGTCTCAGAGTGTGGGAGCGCGCTCTTAATGAA 2136  
DB 12 TAACTACTGTTAGGAACAGAGTGTCTCAGAGTGTGGGAGCGCGCTCTTAATGAA 71  
QY 2137 GACAAATGATATTAACACTGTCTCTTTGGAGTTGATTAAGTAAAGTAAAT 2196  
DB 72 GACAAATGATATTAACACTGTCTCTTTGGAGTTGATTAAGTAAAGTAAAT 131  
QY 2197 GACTGAGCGTAGCATACAG 2215  
DB 132 GACTGAGCGTAGCATACAG 150

RESULT 5  
US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMWU  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZ9pt-F15  
US-08-232-463-14

Query Match  
Best Local Similarity 2.0%; Score 52.4; DB 1; Length 7218;  
Matches 11; Conservative 216; Mismatches 147; Indels 0; Gaps 0;  
QY 277 AGGAGAGGACCCCTCATGATGATGTTCCGCGAGGTGAGAGTATGAGACAGCGC 336  
DB 1422 RRR 1363  
QY 337 AGCAAAATGGCGAGCGCGGTGAAAGATGAGAGAGAGAGAGTGGCTGTAAGCAT 396  
DB 1362 RRR 1303  
QY 397 CATCAGAGTGAACCTGCAACTTACCTCCAGCTATCACAATGAGACCAACAGACA 456  
DB 1302 RRR 1243  
QY 457 CGAAGTTGAAATATATCATCATGTCACCGAGAAATTCACAATATACCAACACC 516  
DB 1242 RRR 1183  
QY 517 AGACTGACAAATGATGTTTTCAGAGACAGTATCATCTGTGGAGAGCAAGAAAGCA 576  
DB 1182 RRR 1123  
QY 577 GAGAGAGCCAGAGTGCATCATGACAGAGACTGTGGCCACAGATATATGCAAGTTG 636  
DB 1122 RRR 1063  
QY 637 CCAGCTTCAGTAC 650  
DB 1062 CAAGCTCCCTGCAC 1049

RESULT 6  
US-09-461-325-118  
; Sequence 118, Application US/09461325A  
; Patent No. 6475753



```

GENERAL INFORMATION:
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P2029P1
CURRENT APPLICATION NUMBER: US/09/461,325A
CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: PCT/US99/13418
EARLIER FILING DATE: 1999-06-15
EARLIER APPLICATION NUMBER: 60/089,507
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,508
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,509
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,510
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/090,112
EARLIER FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: 60/090,113
EARLIER FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 118
LENGTH: 882
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (117)
OTHER INFORMATION: n equals a,t,g, or c
US-09-461-325-118

Query Match
Best Local Similarity 55.8%; Score 51.6; DB 4; Length 882;
Matches 96; Conservative 1; Mismatches 75; Indels 0; Gaps 0;
Pred. No. 0.0065;

406 TGAACCTGGCAAACTTACCTCCCGCATCAATGAGACCAACACAGACAGAGGTTG 465
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

RESULT 7
US-09-128-155-16
Sequence 16, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 152331
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(152331)

```

```

: OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

Query Match      2.0%; Score 51.6; DB 3; Length 152331;
Best Local Similarity 48.6%; Pred. No. 0 078; Indels 0; Gaps 0;
Matches 141; Conservative 0; Mismatches 149;

QY      4 CGCGCTCCCGCAGCCCGCGCCCGCCCGCCCGCGCTCCCGATGTGACCCCGAGCCCG 63
DB      21931 CCCCCCCCCCGCCCCCGCGCCCGCCCGCGCGCCCGCCCGCCCCCCCCCCCCCG 21990

QY      64 GCGGCTCTCCGCGGAGCGAGCATTCAGTCCGCGCCCGCGAGCGCACTGCGTCCAGTC 123
DB      21991 CGCCCCCGCCCCCCCCCGCGCGCCCCCGCCCGCCCCCGCCCCCCCCCCCCCG 22050

QY      124 GGGCGCGCGCGCTGCGGCGCGCAGAGCGAGAGTCCAGCGGCTTGAGGAGCACTGCTGTGCG 183
DB      22051 CCAACCCCCCAACCGGCGCCCAACAGAGACCCCGACCCCGAGCGCCCCCGCCCCCGCC 22110

QY      184 TGTGCTGTGGGCGCGCGGTGTCGCCACGCGCCCCCGCGCTCCGAGGAGGACTTGCGTC 243
DB      22111 CGGAGCGCGAGCGCCCCCCCCCGCGCGCGCGCGCGCGCACCCCGAGCCCCCGCGCC 22170

QY      244 CAGTCAAGCGCGGCGCGCGCTCTAGCTACCGCAGAGAGGAGCCACCTC 293
DB      22171 CGCCCCCGCCCCCCCCCGCGCGCCCCCCCCCGCGCGCGCGCGCGCGCCCGCCAC 22220

RESULT 8
US-08-665-259-19
: Sequence 19, Application US/08665259
: Patent No. 6028173
: GENERAL INFORMATION:
: APPLICANT: Landes, Gregory M.
: APPLICANT: Burn, Timothy C.
: APPLICANT: Comore, Timothy D.
: APPLICANT: Dackowski, William R.
: APPLICANT: Van Raay, Terence J.
: APPLICANT: Klingler, Katherine W.
: TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
: NUMBER OF SEQUENCES: 73
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: GENZYME CORPORATION
: STREET: One Mountain Road
: CITY: Framingham
: STATE: Massachusetts
: COUNTRY: United States of America
: ZIP: 01701
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/665,259
: FILING DATE: 17-JUN-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Dugan, Deborah A.
: REGISTRATION NUMBER: 37,315
: REFERENCE/DOCKET NUMBER: IGS-9.1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (508) 872-8400
: TELEFAX: (508) 872-5415
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6803 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-08-665-259-19

```

Query Match 1.9%; Score 49; DB 3; Length 6803;  
Best Local Similarity 49.8%; Pred. No. 0.073;  
Matches 155; Conservative 0; Mismatches 150; Indels 6; Gaps 1;  
Molecule Type: DNA (genomic)  
US-08-762-500-19

17 CCGGCGCCCGCCGACCGCCGCTCCGATCTGACCCGAGCCCGGCGGCTCCCGGC 76  
2746 CTGACACCGGAGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2805

QY 77 GGGAGCGAGCATCCAGTCCGCGCCGAGCCGCACTCGTCCATTCGGGGCGGGCGT 136  
DB 2806 CCGGAGGCGCGGAGAGCATCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2865

QY 137 CCGGCGCCGACGAGATGAGCGGCTTGGGCGACCTCTGTGCTGCTGCTGCGGCG 196  
DB 2866 GGGCGCTCCGCGGCGGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2925

QY 197 GCGCGTCCCGACCGCCCGCGGCGGCTCCGAGCGGCGGCTCCAGTCAAGCCCGG 256  
DB 2926 GCGGGA-----GAGCGCGCAACATCCCGCTGTGCTGTGCGGCGGCGGCGG 2979

QY 257 CCGGCGCTCTAGCTACCGCGAGAGAGGCGACCTCAATGAGATGTTCCGAGGTTGA 316  
DB 2980 CGCTGCTCCCACTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3039

QY 317 GGAAGTGAATG 327  
DB 3040 GGGCGTGTGG 3050

RESULT 9  
US-08-762-500-19  
Sequence 19, Application US/08762500  
Patent No. 6030806  
GENERAL INFORMATION:  
APPLICANT: Landes, Gregory M.  
APPLICANT: Burn, Timothy C.  
APPLICANT: Connors, Timothy D.  
APPLICANT: Dackowski, William R.  
APPLICANT: Van Raay, Terence J.  
APPLICANT: Klinger, Katherine W.  
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,  
TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME  
NUMBER OF SEQUENCES: 83  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENZYME CORPORATION  
STREET: One Mountain Road  
CITY: Framingham  
STATE: Massachusetts  
COUNTRY: United States of America  
ZIP: 01701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/762,500  
FILING DATE: 09-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/665,259  
FILING DATE: 17-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10469  
FILING DATE: 17-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Dugan, Deborah A.  
REGISTRATION NUMBER: 37,315  
REFERENCE/DOCKET NUMBER: 165-9.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508) 872-8400  
TELEFAX: (508) 872-5415

INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6803 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-762-500-19

Query Match 1.9%; Score 49; DB 3; Length 6803;  
Best Local Similarity 49.8%; Pred. No. 0.073;  
Matches 155; Conservative 0; Mismatches 150; Indels 6; Gaps 1;  
Molecule Type: DNA (genomic)  
US-07-751-891B-24/C

17 CCGGCGCCCGCCGACCGCCGCTCCGATCTGACCCGAGCCCGGCGGCTCCCGGC 76  
2746 CTGACACCGGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2805

QY 77 GGGAGCGAGCATCCAGTCCGCGCCGAGCCGCACTCGTCCATTCGGGGCGGGCGT 136  
DB 2806 CCGGAGGCGCGGAGAGACTCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2865

QY 137 CCGGCGGAGCGGAGATGAGCGGCTTGGGCGACCTCTGTGCTGTGCTGCGGCG 196  
DB 2866 GGGCGCTCCGCGGCGGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2925

QY 197 GCGCGTCCCGACCGCCCGCGGCGGCTCCGAGCGGCGGCACTCGGCTCGTCTGCTGCGGCG 256  
DB 2926 GCGGGA-----GAGCGCGCAACATCCCGCTGTGCTGTGCGGCGGCGGCGG 2979

QY 257 CCGGCGCTCTAGCTACCGCGAGAGAGGCGACCTCAATGAGATGTTCCGCGAGTTGA 316  
DB 2980 CGCTGCTCCCACTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3039

QY 317 GGAAGTGAATG 327  
DB 3040 GGGCGTGTGG 3050

RESULT 10  
US-07-751-891B-24/C  
Sequence 24, Application US/07751891B  
Patent No. 6180337  
GENERAL INFORMATION:  
APPLICANT: Caskey, C. T.  
APPLICANT: Nelson, David L.  
APPLICANT: Pieretti, Maura  
APPLICANT: Warren, Stephen T.  
APPLICANT: Costra, Ben A.  
TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Thomas D. Paul  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/751,891B  
FILING DATE: 29-AUG-1991  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5350  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5325

/ TELEFAX: 713/651-5246  
 / TELFX: 762829  
 / INFORMATION FOR SEQ ID NO: 24:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 1026 base pairs  
 / TYPE: nucleic acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: DNA (genomic)  
 / SEQUENCE DESCRIPTION: SEQ ID NO: 24  
 / US-07-751-8915-24

Query Match	1.9%	Score 48.4	DB 3	Length 1026
Best Local Similarity	47.9%	Pred. No. 0.041		
Matches 139	Conservative 0	Mismatches 151	Indels 0	Gaps 0
QY	2	GCCTGGCTCCGCATCCCGGGCGCCGCCCGCTCCCGCATTTGCATCCCGAGCC	61	
Db	555	GGCCCGCATTCACATCCACAGCTCCTCATCTTTCAGCCCTGTAGCCGCGGAGAC	496	
QY	62	CGCGGAGCTCCCGCGCGGAGCGAGACAGATCAGTCCGCGCCCGAGACGCGCACTCGTCTCAG	121	
Db	495	CGCGCCCGGAGAGTGGGCTGGGGCGCTGAGGCGCCAGCGCGCGCGCGCGCGCGCGCG	436	
QY	122	TTGGGGGCGCGGCTTCGGGCGCGAAGCGGAGATCAGCGGCTTGGGGCCACTGCTGTGG	181	
Db	435	CG	376	
QY	182	CCGTGCTGTGGGCGGCGGCGGTCCCGACGGCCCCCGCGCGCGCTTCGACGGCGCATCTGGCG	241	
Db	375	GTCACGCGCGCGCGCGCGCGCTGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	316	
QY	242	TCCAGTCAAGCCCGGCGCGGCTTTCAGTACCCCGAGAGAGAGCCACCC	291	
Db	315	CGGAGGTGAAACGGAACGGAAGCTGAGGCGCTTGACTGAGGCGCAACCCCC	266	

RESULT 11  
US-07-751-891B-23/c  
Sequence 23, Application US/07751.891B  
Patent No. 6180337  
GENERAL INFORMATION:  
APPLICANT: Caskey, C. T.  
Nelson, David L.  
Pieretti, Maura  
Warren, Stephen T.  
Coastre, Ben A.  
Fu, Ying-hui  
TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Thomas D. Paul  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/751.891B  
FILING DATE: 29-Aug-1991  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5350  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5325  
TELEFAX: 713/651-5246

TELEX: 762829  
 INFORMATION FOR SEQ ID NO: 23:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5222 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 SEQUENCE DESCRIPTION: SEQ ID NO: 23

Query Match	1.9%	Score 48.4%	DB 3	Length 5222
Best Local Similarity	47.9%	Pred. No. 0.09		
Matches 139	Conservative 0	Mismatches 151	Indels 0	Gaps 0
QY	2	GCCTGCTCCCGCA	CCCGCGGCGCCGACCGCGCGCTCCCGAGATTGCACCCGCGACCC	61
Db	2866	GCCCCCGACTTTCAC	CCACCAAGCTCTCTCATTCTTCTTTCAGCCTGTGACGCGCGGGAGC	2807
QY	62	CGCGCGGCTTCCCG	CGGAGAGAGAGATCAGTCCGCGCGCGACGCCAACTTCGATCCAG	121
Db	2806	CCGCGCCCCGAGAG	GTGGGTCTGCGGGCGCTCGAGGCCAGCGCGCGCGCGCGCGCG	2747
QY	122	TTCGGGGGGGGGG	GCTGCGCGGCGCAGAGGGAGATTCAGCGGCTTTGGGGGCCAECTTGTCTGTG	181
Db	2746	CCCGCGCGCGCGCG	CGCGCGCGCGCGCGCGCGCGCGCTGCGCGACGCGCCCTGTGCAGGGGCGCTTC	2687
QY	182	CTGCTGCTGCGCG	CGGCGGCTTCCCAAGGCGCCCGCGCGCGCTTCGACGCGGACCTCGGC	241
Db	2686	GTCACCGCGCGCG	CGCGCTTCGCGCGCGCGCGCGCGCGCGCTGACGCTTGAAGCGGCGCTTCAC	2627
QY	242	TTCAGTAAACCCG	CGCGCGCTCTCAGACTTACCCGACAGAGAGAGGCCAACC	291
Db	2626	CGGAGTGAACCGAA	CGGAGCTTGAAGCGCTTGAAGGCGCGCAACCCC	2577

```

RESULT 12
US-09-252-991A-9441
: Sequence 9441, Application US/09252991A
: Patent No. 6551795
: GENERAL INFORMATION:
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.136
: CURRENT APPLICATION NUMBER: US/09/252,991A
: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 33142
: SEQ ID NO 9441
: LENGTH: 1269
: TYPE: DNA
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9441

Query Match      1.8%; Score 47.4; DB 4; Length 1269;
Best Local Similarity 51.8%; Pred.No.0.079;
Matches 131; Conservative 0; Mismatches 121; Indels 1; Gaps 1;

QY      64  GCGGCTCCCGGCGGGAGCGAGCAGATCCAGTCCGCGCCCGCCAGCGCAACTCGGTCCAGTC 123
Db      831  GCGGGGCGCCGCTCTCTGGCGCGCGGCCAGCCATGCGCGCGCTCGTATCGAGGCCCTGGT 890

QY      124  GGGGCGCGCGCTCGCGGCGCGAGCGCGAGATGACGCGCTTGGGAGCCACCCCTCTGTGCC 183
Db      891  GGGCGGCGAGGCTCAAGTGTG-TG-GAGCTAGCGCTGAGAAAGACGCCCGCGGAGTGA 949

QY      184  TGCTGTGCGCGCGGCGGCGATCCCAAGGCCCCCGCGCCGCTCTCGAGAGGCACTTCGCTC 243
Db      950  CGGTGCGCGGCGAGCGGATTCCTCCGCTTGCCTGCGGAGCGACTGCTGACCCGTGCGCGGCGG 1009

```

QY 244 CAGTCAAGCCCGCCCGGCTTCACTACCGGAGAGAGAGCCACTTCATGATGT 303  
DB 1010 CGGCGCCCGCCGAGCGAGCGGCTGCCGCGCCGCGGTAAAGCCCTTCAGCTGAGC 1069  
QY 304 TCCGCGAGGTGA 316  
DB 1070 TGGTCCAGGTGA 1082

RESULT 13  
US-09-252-991A-9392/c  
Sequence 9392, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 9392  
LENGTH: 1890  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9392

Query Match 1.8%; Score 47.4; DB 4; Length 1890;  
Best Local Similarity 51.8%; Pred. No. 0.096;  
Matches 131; Conservative 0; Mismatches 121; Indels 1; Gaps 1;

QY 64 GGGGCTTCCCGCGGAGAGAGATCCAGTCCCGCCCGGAGGCGCACTCGGTCAATC 123  
DB 502 GCGGGGCGGCTCTGCGCGCGCGCCAGCCATCGCGCGCTGCTATGAGGCCCTGT 443  
QY 124 GCGGCGCGCGCTGCGCGCGCGAGAGAGATGAGAGATGAGAGATGAGATG 183  
DB 442 GCGCGCGCGAGGCTGAGGTCTG-GAGCTGAGGCTGGAAGAACCCCGCGGAGTGA 384  
QY 184 TCGTGTGCGCGCGGCGGTCCCAAGGCGCCCGCGCTCCGAGCGACTTGGCTC 243  
DB 383 CGGTGCGCGCGAGCGGTTCCTGCGCGCGAGCTGCGAGCGTGGCGCGGCGG 324  
QY 244 CAGTCAAGCCCGGCGGCTTCAGTACCGGAGAGAGAGAGAGAGAGAGAGATG 303  
DB 323 CGGCGCGCGCGAGCGGAGCGGCGGCGCGCGGTAAAGCCCTTCAGCTGAGC 264  
QY 304 TCCGCGAGGTGA 316  
DB 263 TGGTCCAGGTGA 251

RESULT 14  
US-08-469-526A-21  
Sequence 21, Application US/08469526A  
Patent No. 5792849  
GENERAL INFORMATION:  
APPLICANT: Goodheart, Andrew  
APPLICANT: Strobant, Paul  
APPLICANT: Minshetti, Luisa  
APPLICANT: Waterfield, Michael  
APPLICANT: Marchionni, Mark  
APPLICANT: Chen, Miao Su  
APPLICANT: Hiles, Ian  
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
PREPARATION AND USE  
NUMBER OF SEQUENCES: 187  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,526A  
FILING DATE: 06 June 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/036,555  
FILING DATE: 24-MAR-1993  
APPLICATION NUMBER: 07/965,173  
FILING DATE: 23-OCT-1992  
APPLICATION NUMBER: 07/940,389  
FILING DATE: 03-SEP-1992  
APPLICATION NUMBER: 07/907,138  
FILING DATE: 03-JUN-1992  
APPLICATION NUMBER: 07/863,703  
FILING DATE: 03-APRIL-1992  
APPLICATION NUMBER: U.K. 91 07566.3  
FILING DATE: 10-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Bleker-Brady, Kristina  
REGISTRATION NUMBER: 39,109  
REFERENCE/DOCKET NUMBER: 04585/00200A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2003  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: N in positions 31 and 32 could be  
either A or G.  
US-08-469-526A-21

Query Match 1.8%; Score 47; DB 1; Length 2003;  
Best Local Similarity 47.5%; Pred. No. 0.12;  
Matches 140; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 94 GTCGCGCGCGCGAGCACTCGGTTCAGTCCGCGCGCGCGCTGCGGCGCGAGCGGAGA 153  
DB 299 GTCCCGCGCGCGCGCGCGCGCGCGCGCGCTCCGCGCGCTGTGCGCGCGCGCTCCG 358  
QY 154 TCGAGCGGCTTGGGCGCACCTGCTGCTGCTGCTGCGCGCGCGCGCGCGCGCG 213  
DB 359 TCGTGCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 418  
QY 214 CCGGCGCGCGCTCCGAGGCGCACTTGGCTTCACTCAAGCGCGCGCGCGCGCTCAGTAC 273  
DB 419 ACAGAGGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTG 478  
QY 274 CCGAGAGAGAGCGCACCTTCATGATGATGTCGCGAGGTTGAGAACTGATGAGAGAGA 333  
DB 479 TCGAGAGAGTAGTCAAGCGCGCGCGCGGTGATGATGAGGAGAAAGTGCAACCGCACCGC 538  
QY 334 CCGAGCAAAATTGCGCGAGCGCGGTGAGAAAGATGAGAGCAAGAAAGTGTGCG 388  
DB 539 GCGAGCAGGCGGCACTGCAACAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 593

RESULT 15  
US-08-734-591A-21

Sequence 21, Application US/08734591A  
Patent No. 5854220  
GENERAL INFORMATION:  
APPLICANT: Goodheart, Andrew  
APPLICANT: Stroobant, Paul  
APPLICANT: Mingshetti, Luisa  
APPLICANT: Waterfield, Michael  
APPLICANT: Hiles, Ian  
APPLICANT: Marchionni, Mark  
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
NUMBER OF SEQUENCES: 187  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible Pentium  
OPERATING SYSTEM: Windows95  
SOFTWARE: WordPerfect (Version 7.0)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/734,591A  
FILING DATE: 22-OCT-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/470,335  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/036,555  
FILING DATE: 03-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,173  
FILING DATE: 23-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/940,389  
FILING DATE: 03-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/907,138  
FILING DATE: 30-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/863,703  
FILING DATE: 03-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: UK 91 07566.3  
FILING DATE: 10-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Bieker-Brady, Kristina  
REGISTRATION NUMBER: 39,109  
REFERENCE/DOCKET NUMBER: 04585/00200P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 428-0200  
TELEFAX: (617) 428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2003  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: N in positions 31 and 32 could be  
OTHER INFORMATION: either A or G.  
US-08-734-591A-21  
Query Match 1.8%; Score 47; DB 2; Length 2003;  
Best Local Similarity 47.5%; Pred. No. 0.12;  
Matches 140; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Oy 94 GTCCGCGCCCGCAGCGCACTCGGTCAGTCGCGGCGCGGCTGCGGCGCAGAGCCGAGA 153  
Db 299 GTCCCGGCCCCCGGCGCCAGCGCCCCCGGCTCCCGCCCGCTGTCGCGCGCTCGCCG 358  
Oy 154 TGCAGCGGCTTGGGGCCACCCTGCTGTGCTGTGCTGCGCGGGGTCCCAAGGCC 213  
Db 359 TGTGCGCACTACTGCTGCTGCTGCTGCGGACCGCGGCTTGGGCGCGGCGCGCGGCA 418  
Oy 214 CCGGCGCCGCTCCGAGCGGCGACCTCGGCTCAGTCAAGCCCGGCGGCTCTCAGCTACG 273  
Db 419 ACGAGCGGCTCCCGCGGCGGCTCGTGTGCTACTGCTCCCGCCAGGCTGGATCGG 478  
Oy 274 CGCAGAGGAGGCGCACCTCAATGAGATGTTCCGCGAGTTGAGAACTGATGAGGACA 333  
Db 479 TGCAGGAGTAGCTCAGCGCGCGCGGTGCTCATCGAGGAGAAAGTGTCACCCGACGCGC 538  
Oy 334 CGCAGCACAATTTGCGCAGCGCGGTGGAAGATGAGAGGAGAGAAAGCTGCTGC 388  
Db 539 GGCAGCGGGGCACTGACAGAGAAAGCGGCGGCGCGGCGGAGGCAAGGGGC 593

Search completed: February 19, 2004, 21:20:51  
Job time : 161 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 20, 2004, 14:52:39 ; Search time 75 Seconds  
(without alignments)  
740.724 Million cell updates/sec

Title: US-10-063-671-8  
Perfect score: 1880  
Sequence: 1 MORTGATLCLILAAVPTA.....EMALGEPAAAAALUGGERI 350

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 segs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database:

1: A\_Geneseq\_19Jun03:\*  
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
25: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1880	100.0	350	19	AAW62595
2	1880	100.0	350	21	AAV92070
3	1880	100.0	350	22	AA680271
4	1880	100.0	350	22	AA682468
5	1880	100.0	350	22	AA687529
6	1880	100.0	350	22	AA680252
7	1880	100.0	350	23	ABG95854
8	1880	100.0	350	23	ABB95447
9	1880	100.0	350	23	ABB90735

10	1880	100.0	350	23	AB684841	Human PRO295 prote
11	1880	100.0	350	24	ABU59662	Novel human secre
12	1880	100.0	350	24	ABU71465	Human PRO polypept
13	1880	100.0	350	24	ABU71509	Human secreted pol
14	1880	100.0	350	24	ABU71931	Human secreted/tira
15	1880	100.0	350	24	ABU71955	Novel human secret
16	1880	100.0	350	24	ABU72112	Human PRO polypept
17	1880	100.0	350	24	ABU67385	Human secreted pro
18	1880	100.0	350	24	ABU64539	Human secreted/tira
19	1880	100.0	350	24	ABU54069	DKK 3 protein. Un
20	1880	100.0	350	24	ABU55915	Human protein DKK3
21	1880	100.0	350	24	ABU54387	Human secreted/tira
22	1880	100.0	350	24	ABU54442	Human tumour endoc
23	1878	99.9	350	20	AAV13384	Amino acid sequenc
24	1859	98.9	350	19	AAW73016	Human cysteine-ric
25	1859	98.9	350	21	AA680874	Amino acid sequenc
26	1859	98.9	350	21	AAW73021	Mouse cysteine-ric
27	1589	84.5	349	19	AA680879	A murine DKKopt
28	1589	84.5	349	21	AAV92069	Murine DKK-3. Mus
29	214.5	11.4	224	19	AAW73017	Human cysteine-ric
30	214.5	11.4	224	21	AA680875	Amino acid sequenc
31	214.5	11.4	224	21	AA680875	Human DKK-4. Homo
32	214.5	11.4	224	21	AA680875	Amino acid sequenc
33	214.5	11.4	224	24	AA684070	Human DKK 4 protein. Un
34	214.5	11.4	224	24	ABU55916	Human protein DKK4
35	174.5	9.3	266	19	AAW73018	Human cysteine-ric
36	174.5	9.3	266	20	AAV41757	Human PRO1008 prot
37	174.5	9.3	266	21	AA680876	Human PRO1008 (UNQ
38	174.5	9.3	266	21	AAV92071	Amino acid sequenc
39	174.5	9.3	266	22	AAW78517	Human DKK-1. Homo
40	174.5	9.3	266	22	AAU12385	Human protein SEO
41	174.5	9.3	266	24	ABU67633	Human PRO1008 poly
42	174.5	9.3	266	24	ABU67059	Human PRO polypept
43	174.5	9.3	266	24	ABU67059	Human secreted/tira
44	174.5	9.3	266	24	ABU67059	Human cancer-relat
45	174.5	9.3	266	24	ABU61143	Novel secreted and

## ALIGNMENTS

AAW62595	AAW62595 standard; Protein, 350 AA.
1	AAW62595
2	AAW62595
3	AAW62595
4	AAW62595
5	AAW62595
6	AAW62595
7	AAW62595
8	AAW62595
9	AAW62595
10	AAW62595
11	AAW62595
12	AAW62595
13	AAW62595
14	AAW62595
15	AAW62595
16	AAW62595
17	AAW62595
18	AAW62595
19	AAW62595
20	AAW62595
21	AAW62595
22	AAW62595
23	AAW62595
24	AAW62595
25	AAW62595
26	AAW62595
27	AAW62595
28	AAW62595
29	AAW62595
30	AAW62595
31	AAW62595
32	AAW62595
33	AAW62595
34	AAW62595
35	AAW62595
36	AAW62595
37	AAW62595
38	AAW62595
39	AAW62595
40	AAW62595
41	AAW62595
42	AAW62595
43	AAW62595
44	AAW62595
45	AAW62595



DR MPI: 1998-377366/32.  
 DR N-PSDB; AAY38798.  
 XX  
 PT New isolated cerebellum and embryo specific polypeptide - used to  
 PT develop products for treating e.g. coronary stenosis, myocardial  
 PT infarction, heart disease and artery or venous thrombosis  
 XX  
 PS Claim 17; Fig 1; 77pp; English.  
 CC The sequence is that of cerebellum and embryo specific protein  
 CC (CBSP). CBSP is involved in: (i) the regulation of collateral  
 CC circulation (particularly in the heart), coronary artery stenosis  
 CC following a revascularisation procedure, apoptosis in myocytes; (ii) the  
 CC modulation of myocyte development in the developing heart; (iii)  
 CC regulation of circulating blood volume, vascular tone, blood pressure and  
 CC cardiac output, diuresis, natriuresis; (iv) facilitation of transudation  
 CC of plasma water to the interstitium, and (iv) inhibition of the release  
 CC or action of hormones such as aldosterone, angiotensin II, endothelin,  
 CC renin and vasopressin. The products can be used in the diagnosis and  
 CC treatment of CBSP related disorders, e.g. coronary stenosis following  
 CC coronary revascularisation, coronary artery thrombus or occlusion,  
 CC myocardial infarction, atrial and/or ventricular arrhythmias, heart  
 CC block, hereditary medial necrosis of small coronary arteries,  
 CC cardiomyopathy, arrhythmogenic right ventricular dysplasia, athero-  
 CC sclerotic heart disease, venous thrombosis or Reynaud's syndrome.  
 XX  
 SQ Sequence 350 AA;  
 Query Match 100.0%; Score 1880; DB 19; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-149;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRIGATLCLLLAAVPTAPAPATATAPKPGPALSTPQEBATLNMREVELEMD 60  
 DB 1 MQRIGATLCLLLAAVPTAPAPATATAPKPGPALSTPQEBATLNMREVELEMD 60  
 QY 61 TQHKRSAYEMEAEEAAKASEVNLALPPSYHNETNTDKVGNNTIHYHREIHKITN 120  
 DB 61 TQHKRSAYEMEAEEAAKASEVNLALPPSYHNETNTDKVGNNTIHYHREIHKITN 120  
 QY 121 NOTGVVSEVTVTSVGEDEGRSHSECTIDEDCGSNVQSPASFOYTQPCPGQMLCTR 180  
 DB 121 NOTGVVSEVTVTSVGEDEGRSHSECTIDEDCGSNVQSPASFOYTQPCPGQMLCTR 180  
 QY 181 DSECCDQLCVMGHCTKMATRSGNGTICDNORDCOPGLCCAFQRLFFVCTPLPVEGEL 240  
 DB 181 DSECCDQLCVMGHCTKMATRSGNGTICDNORDCOPGLCCAFQRLFFVCTPLPVEGEL 240  
 QY 241 CHDPASRLDLITWLEPDPGALDRPCASGLICQPHSHSLVYVCKPTFVSGRDQGEILL 300  
 DB 241 CHDPASRLDLITWLEPDPGALDRPCASGLICQPHSHSLVYVCKPTFVSGRDQGEILL 300  
 QY 301 PRVPPEVEVSGFMEVROLEPDLERSLTEMALGEPAAAAAALGGERT 350  
 DB 301 PRVPPEVEVSGFMEVROLEPDLERSLTEMALGEPAAAAAALGGERT 350

RESULT 2  
 ID AAY92070 standard; Protein; 350 AA.  
 XX  
 AC AAY92070;  
 XX  
 DT 01-AUG-2000 (first entry)  
 XX  
 DE Human DKR-3.  
 XX  
 KW DKR-3; human rlg-1-like 7-1 mRNA; chicken lens fiber protein; cleft 4;  
 KW dkk-1; dickkopf-1; antagonist; wnt-8 signaling; morphogenesis;  
 KW growth factor; cytoskeletal; sonic hedgehog; tissue differentiation.  
 XX  
 OS Homo sapiens.  
 XX

FN Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /label= "signal peptide"  
 FT /note= "putative"  
 FT Peptide 1..21  
 FT /label= "signal peptide"  
 FT /note= "putative"  
 FT Cleavage-site 16..17  
 FT /note= "putative endogenous processing site"  
 FT Region 21..145  
 FT /note= "alpha helical region and region of N-linked glycosylation"  
 FT Cleavage-site 22..23  
 FT /note= "putative endogenous processing site"  
 FT Cleavage-site 32..33  
 FT /note= "putative endogenous processing site"  
 FT Cleavage-site 41..42  
 FT /note= "putative endogenous processing site"  
 FT Modified-site 96  
 FT /note= "N-glycosylated"  
 FT Modified-site 106  
 FT /note= "N-glycosylated"  
 FT Modified-site 121  
 FT /note= "N-glycosylated"  
 FT Modified-site 204  
 FT /note= "N-glycosylated"  
 FT Region 300..350  
 FT /note= "alpha helical region"  
 FN WO200018914-A2.  
 XX 06-Apr-2000.  
 XX 17-SEP-1999; 99WO-US21647.  
 XX 25-SEP-1998; 98US-0161241.  
 XX (AMGE-) AMGEN INC.  
 PI Baas MB, Sullivan JK, Theill LE, Wang D;  
 DR MPI: 2000-229153/25.  
 DR N-PSDB; AAA08839.  
 XX  
 PT New nucleic acid molecule encoding a biologically active DKR  
 PT polypeptide, useful in treatment of cancer, e.g. mammary tumors and  
 PT stem cell tumors  
 PS Claim 18; Page 126-127; 143pp; English.  
 XX  
 XX AAY92069-75 are novel mouse and human DKR polypeptides.  
 CC The human DKR-3 open reading frame has homology to human rlg-1-like 7-1  
 CC mRNA and to chicken lens fiber protein cleft 4 gene. Human DKR-3  
 CC appears to be secreted, with a signal peptide cleavage site after either  
 CC amino acid 20 or 21.  
 CC DKR-1 is a human ortholog of dkk-1 (dickkopf-1), a novel gene identified  
 CC in Xenopus and mouse, purportedly an antagonist of wnt-8 signaling.  
 CC DKR-2, -3 and -4 are each related to DKR-1 by their cysteine pattern,  
 CC therefore a growth factor, by inference DKR polypeptides are also  
 CC growth factors. The DKR polypeptides are useful for treating cancer,  
 CC e.g. mammary tumors, stem cell tumors, or other cancers in which the wnt  
 CC and/or sonic hedgehog (shh) signal transduction pathways are activated.  
 CC They can also be used to enhance tissue differentiation, such as bone  
 CC formation and hematopoietic cell formation.  
 XX  
 SQ Sequence 350 AA;  
 Query Match 100.0%; Score 1880; DB 21; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-149;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRIGATLCLLLAAVPTAPAPATATAPKPGPALSTPQEBATLNMREVELEMD 60

Db 1 MORGATLCLLLAAVPTAPAPATATSAVPKGPALSYQEBATINEMFREVEELMED 60  
 QY 61 TQKLSAVEEMEAERAAKASSEVNLANLPSPYHNETDTKVGNNTHVHREIHKITN 120  
 Db 61 TQKLSAVEEMEAERAAKASSEVNLANLPSPYHNETDTKVGNNTHVHREIHKITN 120  
 QY 121 NOTGQWVFSEVTITVSGDEGRSHSECTIDEDCGPSMYCOPASFOYTQCPKRGQRLCTR 180  
 Db 121 NOTGQWVFSEVTITVSGDEGRSHSECTIDEDCGPSMYCOPASFOYTQCPKRGQRLCTR 180  
 QY 181 DSECCGQOLCVMGHCTKMATRGSNGTICDNORCCOPGLCCAFORGLLPVCTPLPVEGEL 240  
 Db 181 DSECCGQOLCVMGHCTKMATRGSNGTICDNORCCOPGLCCAFORGLLPVCTPLPVEGEL 240  
 QY 241 CHDPASRLDLITWLEBPDGALDRCPGASGLCQPHSHSLVYVCKPTFVGSRDQGEILL 300  
 Db 241 CHDPASRLDLITWLEBPDGALDRCPGASGLCQPHSHSLVYVCKPTFVGSRDQGEILL 300  
 QY 301 PREVPDEYEVGSFMEVROELEDLERSLITEMALGEPMAAAALLGGEI 350  
 Db 301 PREVPDEYEVGSFMEVROELEDLERSLITEMALGEPMAAAALLGGEI 350  
 RESULT 3  
 AAG80271 ID AAG80271 standard; Protein; 350 AA.  
 AC AAG80271;  
 DT 11-FEB-2002 (first entry)  
 XX Human DKK-3 protein.  
 DE Human DKK-3 protein.  
 XX DKK-3; detection; schizophrenia; neuroleptic; vaccine; gene therapy;  
 KM neuralgic defect; neuropsychiatric disorder; human.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN MO200163295-A2.  
 PD 30-AUG-2001.  
 PF 26-FEB-2001; 2001WO-1B00259.  
 XX 24-FEB-2000; 2000GB-0004412.  
 PR 24-FEB-2000; 2000GB-0004415.  
 PR 15-MAR-2000; 2000GB-0006285.  
 PR 24-NOV-2000; 2000GB-0028734.  
 PR 28-NOV-2000; 2000US-0724391.  
 PR 08-DEC-2000; 2000GB-0030050.  
 PR 12-DEC-2000; 2000US-0254830.  
 PR 28-DEC-2000; 2000US-0750395.  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX Herath HNAAC, Parekh RB, Rohlf C, Patel TP;  
 DR WPI; 2001-570652/64.  
 DR N-PSDB; AAI69309.  
 XX Diagnosing and monitoring Schizophrenia by detecting the presence of  
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein  
 PT isoforms in samples of cerebrospinal fluid -  
 XX Claim 1a; Fig 1; 91p; English.  
 PS This invention describes a novel method for detecting the presence of  
 CC schizophrenia associated features (SfEs) and schizophrenia associated  
 CC protein isoforms (SPIs) in samples, e.g. by electrophoresis, immunoassay  
 CC or hybridisation assay, for diagnosing and monitoring schizophrenia,  
 CC studying the effectiveness of treatments and for identifying potential  
 CC therapeutic agents. The products of the invention have neuroleptic

CC activity and can be used in vaccines or for gene therapy. The method (1)  
 CC is used: (1) for screening or diagnosis of schizophrenia and the relative  
 CC abundance of at least 1 chosen feature correlates with the presence or  
 CC absence of schizophrenia and for monitoring the effect of therapy  
 CC administered to a subject with schizophrenia and the relative abundance  
 CC of at least 1 chosen feature which correlates with the severity of  
 CC schizophrenia. The expression and activity of the SfEs, SPIs and related  
 CC molecules (e.g. secondary messengers) are studied to diagnose  
 CC schizophrenia, monitor the progress of the disorder and the effectiveness  
 CC of treatment and as targets to identify and produce potential therapeutic  
 CC agents for the treatment of schizophrenia. The paucity of detectable  
 CC neuroleptic defects distinguishes neuropsychiatric disorders such as  
 CC schizophrenia from neurological disorders, where manifestations of  
 CC anatomical and biochemical changes have been identified in many cases.  
 CC Consequently the identification and characterisation of cellular and/or  
 CC molecular causative defects and neuropathies are necessary for improved  
 CC treatment of neuropsychiatric disorders. This sequence represents the  
 CC human DKK-3 protein described in the method of the invention.  
 XX Sequence 350 AA:  
 SQ  
 Query Match 100.0%; Score 1880; DB 22; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-149;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MORGATLCLLLAAVPTAPAPATATSAVPKGPALSYQEBATINEMFREVEELMED 60  
 Db 1 MORGATLCLLLAAVPTAPAPATATSAVPKGPALSYQEBATINEMFREVEELMED 60  
 QY 61 TQKLSAVEEMEAERAAKASSEVNLANLPSPYHNETDTKVGNNTHVHREIHKITN 120  
 Db 61 TQKLSAVEEMEAERAAKASSEVNLANLPSPYHNETDTKVGNNTHVHREIHKITN 120  
 QY 121 NOTGQWVFSEVTITVSGDEGRSHSECTIDEDCGPSMYCOPASFOYTQCPKRGQRLCTR 180  
 Db 121 NOTGQWVFSEVTITVSGDEGRSHSECTIDEDCGPSMYCOPASFOYTQCPKRGQRLCTR 180  
 QY 181 DSECCGQOLCVMGHCTKMATRGSNGTICDNORCCOPGLCCAFORGLLPVCTPLPVEGEL 240  
 Db 181 DSECCGQOLCVMGHCTKMATRGSNGTICDNORCCOPGLCCAFORGLLPVCTPLPVEGEL 240  
 QY 241 CHDPASRLDLITWLEBPDGALDRCPGASGLCQPHSHSLVYVCKPTFVGSRDQGEILL 300  
 Db 241 CHDPASRLDLITWLEBPDGALDRCPGASGLCQPHSHSLVYVCKPTFVGSRDQGEILL 300  
 QY 301 PREVPDEYEVGSFMEVROELEDLERSLITEMALGEPMAAAALLGGEI 350  
 Db 301 PREVPDEYEVGSFMEVROELEDLERSLITEMALGEPMAAAALLGGEI 350  
 RESULT 4  
 AAG62468 ID AAG62468 standard; Protein; 350 AA.  
 AC AAG62468;  
 DT 10-SEP-2001 (first entry)  
 XX Human reduced expression in immortalised cells protein.  
 DE Human reduced expression in immortalised cells protein.  
 KM REIC; reduced expression in immortalised cells; cancer; tumour;  
 KM proliferation inhibitor; viral infection; human.  
 OS Homo sapiens.  
 PN WO200138528-A1.  
 PD 31-MAY-2001.  
 PF 30-AUG-2000; 2000WO-JP05879.  
 PR 19-NOV-1999; 99JP-0330604.  
 XX

PA (HISM ) HISAMITSU PHARM CO LTD.  
XX Namba M, Tsuji T,  
XX WPI: 2001-367688/38.  
DR N-PSDB; AAA45489, AAA45490, AAA45491.  
XX  
PT Cell proliferation inhibiting protein REIC and polynucleotide encoding  
PT it for diagnosis and therapy of cancer and as an antiviral agent -  
PS Claim 2; Page 56-57; 66pp; Japanese.  
XX  
CC This invention relates to a protein designated REIC (reduced expression  
CC in immortalised cells) which inhibits proliferation. REIC shows reduced  
CC or suppressed expression in immortalised cells such as cancer cells. The  
CC invention includes DNA and protein sequences for REIC. The protein is  
CC useful for the treatment and diagnosis of a wide range of benign and  
CC malignant tumours and of viral infections (including HIV, influenza,  
CC hepatitis and Epstein-Barr virus). The present sequence represents REIC.  
XX  
SQ Sequence 350 AA;  
Query Match 100.0%; Score 1880; DB 22; Length 350;  
Best Local Similarity 100.0%; Pred. No. 6.5e-149;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MORTGATLCLILAAVPTAPAPATPATSAPVKGPAALSTPOEATLNEMFREVELMED 60  
DB 1 MORTGATLCLILAAVPTAPAPATPATSAPVKGPAALSTPOEATLNEMFREVELMED 60  
QY 61 TQHKLSAVEEMAEBAKASSEVNLANLPPSYHNENTDTKVGNNTHVHREIHKITN 120  
DB 61 TQHKLSAVEEMAEBAKASSEVNLANLPPSYHNENTDTKVGNNTHVHREIHKITN 120  
QY 121 NOTGQWVFSEVITVSVDDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRM LCTR 180  
DB 121 NOTGQWVFSEVITVSVDDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRM LCTR 180  
QY 181 DSECCGDCQVCWGHCTKMAKTRGNSNGTICNORDCQGLCCAFRGILLFPVCTPLPYEGEL 240  
DB 181 DSECCGDCQVCWGHCTKMAKTRGNSNGTICNORDCQGLCCAFRGILLFPVCTPLPYEGEL 240  
QY 241 CHDPASRLDLITWLEPDPGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDEIILL 300  
DB 241 CHDPASRLDLITWLEPDPGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDEIILL 300  
QY 301 PREVPDEYEVGSFMEVROELDLERSLITEMALGEPAAAAALLGGEEL 350  
DB 301 PREVPDEYEVGSFMEVROELDLERSLITEMALGEPAAAAALLGGEEL 350

PR 07-DEC-1999; 99US-0169495.  
PR 09-DEC-1999; 99US-0170262.  
PR 11-JAN-2000; 2000US-0175481.  
PR 18-FEB-2000; 2000MO-US04341.  
PR 18-FEB-2000; 2000MO-US04342.  
PR 22-FEB-2000; 2000MO-US04414.  
PR 01-MAR-2000; 2000MO-US05601.  
PR 03-MAR-2000; 2000US-0187202.  
PR 25-APR-2000; 2000US-0199397.  
PR 22-MAY-2000; 2000MO-US14042.  
PR 05-JUN-2000; 2000US-0209832.  
XX  
PA (GETH ) GENENTECH INC.  
XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Matanabe CK, Wood WI,  
XX WPI: 2001-183260/18.  
DR N-PSDB; AAF92061.  
XX  
XX Eighty four nucleic acids encoding PRO polypeptides, useful in  
PT molecular biology, including use as hybridization probes, and in  
PT chromosome and gene mapping. -  
PS Claim 12; Fig 8; 278pp; English.  
XX  
CC The present sequence is a human PRO polypeptide (secreted and  
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or  
CC anti-PRO antibodies are useful for preparation of a medicament useful in  
CC the treatment of a condition which is responsive to the PRO protein,  
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be  
CC employed as molecular weight markers for protein electrophoresis. The PRO  
CC coding sequence has applications in molecular biology, including use as  
CC hybridisation probes, and in chromosome and gene mapping.  
XX  
SQ Sequence 350 AA;  
Query Match 100.0%; Score 1880; DB 22; Length 350;  
Best Local Similarity 100.0%; Pred. No. 6.5e-149;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MORTGATLCLILAAVPTAPAPATPATSAPVKGPAALSTPOEATLNEMFREVELMED 60  
DB 1 MORTGATLCLILAAVPTAPAPATPATSAPVKGPAALSTPOEATLNEMFREVELMED 60  
QY 61 TQHKLSAVEEMAEBAKASSEVNLANLPPSYHNENTDTKVGNNTHVHREIHKITN 120  
DB 61 TQHKLSAVEEMAEBAKASSEVNLANLPPSYHNENTDTKVGNNTHVHREIHKITN 120  
QY 121 NOTGQWVFSEVITVSVDDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRM LCTR 180  
DB 121 NOTGQWVFSEVITVSVDDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRM LCTR 180  
QY 181 DSECCGDCQVCWGHCTKMAKTRGNSNGTICNORDCQGLCCAFRGILLFPVCTPLPYEGEL 240  
DB 181 DSECCGDCQVCWGHCTKMAKTRGNSNGTICNORDCQGLCCAFRGILLFPVCTPLPYEGEL 240  
QY 241 CHDPASRLDLITWLEPDPGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDEIILL 300  
DB 241 CHDPASRLDLITWLEPDPGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDEIILL 300  
QY 301 PREVPDEYEVGSFMEVROELDLERSLITEMALGEPAAAAALLGGEEL 350  
DB 301 PREVPDEYEVGSFMEVROELDLERSLITEMALGEPAAAAALLGGEEL 350



28-FEB-2001; 2001WO-US06520.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 XX  
 PA (GENENTECH INC.)  
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurney AL, Matanabe CK, Wood WI,  
 DR N-PSDB; ABB514381.  
 XX WPI; 2002-731348/79.  
 XX  
 PT New isolated secreted and transmembrane PRO polypeptide useful for  
 PT modulating biological activity of a cell, or for treating  
 PT sports-related joint problems, osteoarthritis or rheumatoid arthritis  
 XX  
 XX Claim 20; Fig 8; 399pp; English.

CC The invention relates to an isolated secreted and transmembrane PRO  
 CC polypeptide having 80 % sequence identity to a sequence appearing  
 CC as ABG5851-ABG5334 or their associated signal peptide, or a sequence of  
 CC an extracellular domain of the proteins with their associated signal  
 CC peptide, or lacking its associated signal peptide. Also included are  
 CC the nucleic acids encoding the proteins, vectors, host cells,  
 CC fusion proteins and antibodies which specifically bind to the proteins.  
 CC The proteins are useful for detecting a polypeptide designated as A, B, C  
 CC or D in a sample suspected of containing an A, B, C or D polypeptide,  
 CC by contacting the sample with a polypeptide designated as E, F, G, H or  
 CC I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H  
 CC or D/I polypeptide conjugate in the sample, where the formation of C/H  
 CC conjugate is indicative of the presence of an A, B, C or D polypeptide  
 CC in the sample, where A is a PRO10272 polypeptide, B is a PRO20110  
 CC polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide,  
 CC E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040  
 CC polypeptide, H is a PRO20233 polypeptide and I is a PRO1890  
 CC polypeptide. The sample comprises a cell suspected of expressing the A,  
 CC B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with  
 CC a detectable label or is attached to a solid support. The proteins are  
 CC useful for linking a bioactive molecule to a cell expressing a  
 CC polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive  
 CC molecule is a toxin, a radiolabel or an antibody. The bioactive molecule  
 CC causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies  
 CC against them are useful for modulating a biological activity of a cell  
 CC expressing a polypeptide designated as A, B, C or D or E, F, G, H, or  
 CC I. The cell is killed. The proteins are useful for identifying  
 CC agonists or antagonists, for the preparation of a medicament useful in  
 CC the treatment of a condition which is responsive to the proteins, as  
 CC molecular weight markers for protein electrophoresis purposes, and as  
 CC therapeutic agents for treating sports-related joint problems, and as  
 CC articular cartilage defects, osteoarthritis or rheumatoid arthritis.  
 CC Nucleic acids encoding the proteins are useful as hybridization probes,  
 CC in chromosome and gene mapping, in the generation of anti-sense RNA and  
 CC DNA, for the preparation of the proteins, to generate transgenic or  
 CC knockout animals which are useful in the development and screening of  
 CC therapeutic useful reagents, for chromosome identification, and in gene  
 CC therapy. The antibody is useful as a therapeutic agent, in a diagnostic  
 CC assay and for affinity purification of the protein from recombinant  
 CC cell culture natural sources. The present sequence represents a novel  
 CC secreted or transmembrane protein of the invention.

XX  
 XX Sequence 350 AA;

Query Match 100.0%; Score 1880; DB 23; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 6-5e-149;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORIGATLLCLLAAVFPAPAPATSAVPKPGALSTPQEEATLNFREVEELMD 60  
 DB 1 MORIGATLLCLLAAVFPAPAPATSAVPKPGALSTPQEEATLNFREVEELMD 60  
 QY 61 TORHLSAIVEMEAFAAKASSEVNLANLPSTYHNETNTDTKVGNNTHVREIHKTN 120

DB 61 TORHLSAIVEMEAFAAKASSEVNLANLPSTYHNETNTDTKVGNNTHVREIHKTN 120  
 QY 121 NOTGQWFSEETVITVSQDEBGRSRSHCEIIDDGCPSPMYCQFASFOYTCPCRGQMLCTR 180  
 DB 121 NOTGQWFSEETVITVSQDEBGRSRSHCEIIDDGCPSPMYCQFASFOYTCPCRGQMLCTR 180  
 QY 181 DSECCGQQLCVMGHCNTRMATRGSNGTICDNQDCQGLCCAFQGLLFPYCTLPVEGEL 240  
 DB 181 DSECCGQQLCVMGHCNTRMATRGSNGTICDNQDCQGLCCAFQGLLFPYCTLPVEGEL 240  
 QY 241 CHDPASRLDLITWLEPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQGEILL 300  
 DB 241 CHDPASRLDLITWLEPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQGEILL 300  
 QY 301 PREVPDEYGVSGFMEEYRQELDLERSLTFEMALGPAAALALGGEI 350  
 DB 301 PREVPDEYGVSGFMEEYRQELDLERSLTFEMALGPAAALALGGEI 350

RESULT 8  
 ABB95447  
 ID ABB95447 standard; Protein; 350 AA.

XX ABB95447;

DT 19-JUN-2002 (first entry)

XX Human angiogenesis related protein PRO295 SEQ ID NO: 50.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiatic; cytosolic; antiangiogenic; hypotensive; vulnerability;  
 KW antiarteriosclerotic.

XX Homo sapiens.

OS WC0200208284-A2.

XX 31-JAN-2002.

PF 09-JUN-2001; 2001WO-US21735.

XX 20-JUN-2000; 2000US-219556P.  
 PR 25-JUN-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220644P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 02-AUG-2000; 2000US-222695P.  
 PR 17-AUG-2000; 2000US-0643657.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 15-SEP-2000; 2000US-000000P.  
 PR 18-SEP-2000; 2000US-064610.  
 PR 18-SEP-2000; 2000US-066350.  
 PR 24-OCT-2000; 2000US-242922P.  
 PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-082366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.

XX	25-MAY-2001; 2001MO-US17092.
PR	30-MAY-2001; 2001US-0870574.
PR	30-MAY-2001; 2001MO-US17443.
PR	01-JUN-2001; 2001MO-US17800.
PR	20-JUN-2001; 2001MO-US19692.
XX	28-JUN-2001; 2001WO-US00000.
PA	(GETH) GENENTECH INC.
PA	(BAKE/) BAKER K P.
PA	(FERA/) FERRARA N.
PA	(GERB/) GERBER H.
PA	(GERR/) GERRITSEN M E.
PA	(GODD/) GODDARD A.
PA	(GODO/) GODOWSKI P J.
PA	(GURN/) GURNEY A L.
PA	(HILL/) HILLAN K J.
PA	(MARS/) MARSTERS S A.
PA	(PANU/) PAN J.
PA	(PAON/) PAONI N F.
PA	(STEP/) STEPHAN J F.
PA	(WATA/) WATANABE C K.
PA	(WILL/) WILLIAMS P M.
PA	(WOOD/) WOOD W I.
XX	Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI	Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
PI	Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
XX	WFI; 2002-171999/22.
DR	N-PDB; ABL95565.
PT	One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT	useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT	infarction), endothelial or angiogenic disorders in a mammal -
XX	
PS	Claim 11; Fig 50; 567pp; English.
XX	
CC	The present invention provides the protein and coding sequences of human
CC	PRO proteins. These are useful for treating or diagnosing a
CC	cardiovascular, endothelial or angiogenic disorder, including cardiac
CC	hypertrophy, trauma, cancer, age-related macular degeneration,
CC	atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC	angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumor
CC	healing. The present sequence is a PRO protein of the invention.
XX	
SQ	Sequence 350 AA;
	Query Match 100.0%; Score 1880; DB 23; Length 350;
	Best Local Similarity 100.0%; Pred. No. 6,5e-149;
	Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 MGRIGATLILCLIAAAVPTAPAPAPATATSAIPVKFGPALSYPOEBALINEMFREVEIMED 60
DB	1 MORLTGLTLLCLLIAAVPTAPAPATATSAIPVKFGPALSYPOEBALINEMFREVEIMED 60
QY	61 TORKLSAAYEWEAEBAAKASSEYNLANLPYSYHNENETDTKYGNNTIHVHEIKITN 120
DB	61 TORKLSAAYEWEAEBAAKASSEYNLANLPYSYHNENETDTKYGNNTIHVHEIKITN 120
QY	121 NOTGVWFSEVTIVTSVGDEGRSRSECTIIDDCGFSMYCQFASFQYTQPCRCQRMLCTR 180
DB	121 NOTGVWFSEVTIVTSVGDEGRSRSECTIIDDCGFSMYCQFASFQYTQPCRCQRMLCTR 180
QY	181 DSCCGCDQLCWCHCKKATRGNSNGTICDNORDCPGLCAFORGLFPVCTPLPYEGEL 240
DB	181 DSECCGGQLCWCHCKKATRGNSNGTICDNORDCPGLCAFORGLFPVCTPLPYEGEL 240
QY	241 CHDPASRLIDLITWLEPDPDALDRPCASGLLCQPHSHSLVYVKKPTFVSRRDDGEILL 300
DB	241 CHDPASRLIDLITWLEPDPDALDRPCASGLLCQPHSHSLVYVKKPTFVSRRDDGEILL 300
QY	301 PREVPDEVGVGSFMEEVRQLEDLRSLTEEWALGFAPAAAAALLGGEI 350

```

Db      301 PREPDEYEVGFMEYRQLEEDLERSTFEMALGEPAAAAALLGGEEL 350

RESULT 9
ID      ABB90735
XX      ABB90735 standard; Protein; 350 AA.
AC      ABB90735;
XX      30-MAY-2002 (first entry)
DE      Human Tumour Endothelial Marker polypeptide SEQ ID NO 202.
XX      Human Tumour Endothelial Marker polypeptide SEQ ID NO 202.
XX      Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
XX      normal endothelial marker; pan-endothelial marker; immunostimulant;
XX      antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
XX      polyarthritis; kidney disease; diabetes; retinopathy; rheumatoid arthritis;
XX      polyarthritis.
XX      Homo sapiens.
OS      Homo sapiens.
XX      WO200210217-A2.
XX      07-FEB-2002.
XX      01-AUG-2001; 2001WO-US24031.
XX      02-AUG-2000; 2000US-222599P.
XX      11-AUG-2000; 2000US-224360P.
XX      11-APR-2001; 2001US-282850P.
XX      (UYUO ) UNIV JOHNS HOPKINS.
XX      St Croix B, Kinzler KM, Vogelstein B;
XX      WPI; 2002-291856/33.
XX      N-PSDB; ABL92089.
XX      An isolated molecule comprising an antibody variable region which
XX      specifically binds to an extracellular domain of a tumor endothelial
XX      marker (TEM) protein, useful for inhibiting tumor growth -
XX      Claim 54; Page 156-157; 31pp; English.
XX      The invention relates to an isolated molecule comprising an antibody
XX      variable region which specifically binds to an extracellular domain of a
XX      tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
XX      ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
XX      proteins have cytostatic, immunostimulant and antiangiogenic activity.
XX      They are useful for inhibiting tumour growth, neoangiogenesis in
XX      subjects bearing a vascularised tumour, polycystic kidney disease,
XX      diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
XX      and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
XX      ABB90721-ABB90789) are disclosed, as are marker oligonucleotide and
XX      sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
XX      ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
XX      and pan-endothelial markers (PEM) ABL91903-ABL91995.
XX      Sequence 350 AA;
XX      Query Match 100.0%; Score 1880; DB 23; Length 350;
XX      Best Local Similarity 100.0%; Pred. No. 6,5e-149; Indels 0; Gaps 0;
XX      Matches 350; Conservative 0; Mismatches 0;
QY      1 MORIGATTCCTLAAVPTAPAPATATSAVPGKGPALSYQCEATINEMPREVEELMED 60
DB      1 MORIGATTCCTLAAVPTAPAPATATSAVPGKGPALSYQCEATINEMPREVEELMED 60
QY      61 TOHKLRSAVEEMEAEEAAKASSEVNLANIPPSYHNETNTDTKYGNNTIYHREIHKITN 120
DB      61 TOHKLRSAVEEMEAEEAAKASSEVNLANIPPSYHNETNTDTKYGNNTIYHREIHKITN 120

```



QY 121 NOTGQWVSEFVITVSVDDEGRSHCEITIDEDCGPSMYCQFASFOYTCQPCRGQMLCTR 180  
 Db 121 NOTGQWVSEFVITVSVDDEGRSHCEITIDEDCGPSMYCQFASFOYTCQPCRGQMLCTR 180  
 QY 181 DSECCGDLQVWGHCCTKATRGNSGTICNORDCQPGGLCAFGGLFPVCTPLPVEGEL 240  
 Db 181 DSECCGDLQVWGHCCTKATRGNSGTICNORDCQPGGLCAFGGLFPVCTPLPVEGEL 240  
 QY 241 CHDPASRLDLITWLEPDGALDRCPASGLLCPHSHSLVYVCKPTFVGSRDQGEILL 300  
 Db 241 CHDPASRLDLITWLEPDGALDRCPASGLLCPHSHSLVYVCKPTFVGSRDQGEILL 300  
 QY 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350  
 Db 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350

## RESULT 10

AB84841  
 ID ABB84841 standard, Protein, 350 AA.

AC ABB84841;  
 XX

DT 16-MAY-2002 (first entry)  
 XX

DE Human PRO295 protein sequence SEQ ID NO:50.  
 XX

Human, angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
 KM vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KM gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KM angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KM age-related macular degeneration; arterial restenosis; angina;  
 KM rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KM lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KM wound healing; chromosome mapping; gene mapping.

XX Homo sapiens.  
 OS

PN WO200200690-A2.  
 XX

PD 03-JAN-2002.  
 XX

PF 20-JUN-2001; 2001WO-US19692.  
 XX

PR 23-JUN-2000; 2000US-213637P.  
 XX

PR 20-JUL-2000; 2000US-219556P.  
 XX

PR 25-JUL-2000; 2000US-220624P.  
 XX

PR 28-JUL-2000; 2000US-220644P.  
 XX

PR 02-AUG-2000; 2000US-222695P.  
 XX

PR 17-AUG-2000; 2000US-0643657.  
 XX

PR 23-AUG-2000; 2000WO-US23522.  
 XX

PR 24-AUG-2000; 2000US-230978P.  
 XX

PR 07-SEP-2000; 2000US-230978P.  
 XX

PR 18-SEP-2000; 2000US-0644610.  
 XX

PR 18-SEP-2000; 2000US-0663550.  
 XX

PR 24-OCT-2000; 2000US-242922P.  
 XX

PR 08-NOV-2000; 2000US-0709238.  
 XX

PR 08-NOV-2000; 2000WO-US30952.  
 XX

PR 10-NOV-2000; 2000WO-US30952.  
 XX

PR 01-DEC-2000; 2000WO-US32678.  
 XX

PR 20-DEC-2000; 2000US-0747259.  
 XX

PR 20-DEC-2000; 2000WO-US34956.  
 XX

PR 22-JAN-2001; 2001US-0767609.  
 XX

PR 28-FEB-2001; 2001US-0796498.  
 XX

PR 01-MAR-2001; 2001WO-US06520.  
 XX

PR 09-MAR-2001; 2001US-0802706.  
 XX

PR 14-MAR-2001; 2001US-0808489.  
 XX

PR 22-MAR-2001; 2001US-0816744.  
 XX

PR 05-APR-2001; 2001US-0828366.  
 XX

PR 10-MAY-2001; 2001US-0854208.  
 XX

PR 10-MAY-2001; 2001US-0854280.  
 XX

PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.

XX (GENTH) GENENTECH INC.  
 PA

XX Baker KP, Ferrara N, Gerber H, Gertzen ME, Goddard A, Goddard PJ, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephens JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 PI

XX WPI; 2002-090516/12.  
 XX

DR N-PSDB; ABL88096.  
 XX

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 11, Fig 50; 565pp; English.  
 XX

XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 XX ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
 CC antiangiogenic, hypotensive, vulnerable and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
 CC carcinoma) and wound healing. The PRO polynucleotides have applications  
 CC in molecular biology, including use as hybridisation probes, and in  
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
 CC probes used in the exemplification of the present invention.  
 XX

Sequence 350 AA;  
 SQ  
 Query Match 100.0%; Score 1880; DB 23; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-149;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORIGATILCLILAAVPTAPAPPTATSAVYKGPALSTPOEBATINEMFREVEIMED 60  
 Db 1 MORIGATILCLILAAVPTAPAPPTATSAVYKGPALSTPOEBATINEMFREVEIMED 60

QY 61 TOHKLRSVEMEEMAEAAKASSEVNLANLPSSYHNETNDITKGNNTIHVREIHKITT 120  
 Db 61 TOHKLRSVEMEEMAEAAKASSEVNLANLPSSYHNETNDITKGNNTIHVREIHKITT 120

QY 121 NOTGQWVSEFVITVSVDDEGRSHCEITIDEDCGPSMYCQFASFOYTCQPCRGQMLCTR 180  
 Db 121 NOTGQWVSEFVITVSVDDEGRSHCEITIDEDCGPSMYCQFASFOYTCQPCRGQMLCTR 180

QY 121 NOTGQWVSEFVITVSVDDEGRSHCEITIDEDCGPSMYCQFASFOYTCQPCRGQMLCTR 180  
 Db 121 NOTGQWVSEFVITVSVDDEGRSHCEITIDEDCGPSMYCQFASFOYTCQPCRGQMLCTR 180

QY 181 DSECCGDLQVWGHCCTKATRGNSGTICNORDCQPGGLCAFGGLFPVCTPLPVEGEL 240  
 Db 181 DSECCGDLQVWGHCCTKATRGNSGTICNORDCQPGGLCAFGGLFPVCTPLPVEGEL 240

QY 241 CHDPASRLDLITWLEPDGALDRCPASGLLCPHSHSLVYVCKPTFVGSRDQGEILL 300  
 Db 241 CHDPASRLDLITWLEPDGALDRCPASGLLCPHSHSLVYVCKPTFVGSRDQGEILL 300

QY 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350  
 Db 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350

QY 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350  
 Db 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350

QY 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350  
 Db 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350

QY 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350  
 Db 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350

QY 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350  
 Db 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350

QY 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350  
 Db 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350

QY 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350  
 Db 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350

QY 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350  
 Db 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350

QY 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350  
 Db 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350

QY 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350  
 Db 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350

QY 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350  
 Db 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350

QY 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350  
 Db 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350

QY 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350  
 Db 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350

QY 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350  
 Db 301 PREVPDEYVGSFMEVRQLEDLERSLTETMALGEPAAAAALLGGEET 350

XX 05-JUN-2003 (first entry)  
 XX Novel human secreted and transmembrane protein PRO295.  
 XX  
 KM Human, secreted and transmembrane protein; gene therapy; psoriasis;  
 KM enterocolitis; gastrointestinal ulceration; skin disease;  
 KM keratinocyte differentiation; epithelial cancer; Alzheimer's disease;  
 KM squamous cell carcinoma; Parkinson's disease; inflammatory disease;  
 KM amyotrophic lateral sclerosis; rheumatoid arthritis; asthma;  
 KM multiple sclerosis; organ failure; atherosclerosis; cardiac injury;  
 KM infertility; birth defect; premature aging; AIDS; cancer;  
 KM diabetic complication; wound repair; tissue re-growth.  
 OS Homo sapiens.  
 XX US2003017463-A1.  
 XX  
 PD 23-JAN-2003.  
 XX  
 PF 11-JUL-2001; 2001US-0903640.  
 XX  
 XX 10-SEP-1998; 98WO-US18824.  
 PR 14-SEP-1998; 98WO-US19177.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 06-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 11-FEB-2000; 2000WO-US03555.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 02-MAY-2000; 2000WO-US14042.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 17-SEP-1997; 97US-059113P.  
 PR 17-SEP-1997; 97US-059115P.  
 PR 17-SEP-1997; 97US-059117P.  
 PR 17-SEP-1997; 97US-059119P.  
 PR 17-SEP-1997; 97US-059121P.  
 PR 17-SEP-1997; 97US-059122P.  
 PR 17-SEP-1997; 97US-059124P.  
 PR 17-SEP-1997; 97US-059126P.  
 PR 18-SEP-1997; 97US-059263P.  
 PR 15-OCT-1997; 97US-062125P.  
 PR 17-OCT-1997; 97US-062285P.  
 PR 17-OCT-1997; 97US-062287P.  
 PR 21-OCT-1997; 97US-063486P.  
 PR 24-OCT-1997; 97US-062814P.  
 PR 24-OCT-1997; 97US-062816P.  
 PR 24-OCT-1997; 97US-063045P.  
 PR 24-OCT-1997; 97US-063120P.  
 PR 24-OCT-1997; 97US-063127P.  
 PR 24-OCT-1997; 97US-063128P.  
 PR 27-OCT-1997; 97US-063327P.  
 PR 27-OCT-1997; 97US-063329P.

PR 28-OCT-1997; 97US-063541P.  
 PR 28-OCT-1997; 97US-063542P.  
 PR 28-OCT-1997; 97US-063544P.  
 PR 28-OCT-1997; 97US-063549P.  
 PR 28-OCT-1997; 97US-063550P.  
 PR 28-OCT-1997; 97US-063564P.  
 PR 29-OCT-1997; 97US-063335P.  
 PR 29-OCT-1997; 97US-063704P.  
 PR 29-OCT-1997; 97US-063732P.  
 PR 29-OCT-1997; 97US-063734P.  
 PR 29-OCT-1997; 97US-063735P.  
 PR 29-OCT-1997; 97US-063738P.  
 PR 29-OCT-1997; 97US-064215P.  
 PR 31-OCT-1997; 97US-063870P.  
 PR 31-OCT-1997; 97US-064103P.  
 PR 03-NOV-1997; 97US-064248P.  
 PR 07-NOV-1997; 97US-064809P.  
 PR 12-NOV-1997; 97US-065186P.  
 PR 17-NOV-1997; 97US-065846P.  
 PR 18-NOV-1997; 97US-065693P.  
 PR 21-NOV-1997; 97US-066120P.  
 PR 21-NOV-1997; 97US-066364P.  
 PR 24-NOV-1997; 97US-066453P.  
 PR 24-NOV-1997; 97US-066466P.  
 PR 24-NOV-1997; 97US-066511P.  
 PR 24-NOV-1997; 97US-066770P.  
 PR 25-NOV-1997; 97US-066772P.  
 PR 25-NOV-1997; 97US-066840P.  
 PR 12-DEC-1997; 97US-069425P.  
 PR 04-JUN-1998; 98US-088026P.  
 PR 10-SEP-1998; 98US-099603P.  
 PR 14-SEP-1998; 98US-100262P.  
 PR 17-SEP-1998; 98US-100858P.  
 PR 13-OCT-1998; 98US-104080P.  
 PR 20-NOV-1998; 98US-109304P.  
 PR 22-DEC-1998; 98US-113296P.  
 PR 07-JUL-1999; 99US-143048P.  
 PR 26-JUL-1999; 99US-145698P.  
 PR 28-JUL-1999; 99US-146222P.  
 PR 18-SEP-2000; 2000US-0665350.  
 XX  
 PA (GENT ) GENENTECH INC.  
 XX  
 PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
 PI Filvarski E, Fong S, Gao W, Gerber H, Gerritsen WE, Goddard A;  
 PI Gadowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavlin IJ;  
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WI;  
 XX  
 DR WPI, 2003-341586/32.  
 DR N-PSDB; ACAS5002.  
 XX  
 PT New PRO polypeptides and nucleic acid molecules, useful in diagnosing  
 PT or treating inflammatory diseases, organ failure, atherosclerosis,  
 PT cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or  
 PT Parkinson's disease -  
 XX  
 PS Claim 12; Fig 84; 473pp; English.  
 XX  
 CC The invention describes sixty one nucleic acids encoding PRO polypeptides  
 CC (secreted and transmembrane). The PRO polypeptides and nucleic acids are  
 CC useful in diagnosing or treating enterocolitis, gastrointestinal  
 CC ulceration, skin diseases associated with abnormal keratinocyte  
 CC differentiation, e.g. psoriasis or epithelial cancers such as squamous  
 CC cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic  
 CC lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis,  
 CC asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac  
 CC injury, infertility, birth defects, premature aging, AIDS, cancer,  
 CC diabetic complications, or mutations in general. The polypeptides are  
 CC also useful for wound repair and associated therapies concerned with  
 CC re-growth of tissue. The PRO polypeptides and nucleic acid molecules  
 CC are also useful in gene therapy, and as molecular weight markers for  
 CC protein electrophoresis purposes. The anti-PRO antibodies may be used



QY 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEEI 350  
 DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEEI 350

## RESULT 13

ID ABU71509 standard; Protein; 350 AA.

AC ABU71509;

DT 10-JUN-2003 (first entry)

DE Human secreted polypeptide PRO295.

KW Human; gene therapy; tumour; cancer.

OS Homo sapiens.

PN US2003013855-A1.

PD 16-JAN-2003.

PF 03-MAY-2002; 2002US-0063616.

PR 30-DEC-1999; 98KR-0062142.

PR 08-MAR-1999; 99MO-US05028.

PR 14-MAY-1999; 99MO-US10733.

PR 30-DEC-1999; 99MO-US11274.

PR 18-FEB-2000; 2000MO-US04341.

PR 01-MAR-2000; 2000MO-US05601.

PR 02-MAR-2000; 2000MO-US05841.

PR 21-MAR-2000; 2000MO-US07532.

PR 22-MAY-2000; 2000MO-US14042.

PR 02-JUN-2000; 2000MO-US15264.

PR 24-AUG-2000; 2000MO-US23328.

PR 10-NOV-2000; 2000MO-US30873.

PR 01-DEC-2000; 2000MO-US32678.

PR 20-DEC-2000; 2000MO-US34956.

PR 28-FEB-2001; 2001MO-US06520.

PR 01-JUN-2001; 2001MO-US11780.

PR 14-MAY-1999; 99US-0311832.

PR 25-AUG-1999; 99US-0380137.

PR 25-AUG-1999; 99US-0380138.

PR 25-AUG-1999; 99US-0380139.

PR 15-SEP-1999; 99US-0380142.

PR 18-OCT-1999; 99US-0403297.

PR 12-NOV-1999; 99US-0423844.

PR 22-AUG-2000; 2000US-0644848.

PR 18-SEP-2000; 2000US-064610.

PR 18-SEP-2000; 2000US-0665350.

PR 08-NOV-2000; 2000US-0709238.

PR 20-DEC-2000; 2000US-0747259.

PR 22-MAR-2001; 2001US-0816744.

PR 10-MAY-2001; 2001US-0854208.

PR 10-MAY-2001; 2001US-0854280.

PR 30-MAY-2001; 2001US-0870574.

PR 05-JUN-2001; 2001US-0874503.

PR 29-JUN-2001; 2001US-0869599.

PR 18-JUL-2001; 2001US-0908827.

PR 06-DEC-2001; 2001US-0006867.

PA (GETH ) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,

PI Grimaldi JC, Gurney AL, Matarane CX, Wood WI,

XX WPI; 2003-330485/31.

DR N-PSDB; ACAS8613.

XX New isolated antibody specifically binding a PRO polypeptide; useful

PT for the preparation of a medicament for treating disorders with the

PT aberrant expression or activity of the PRO polypeptide, such as tumor  
 PT conditions and cancer -  
 XX  
 PS Example 17; Page 73; 406pp; English.

CC The invention relates to an antibody that binds to a polypeptide with a  
 CC fully defined sequence given in the specification. The methods and  
 CC compositions (containing antibodies that specifically bind a PRO  
 CC polypeptide) of the present invention are useful for the preparation of a  
 CC medicament for the treatment of disorders associated with the aberrant  
 CC expression or activity of the PRO polypeptide, such as tumor conditions  
 CC and cancer. They can also be used to generate transgenic or knockout  
 CC animals useful in the development and screening of therapeutically useful  
 CC reagents. The PRO polypeptides and encoding nucleic acids can be used as  
 CC molecular weight markers for protein electrophoresis, chromosome  
 CC identification and tissue typing. The PRO polypeptides are useful to  
 CC induce angiogenesis e.g wound healing; in the treatment of sports-related  
 CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid  
 CC arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The  
 CC antibodies may be used in various diagnostic, competitive binding and/or  
 CC immunoprecipitation assays. The present sequence represents the amino  
 CC acid sequence of a PRO polypeptide of the invention.

CC Sequence 350 AA;

Query Match 100.0%; Score 1880; DB 24; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 6, 5e-149;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORGATLLCLLLAAVPTAPAPATSAVKGPAALSTPOEATLNEMFREVEELMED 60

DB 1 MORGATLLCLLLAAVPTAPAPATSAVKGPAALSTPOEATLNEMFREVEELMED 60

QY 61 TQHLKRSVEMEAEAAKASSEVNLANLPSSYHNETNDTKYNNNTIHYRRIHKITN 120

DB 61 TQHLKRSVEMEAEAAKASSEVNLANLPSSYHNETNDTKYNNNTIHYRRIHKITN 120

QY 121 NOTQMWSEETVITSVDEBGRSHCEIIDDCGPMYCFASFQYTCQPCRGRLCTR 180

DB 121 NOTQMWSEETVITSVDEBGRSHCEIIDDCGPMYCFASFQYTCQPCRGRLCTR 180

QY 121 NOTQMWSEETVITSVDEBGRSHCEIIDDCGPMYCFASFQYTCQPCRGRLCTR 180

DB 121 NOTQMWSEETVITSVDEBGRSHCEIIDDCGPMYCFASFQYTCQPCRGRLCTR 180

QY 181 DSECCGDLCTWGHCTKATGNSGTICDNORDCPGLCAFGGLLPVCTPLPVEGEL 240

DB 181 DSECCGDLCTWGHCTKATGNSGTICDNORDCPGLCAFGGLLPVCTPLPVEGEL 240

QY 241 CHDPASRLDLITTELEBDGALDRCPASGLCCPHSHSLVYVCKPTFVSGRDGDGELL 300

DB 241 CHDPASRLDLITTELEBDGALDRCPASGLCCPHSHSLVYVCKPTFVSGRDGDGELL 300

QY 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEEI 350

DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEEI 350

DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEEI 350

DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEEI 350

DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEEI 350

DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEEI 350

DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEEI 350

DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEEI 350

DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEEI 350

DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEEI 350

DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEEI 350

DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEEI 350

DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEEI 350

DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEEI 350

PR 11-JUL-2001; 2001US-0904011.  
 XX 10-SEP-1998; 98WO-US18824.  
 PR 14-SEP-1998; 98WO-US19177.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 08-SEP-1999; 98WO-US20594.  
 PR 13-SEP-1999; 98WO-US20944.  
 PR 15-SEP-1999; 98WO-US21090.  
 PR 15-SEP-1999; 98WO-US21547.  
 PR 05-OCT-1999; 98WO-US23089.  
 PR 29-NOV-1999; 98WO-US28213.  
 PR 30-NOV-1999; 98WO-US28313.  
 PR 01-DEC-1999; 98WO-US28301.  
 PR 02-DEC-1999; 98WO-US28564.  
 PR 02-DEC-1999; 98WO-US28565.  
 PR 16-DEC-1999; 98WO-US30095.  
 PR 20-DEC-1999; 98WO-US30911.  
 PR 20-DEC-1999; 98WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 22-MAY-2000; 2000WO-US10442.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 17-SEP-1997; 97US-059113P.  
 PR 17-SEP-1997; 97US-059115P.  
 PR 17-SEP-1997; 97US-059117P.  
 PR 17-SEP-1997; 97US-059119P.  
 PR 17-SEP-1997; 97US-059121P.  
 PR 17-SEP-1997; 97US-059122P.  
 PR 17-SEP-1997; 97US-059124P.  
 PR 18-SEP-1997; 97US-059263P.  
 PR 18-SEP-1997; 97US-059266P.  
 PR 15-OCT-1997; 97US-062125P.  
 PR 17-OCT-1997; 97US-062285P.  
 PR 17-OCT-1997; 97US-062287P.  
 PR 21-OCT-1997; 97US-063486P.  
 PR 24-OCT-1997; 97US-062814P.  
 PR 24-OCT-1997; 97US-062816P.  
 PR 24-OCT-1997; 97US-063104P.  
 PR 24-OCT-1997; 97US-063120P.  
 PR 24-OCT-1997; 97US-063121P.  
 PR 24-OCT-1997; 97US-063127P.  
 PR 24-OCT-1997; 97US-063128P.  
 PR 27-OCT-1997; 97US-063327P.  
 PR 27-OCT-1997; 97US-063329P.  
 PR 28-OCT-1997; 97US-063541P.  
 PR 28-OCT-1997; 97US-063542P.  
 PR 28-OCT-1997; 97US-063544P.  
 PR 28-OCT-1997; 97US-063549P.  
 PR 28-OCT-1997; 97US-063550P.  
 PR 28-OCT-1997; 97US-063556P.  
 PR 29-OCT-1997; 97US-063435P.  
 PR 29-OCT-1997; 97US-063704P.  
 PR 29-OCT-1997; 97US-063722P.  
 PR 29-OCT-1997; 97US-063734P.  
 PR 29-OCT-1997; 97US-063735P.  
 PR 29-OCT-1997; 97US-063738P.  
 PR 29-OCT-1997; 97US-064215P.  
 PR 31-OCT-1997; 97US-063870P.  
 PR 31-OCT-1997; 97US-064103P.  
 PR 03-NOV-1997; 97US-064248P.  
 PR 07-NOV-1997; 97US-064809P.  
 PR 12-NOV-1997; 97US-065186P.  
 PR 17-NOV-1997; 97US-065846P.  
 PR 18-NOV-1997; 97US-065633P.

PR 21-NOV-1997; 97US-066120P.  
 PR 21-NOV-1997; 97US-066354P.  
 PR 24-NOV-1997; 97US-066453P.  
 PR 24-NOV-1997; 97US-066466P.  
 PR 24-NOV-1997; 97US-066511P.  
 PR 24-NOV-1997; 97US-066770P.  
 PR 24-NOV-1997; 97US-066772P.  
 PR 18-SEP-2000; 2000US-0665350.  
 XX (GETH ) GENENTECH INC.  
 XX Asikenzai A, Botstein D, Desnuyers L, Eaton DL, Ferrara N;  
 PI Filvaroff E, Fong S, Gao W, Geider H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavlin ID;  
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WI;  
 XX WPI; 2003-329602/31.  
 DR N-PSDB; ACA60194.  
 XX New transmembrane polypeptides and nucleic acids encoding the  
 PT polypeptides, useful in gene therapy, in chromosome identification, as  
 PT chromosome markers, in generating probes and in tissue typing -  
 XX Claim 12; Fig 84; 484pp; English.  
 XX The invention relates to an isolated nucleic acid with at least 80%  
 CC nucleic acid sequence identity to a nucleotide sequence encoding one of  
 CC 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a  
 CC PRO protein extracellular domain. Also included are a vector comprising  
 CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO  
 CC polypeptide (by culturing the host cell for the expression of the PRO  
 CC polypeptide, and recovering the PRO polypeptide from the cell culture),  
 CC an isolated PRO polypeptide (having at least 80% sequence identity  
 CC to: (a) an amino acid sequence selected from the 61 PRO proteins;  
 CC (b) an amino acid sequence encoded by a nucleic acid molecule deposited  
 CC with an ATCC number (detailed in the specification); or (c) an  
 CC extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking  
 CC its associated signal peptide), a chimeric molecule comprising a PRO  
 CC polypeptide of fused to a heterologous amino acid sequence, an anti-PRO  
 CC antibody, detecting a PRO245 or PRO186 in a sample suspected of  
 CC containing the polypeptide, linking a bioactive molecule to a cell  
 CC expressing a PRO245 or PRO186 and modulating at least one biological  
 CC activity of a cell expressing a PRO245 or PRO186. Nucleic acids which  
 CC encode PRO can be used to generate either transgenic animals or knock-out  
 CC animals which may be used in the development and screening of  
 CC therapeutically useful reagents. The nucleic acids may also be used in  
 CC gene therapy, in chromosome identification, as chromosome markers, or in  
 CC generating probes. The PRO polypeptides are useful as molecular markers  
 CC for protein electrophoresis, and the isolated nucleic acids may be used  
 CC for recombinantly expressing those markers. The PRO polypeptides and  
 CC nucleic acids may also be used in tissue typing. Anti-PRO antibodies  
 CC are useful in diagnostic assays for PRO, and in affinity purification  
 CC of PRO from recombinant cell culture or natural sources. The  
 CC present sequence represents a PRO protein.  
 XX  
 SQ Sequence 350 AA;  
 Query Match 100.0%; Score 1880; DB 24; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 6; 5e-149;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MORGATLILCLIAAAYTAPAPATPATSAPKGPALSTPOEBALTNMFREVEELMED 60  
 DB 1 MORGATLILCLIAAAYTAPAPATPATSAPKGPALSTPOEBALTNMFREVEELMED 60  
 QY 61 TQHLRSVAVEMEAEBAKASSEVNLNLPSPSYHNETNTDTKGNNTIIVHREIKITN 120  
 DB 61 TQHLRSVAVEMEAEBAKASSEVNLNLPSPSYHNETNTDTKGNNTIIVHREIKITN 120  
 QY 121 NOTGQWFSSETVITSVDEGRSRSHCEIIDDCGSPSYCQFASFOYTQPCRGQRMLCTR 180  
 DB 121 NOTGQWFSSETVITSVDEGRSRSHCEIIDDCGSPSYCQFASFOYTQPCRGQRMLCTR 180

QY 181 DSECCGDLQVWGHCTKMATRSGNGTICDNQRCQPGILCCAFQRLFPVCTPLPVEGEL 240  
 DB 181 DSECCGDLQVWGHCTKMATRSGNGTICDNQRCQPGILCCAFQRLFPVCTPLPVEGEL 240  
 QY 241 CHDPASRLDLITWELBPDGALDRCPGASGLLCPHSHSLVYCKPTFVGSRRDQDEILL 300  
 DB 241 CHDPASRLDLITWELBPDGALDRCPGASGLLCPHSHSLVYCKPTFVGSRRDQDEILL 300  
 QY 301 PREVPDEYEVGSFMEYVRQELDLERSLITEMALGEPAAAAALLGGEI 350  
 DB 301 PREVPDEYEVGSFMEYVRQELDLERSLITEMALGEPAAAAALLGGEI 350  
 RESULT 15  
 ABU71955 standard, Protein, 350 AA.  
 ID ABU71955  
 AC ABU71955;  
 XX 11-JUN-2003 (first entry)  
 DE Novel human secreted and transmembrane protein PRO295.  
 XX  
 XX Human; secreted and transmembrane polypeptide;  
 XX chromosome mapping; gene mapping; transgenic animal; knockout animal;  
 XX therapeutic agent screening; chromosome identification; tissue typing;  
 XX gene therapy.  
 XX Homo sapiens.  
 OS  
 XX  
 XX US2003018183-A1.  
 PN 23-JAN-2003.  
 PD  
 XX  
 XX 01-MAY-2002; 2002US-0063512.  
 PF  
 XX  
 XX 06-DEC-2001; 2001US-0006867.  
 PR  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX  
 XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
 XX WPI; 2003-330984/31.  
 DR N-PSDB; ACA60366.  
 XX  
 XX New secreted and transmembrane PRO polypeptides and nucleic acid  
 PT molecules encoding the polypeptides, useful in gene therapy or  
 PT preparing a medicament for treating a condition that is responsive to  
 PT the PRO polypeptide or antibody -  
 PS  
 PS Claim 1; Fig 8; 409pp; English.  
 XX  
 XX The invention describes novel isolated PRO polypeptides. The PRO  
 CC polypeptides or anti-PRO antibodies are useful in preparing a medicament  
 CC for treating a condition that is responsive to the PRO polypeptide or  
 CC antibody. The PRO nucleotide sequences may be used as hybridisation  
 CC probes in chromosome and gene mapping, or in generating antisense RNA  
 CC and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,  
 CC in assays to identify other proteins or molecules involved in binding  
 CC reaction, to generate transgenic animals or knockout animals, which in  
 CC turn are useful in the development and screening of therapeutically  
 CC useful reagents, for chromosome identification, and tissue typing. The  
 CC PRO polypeptides and nucleic acid molecules are also useful in gene  
 CC therapy, and as molecular weight markers for protein electrophoresis  
 CC purposes. The anti-PRO antibodies may be used in diagnostic assays for  
 CC PRO, or for the affinity purification of PRO from recombinant cell  
 CC culture or natural sources. This is the amino acid sequence of a novel  
 CC human secreted and transmembrane PRO polypeptide.  
 XX  
 XX Sequence 350 AA;  
 SQ

Query Match 100.0%; Score 1880; DB 24; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 6, se-149;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MORIGATLTCILLAAVPTAPAPATSAVPKPGPALSYQEEATINEMREYEEIMED 60  
 DB 1 MORIGATLTCILLAAVPTAPAPATSAVPKPGPALSYQEEATINEMREYEEIMED 60  
 QY 61 TOHKLRSAVEEMEAEEAAKASSSVNLANLPPSYHNETNTDTKVGNNTIHVREIHKITN 120  
 DB 61 TOHKLRSAVEEMEAEEAAKASSSVNLANLPPSYHNETNTDTKVGNNTIHVREIHKITN 120  
 QY 121 NOTGQWFSSETVITSVGDEGRSHCECTIDEDCGPSMYCOPASFQYTCOPRGQRMCTR 180  
 DB 121 NOTGQWFSSETVITSVGDEGRSHCECTIDEDCGPSMYCOPASFQYTCOPRGQRMCTR 180  
 QY 181 DSECCGDLQVWGHCTKMATRSGNGTICDNQRCQPGILCCAFQRLFPVCTPLPVEGEL 240  
 DB 181 DSECCGDLQVWGHCTKMATRSGNGTICDNQRCQPGILCCAFQRLFPVCTPLPVEGEL 240  
 QY 241 CHDPASRLDLITWELBPDGALDRCPGASGLLCPHSHSLVYCKPTFVGSRRDQDEILL 300  
 DB 241 CHDPASRLDLITWELBPDGALDRCPGASGLLCPHSHSLVYCKPTFVGSRRDQDEILL 300  
 QY 301 PREVPDEYEVGSFMEYVRQELDLERSLITEMALGEPAAAAALLGGEI 350  
 DB 301 PREVPDEYEVGSFMEYVRQELDLERSLITEMALGEPAAAAALLGGEI 350

Search completed: February 20, 2004, 18:49:00  
 Job time : 79 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 20, 2004, 18:26:02 ; Search time 38 Seconds  
(without alignments)  
885.764 Million cell updates/sec

Title: US-10-063-671-8

Perfect score: 1880

Sequence: 1 MQRIGATLCLLLAAVPTA.....EMALGEPAAAAALLGSEI 350

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: p1r1:\*
- 2: p1r2:\*
- 3: p1r3:\*
- 4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1873	99.6	350	2 UC7188	REIC protein - hum
2	138	7.3	577	2 B37057	integrin beta-6 ch
3	131.5	7.0	676	1 KXHU5	plasma protein S p
4	128	6.8	1620	2 T27283	hypothetical prote
5	126	6.7	788	2 A37057	integrin beta-6 ch
6	126	6.7	1394	2 A35626	transforming growt
7	126	6.7	1748	1 UN0786	integrin beta-4 ch
8	123	6.5	1170	2 A53612	laminin B1X chain
9	119	6.3	2318	2 A43506	notch 3 protein -
10	117.5	6.2	996	2 JE0237	apolipoprotein B r
11	117	6.2	3712	2 S18253	laminin alpha-1 ch
12	116	6.2	788	2 I51530	integrin beta-3 su
13	116	6.2	1251	2 A57293	latent transformin
14	116	6.2	2135	2 A35672	crumbs protein - f
15	115	6.1	1807	2 UC6319	integrin beta-4 ch
16	113	6.0	3562	2 A47171	chondroitin sulfat
17	111.5	5.9	1188	2 D86236	protein F1AN23.5 l
18	111.5	5.9	1820	2 A55494	latent transformin
19	110.5	5.9	293	2 B26637	neurogenic repetit
20	110.5	5.9	862	1 CRM5LD	IDL receptor precu
21	110	5.9	2524	2 A35844	notch protein - Af
22	109.5	5.8	656	2 UC2005	integrin beta-5 ch
23	109.5	5.8	799	2 A38308	integrin beta-5 ch
24	109.5	5.8	964	2 JCS545	integrin beta-4 pr
25	109.5	5.8	1712	2 A38261	masking protein pr
26	109.5	5.8	1875	2 A36429	integrin beta-4 ch
27	109.5	5.8	2531	2 T31070	notch homolog - se
28	109	5.8	1168	2 I56985	kalinin B1 - mouse
29	109	5.8	1348	2 S27812	probable epidermal

30	109	5.8	1574	2 T13954	MEGF6 protein - ra
31	108.5	5.8	852	2 A34373	histidine-rich cal
32	108.5	5.8	2195	2 T34264	hypothetical prote
33	108	5.7	1170	1 TSHU01	thrombospondin 1 p
34	108	5.7	2111	2 T15390	hypothetical prote
35	107	5.7	755	2 A44315	cartilage oligomer
36	106	5.6	227	1 LNRZ	lectin precursor -
37	106	5.6	1221	2 A49457	fibulin-2 precursor
38	106	5.6	2945	2 T15840	hypothetical prote
39	105.5	5.6	585	2 S43572	CO5B5.5 protein (c
40	105.5	5.6	585	2 B88571	protein CO5B5.5 (l
41	105.5	5.6	753	2 B36268	platelet glycoprot
42	105.5	5.6	778	2 A60798	platelet glycoprot
43	105.5	5.6	788	2 A26547	platelet glycoprot
44	105.5	5.6	788	2 I77349	platelet glycoprot
45	105.5	5.6	1469	2 B36655	salt protein 2 pre

ALIGNMENTS

RESULT 1	
UC7188	REIC protein - human
C/Species: Homo sapiens (man)	
C/Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000	
C/Accession: UC7188	
R/Tsugi, T.; Miyazaki, M.; Sakaguchi, M.; Inoue, Y.; Namba, M.	
Biochem. Biophys. Res. Commun. 268, 20-24, 2000	
A/Title: A REIC gene shows down-regulation in human immortalized cells and human tumor-de	
A/Reference number: UC7188; MUID:20119095; PMID:10652205	
A/Accession: UC7188	
A/Molecule type: mRNA	
A/Residues: 1-350 <TSU>	
A/Cross-references: DBJ:AB034203	
A/Experimental source: heart	
C/Comment: This protein is a secreted glycoprotein for head induction in amphibian embryo/	
C/Keywords: cardiac muscle; coiled coil; glycoprotein; heart; tumor	
A/Genes: reic	
C/Superfamily: human REIC protein	
C/Keywords: cardiac muscle; coiled coil; glycoprotein; heart; tumor	
Query Match	
Best Local Similarity 99.6%; Score 1873; DB 2; Length 350;	
Matches 349; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 MQRIGATLCLLLAAVPTAAPTATSAVYKGPALSYQEEATLNMREVEELMED 60
DB	1 MQRIGATLCLLLAAVPTAAPTATSAVYKGPALSYQEEATLNMREVEELMED 60
QY	61 TOHKRSAYEEMEAEEAAXKASSEVNLANLPSSYNENNTDTKYGNNTIHYHREIKITN 120
DB	61 TOHKRSAYEEMEAEEAAXKASSEVNLANLPSSYNENNTDTKYGNNTIHYHREIKITN 120
QY	121 NOTGQVSEFVITVSVDSEGRSHSECTIDDCGSMYQCPASFOYTQCPRGQMLCTR 180
DB	121 NOTGQVSEFVITVSVDSEGRSHSECTIDDCGSMYQCPASFOYTQCPRGQMLCTR 180
QY	122 NOTGQVSEFVITVSVDSEGRSHSECTIDDCGSMYQCPASFOYTQCPRGQMLCTR 180
DB	122 NOTGQVSEFVITVSVDSEGRSHSECTIDDCGSMYQCPASFOYTQCPRGQMLCTR 180
QY	181 DSECCGDLQVWGHCCTKATGNSNGTICDNORDCOPGACGAFORGLFPVCTPLPVEGEL 240
DB	181 DSECCGDLQVWGHCCTKATGNSNGTICDNORDCOPGACGAFORGLFPVCTPLPVEGEL 240
QY	241 CHDPASRLDLITWELPFDGALDRCPGASGLICOPHSHLYVYCKPTFVGRDQGEILL 300
DB	241 CHDPASRLDLITWELPFDGALDRCPGASGLICOPHSHLYVYCKPTFVGRDQGEILL 300
QY	301 PREVPDEYVGSFMEVEVQELDLERSLTTEMALGEPAAAAALLGSEI 350
DB	301 PREVPDEYVGSFMEVEVQELDLERSLTTEMALGEPAAAAALLGSEI 350
RESULT 2	
B37057	

A: Molecule type: mRNA  
A: Residues: 27-220, 'L', 222-262, 'H', 264-344, 'Y', 346-676 <LUND>  
A: Cross-references: GB:MIJ38; NID:9190449; PID:9190449  
A: Note: part of this sequence, including the amino end of the mature protein, was detected  
R: Benmrad, C.M., Lundell, A., Wyder, R., Stefflo, J.  
Biochemistry 29, 7861-7868, 1990  
A: Title: Molecular analysis of the gene for vitamin K dependent protein S and its pseudoc  
A: Reference number: A35612; MUID:91084446; PMID:214912  
A: Accession: A35612  
A: Status: not compared with conceptual translation  
A: Molecule type: DNA  
A: Residues: 284-676 <EDE>  
A: Cross-references: GB:J02919  
R: Ploos van Amstel, J.K., van der Zanden, A.L., Bakker, E., Reitsma, P.H., Bertina, R.M.  
Thromb. Haemost. 58, 962-987, 1987  
A: Title: Two genes homologous with human protein S cDNA are located on chromosome 3.  
A: Reference number: A60903; MUID:88178564; PMID:2895503  
A: Accession: A60903  
A: Molecule type: mRNA  
A: Residues: 351-676 <PRO>  
R: Ploos van Amstel, H.K., van der Zanden, A.L., Reitsma, P.H., Bertina, R.M.  
FEBS Lett. 222, 186-190, 1987  
A: Title: Human protein S cDNA encodes Phe-16 and Tyr 222 in consensus sequences for the  
A: Reference number: S02424; MUID:88005138; PMID:2820795  
A: Accession: S02424  
A: Molecule type: mRNA  
A: Residues: 1-676 <PL2>  
A: Cross-references: EMBL:X00692; NID:g36578; PID:CA66687.1; PID:g36579  
C: Genetics:  
A: Gene: GDB:PROS1, PROS  
A: Cross-references: GDB:120721; OMIM:176880  
A: Map position: 3p11.1-3p11.2  
A: Introns: 26/1; 78/3; 87/1; 116/1; 157/1; 201/1; 243/1; 283/3; 322/2; 385/3; 441/3; 498/  
C: Complex: in plasma forms a complex with C4b binding protein  
C: Function:  
A: Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage destr  
C: Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat homol  
C: Keywords: beta-hydroxyaspartic; beta-hydroxyaspartic acid; blood coagulation; carboxy  
F: 1-24/Domain: signal sequence #status predicted <SIG>  
F: 25-41/Domain: propeptide #status predicted <PRO>  
F: 26-85/Domain: Gla domain homology <GLA>  
F: 42-676/Product: plasma protein S #status predicted <MNT>  
F: 121-154/Domain: EGF homology <EG1>  
F: 161-199/Domain: EGF homology <EG2>  
F: 205-241/Domain: EGF homology <EG3>  
F: 247-282/Domain: EGF homology <EG4>  
F: 315-657/Domain: sex hormone-binding globulin homology <SHB>  
F: 325-498/Domain: laminin G repeat homology <LGR>  
F: 47/48, 55, 57, 60, 61, 63, 67, 70, 73, 77/Modified site: gamma-carboxyglutamic acid (Glu) #statu  
F: 58-67, 88-113, 121-134, 126-141, 145-154, 161-175, 171-184, 186-199, 205-217, 212-226, 228-241, 22  
F: 111-112/Cleavage site: Arg-Ser (thrombin) #status predicted  
F: 116/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F: 177, 219, 258/Modified site: erythro-beta-hydroxyaspartic (Asn) #status predicted  
F: 499, 509, 530/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	7.0%	Score 131.5	DB 1	Length 676
Best Local Similarity	24.0%	Pred. No. 0.091	Indels 91	Gaps 21
Matches	83	Conservative 43	Mismatches 129	Indels 91

3 RLGATTTCTLLAAVTPAPATAPATATAPKCGPALSTPQEEATINMEFVEVELMEDTQ 62  
7 RCGALLACLLT-----LPSANFLSKQAQVLRKRRANSILLETIK 50  
63 --KLSAVDEMAEBAAKASSEVNLALPSYHNENTDVKGNNTLHVAREHIXITN 120  
51 QGNLHECIELDNCKEAREV-----FENDPDT-----YFYKVLVCARS 91  
121 NOTQWVSEFTVTSVGDEGRSRSHCEITDEGCP-----SMTQQ--PASFOYTCOP- 170  
92 FQGLFLTAAGSTNAFV--LRSYVNAIPDCCSPICNEDGYMCKCKGKASFTCTCKRG 148  
171 CRGPMICRDRSBCGDOLCWVGHCTKMA--TRGS-----NG-TICDNORDC----- 214

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 20, 2004, 18:04:23 ; Search time 85 Seconds

(without alignments)  
1062.570 Million cell updates/sec

Title: US-10-063-671-8

Perfect score: 1880

Sequence: 1 MORLGATLTLTLAAVPTA.....EMALGPAAALALGGERI 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SPTRMBL\_23:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_phase:\*  
11: sp\_plant:\*  
12: sp\_ricent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*  
16: sp\_virus:\*  
17: sp\_bacterioplasmid:\*  
18: sp\_bacteriophage:\*  
19: sp\_archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1217	64.7	277	11	Q9ES33
2	876	46.6	171	4	Q43532
3	703.5	37.4	215	4	Q8N234
4	182.5	9.7	221	11	Q8VEJ3
5	175	9.3	259	13	Q57464
6	170	9.0	255	13	Q9DDA4
7	165	8.8	240	13	Q9PWH3
8	157	8.4	241	13	Q9WED9
9	156	8.3	259	11	Q8BFW0
10	143	7.6	420	5	Q81459
11	132.5	7.0	230	11	Q9EQT4
12	129.5	6.9	128	11	Q9ERW0
13	129.5	6.9	230	11	Q9ERW1
14	128.5	6.8	788	6	Q8SCB8
15	124.5	6.6	1664	5	Q9TVQ2
16	119	6.3	969	4	Q96KG6

17	119	6.3	1168	11	Q91V90	Q91V90 mus musculu
18	118.5	6.3	96	13	Q8UDX3	Q8UDX3 gallus gall
19	117.5	6.2	996	6	Q924X6	Q924X6 mus musculu
20	117	6.2	420	6	Q9XS50	Q9XS50 bos taurus
21	117	6.2	3712	5	Q9VRW0	Q9VRW0 drosophila
22	116	6.2	788	13	Q07012	Q07012 xenopus lae
23	116	6.2	836	13	Q8AW87	Q8AW87 cynops pyr
24	116	6.2	870	11	Q921B6	Q921B6 mus musculu
25	116	6.2	1253	11	Q61810	Q61810 mus musculu
26	116	6.2	2146	5	Q9VC97	Q9VC97 drosophila
27	115	6.1	2376	5	Q9V5J0	Q9V5J0 drosophila
28	115	6.1	2376	5	Q966V1	Q966V1 drosophila
29	114.5	6.1	96	13	Q8JFX8	Q8JFX8 bombina max
30	114.5	6.1	746	4	Q9EBH9	Q9EBH9 homo sapien
31	114.5	6.1	1256	4	Q9NS15	Q9NS15 homo sapien
32	114.5	6.1	1382	4	Q9H7K2	Q9H7K2 homo sapien
33	114	6.1	755	11	Q9R0G6	Q9R0G6 mus musculu
34	114	6.1	755	11	Q8V154	Q8V154 mus musculu
35	114	6.1	1713	11	Q88349	Q88349 mus musculu
36	113.5	6.0	421	5	Q9NKE1	Q9NKE1 drosophila
37	113.5	6.0	817	4	Q14592	Q14592 homo sapien
38	112	6.0	963	4	Q14114	Q14114 homo sapien
39	112	6.0	1389	11	Q8CG18	Q8CG18 mus musculu
40	112	6.0	1713	11	Q8CG19	Q8CG19 mus musculu
41	111.5	5.9	96	13	Q8JFX9	Q8JFX9 bombina max
42	111.5	5.9	96	13	Q8JFX0	Q8JFX0 bombina max
43	111.5	5.9	96	13	Q8JFX6	Q8JFX6 bombina max
44	111.5	5.9	487	5	Q8MSX5	Q8MSX5 drosophila
45	111.5	5.9	1188	10	Q9SV59	Q9SV59 arabidopsis

## ALIGNMENTS

RESULT 1	Q9ES33	PRELIMINARY	PRT:	277 AA.
ID	Q9ES33			
AC	Q9ES33			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Substrate binding subunit of type II 5'-deiodinase D2p29.			
OS	Rattus norvegicus (Rat)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley; TISSUE=Brain;			
RX	MEDLINE=20400444; PubMed=10829019;			
RA	Leonard D.M., Stacherek S.T., Saffran M., Farwell A.P., Kowalik T.F.,			
RA	Leonard J.U.,			
RT	"Cloning, expression, and functional characterization of the substrate			
RT	binding subunit of rat type II iodothyronine 5'-deiodinase";			
RL	J. Biol. Chem. 275:25194-25201 (2000).			
DR	EMBL; AF245040; AAG15890.1; -			
DR	InterPro; IPR006796; dckkopf.N.			
DR	Ffam; PF04706; dckkopf.N.1.			
DR	SEQUENCE 277 AA; 30763 MW; 8025F66DFE4C205E CRC64;			
QY	Query Match	64.7%; Score 1217; DB 11; Length 277;		
QY	Best Local Similarity	78.1%; Pred. No. 2.5e-98;		
QY	Matches 218; Conservative 26; Mismatches 33; Indels 2; Gaps 1;			
QY	72	MAEEAAKASSEVLANLPSSVHNETGDKVGNNTIHYREIKRINNOGQWVFSET	131	Q91V90 mus musculu
QY	1	MAEEAAKASSEVLANLPSSVHNETGDKVGNNTIHYREIKRINNOGQWVFSET	60	Q91V90 mus musculu
QY	132	VITTSVDEBGRSHHCITIDEDCGPDMYQCPASFOYTCPCGQRMCTRDSECCDQICV	191	Q91V90 mus musculu
QY	61	VITTSVDEBGRSHHCITIDEDCGPDMYQCPASFOYTCPCGQRMCTRDSECCDQICV	120	Q91V90 mus musculu
QY	192	WCHCKRMATRGNSNGRTICNQRDCQGLCCAFQRLGLFVCTPLPVEGSLCHDPASRLDL	251	Q91V90 mus musculu

```

DB 121 WGHCTOKATGNSGTTICDNRDCCQPCGACFQGLLFPVCTPLPVEGELCHPPTSQMDL 180
QY 252 ITTELPPDGLDPCSPASGLLQPHSHSLVYVCKPTFVSGRDDGILLPREVPPEYVG 311
DB 181 ITTELPEBGLMDLCPGSCGLLQPHSHSLVYVCKPFPVSGHIDNEISQLPREALDDYEDV 240
QY 312 SFMEVYRQLEDEJERSITTEEMALGEPAAAAALLGGEI 350
DB 241 GFICEVQLEDEJERSIAQEMAFEE--ATPVSLGGEKI 277

```

## RESULT 2

```

ID 043532 PRELIMINARY; PRT; 171 AA.
AC 043532;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE RIG-like 7.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SOURCE FROM N.A.
RC TISSUE=Brain;
RA Ligon A.H., Peirhouse M.A., Jasser S., Hong Y.K., Yung W.K.A.,
RA Steck P.A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034208; AAB92664.1; -
DR InterPro; IPR006796; dickleopf_N.
DR InterPro; IPR005805; Rieseke_2.
DR Pfam; PF04706; dickleopf_N.1.
DR PROSITE; PS00200; RIESEKE_2.1.
SQ SEQUENCE 171 AA; 19283 MW; B890E38F873D0562 CRC64;

```

```

Query Match 46.6%; Score 876; DB 4; Length 171;
Best Local Similarity 96.8%; Pred. No. 9.2e-69;
Matches 151; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 157 MCGQFASFOYTCQPCRGRLCTRDSECCDQLCWGHCTKATRSNGTICDNRDCCP 216
DB 1 MCGQFASFOYTCQPCRGRLCTRDSECCDQLCWGHCTKATRSNGTICDNRDCCP 60
QY 217 GLCCAFQGLLFPVCTPLPVEGELCHDPAARLLDITTELPPDGLDPCSPASGLLQCPH 276
DB 61 GLCCAFQGLLFPVCTPLPVEGELCHDPAARLLDITTELPPDGLDPCSPASGLLQCPH 120
QY 277 SHSLVYVCKPTFVSGRDDGILLPREVPPEYVG 312
DB 121 SHSLVYVCKPTFVSGRDDGILLPREVPPEYKLA 156

```

## RESULT 3

```

ID 08N294 PRELIMINARY; PRT; 215 AA.
AC 08N294;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Hypothetical protein FLJ33633.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amygdala;
RA Niinomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki T., Irie K.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,

```

```

RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanchori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isegai T.;
RT "NEO human cDNA sequencing project."
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090952; BAC03555.1; -
KW Hypothetical protein.
SQ SEQUENCE 215 AA; 23904 MW; 2D9DEABCAFAB80B0 CRC64;

```

```

Query Match 37.4%; Score 703.5; DB 4; Length 215;
Best Local Similarity 92.5%; Pred. No. 1.5e-53;
Matches 136; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

```

```

QY 25 PTATAPAYKP-GPALSYPOEBATINEMFREVEIMEDTQKRSVEMEAEAAAYASS 83
DB 69 PCAGLLCQPHSHSLSYPOEBATINEMFREVEIMEDTQKRSVEMEAEAAAYASS 128
QY 84 EVNLANLPPSYHNETNTDTKVGNNTHVHREIKHTNNOTGOMVSETVITSVGDEGR 143
DB 129 EVNLANLPPSYHNETNTDTKVGNNTHVHREIKHTNNOTGOMVSETVITSVGDEGR 188
QY 144 SHECIIDDCGSPMYCQFASFOYTCOP 170
DB 189 SHECIIDDCGSPMYCQFASFOYTCOP 215

```

## RESULT 4

```

ID 08VEJ3 PRELIMINARY; PRT; 221 AA.
AC 08VEJ3;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Similar to dickleopf (Xenopus laevis) homolog 4.
GN DK4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strubeberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018400; AAH18400.1; -
DR MGI; MGI:2385299; Dk4.
SQ SEQUENCE 221 AA; 24260 MW; 670AD9F750BF1715 CRC64;

```

```

Query Match 9.7%; Score 182.5; DB 11; Length 221;
Best Local Similarity 24.3%; Pred. No. 6.3e-08;
Matches 50; Conservative 20; Mismatches 71; Indels 65; Gaps 7;

```

```

QY 133 ITSVDDEGR-RSECIIDDCGSPMYC-QFASFOYTCOPRGQRLCTRDSECCDQLC 190
DB 26 IKSSADYQAGKAGSLCASDRDCSEGRCLAFHDERSPCATCRVRRRCQGSAAVCCPTVC 85
QY 191 VMGHT-----KATRSNGTIC 208
DB 86 VNDVCTAYEDTRPYMDNRDQDGAVALGTTKWAENRPOGRSTKSSQSSKQGBSNC 145
QY 209 DNDRDQPCGLCCAFQGLLFPVCTPLPVEGELC---HDPASRLDITTELPPDGLD 264
DB 146 LRTSPCGPGLCCA--RHFWTKICKPVAREGQVCSRGHKTDAQAPEL-----FOR 193
QY 265 CPCASGLICP-----SHSLVYVCK 285
DB 194 CDCGPGILCRSQVTSNRQHSRLVCO 219

```

## RESULT 5

```

ID 057464 PRELIMINARY; PRT; 259 AA.
AC 057464;

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 20, 2004, 18:47:56 ; Search time 28 Seconds

(without alignments)  
528.886 Million cell updates/sec

Title: US-10-063-671-8

Perfect score: 1880

Sequence: 1 MQRIGATLILCLLAAAVPTA.....EMALGEPAAAAALGGEI 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.dep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.dep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.dep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.dep.\*  
5: /cgn2\_6/ptodata/2/1aa/PTCUS.COMB.dep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.dep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1880	100.0	350	4 US-09-161-241-9	Sequence 9, Appli
2	1589	84.5	349	4 US-09-161-241-8	Sequence 8, Appli
3	214.5	11.4	224	4 US-09-161-241-14	Sequence 14, Appli
4	174.5	9.3	266	4 US-09-161-241-10	Sequence 10, Appli
5	169	9.0	207	4 US-09-161-241-13	Sequence 13, Appli
6	162	8.6	259	4 US-09-161-241-12	Sequence 12, Appli
7	156	8.3	259	4 US-09-161-241-11	Sequence 11, Appli
8	138	7.3	577	2 US-07-728-215-29	Sequence 29, Appli
9	138	7.3	577	4 US-08-938-085A-29	Sequence 29, Appli
10	138	7.3	577	4 US-10-072-844-29	Sequence 29, Appli
11	133.5	7.0	676	1 US-08-282-141-4	Sequence 4, Appli
12	131.5	7.0	676	1 US-08-435-434-3	Sequence 3, Appli
13	131.5	7.0	676	1 US-08-435-434-3	Sequence 3, Appli
14	131.5	7.0	676	2 US-08-438-863-3	Sequence 3, Appli
15	131.5	7.0	676	2 US-08-438-864-3	Sequence 3, Appli
16	131.5	7.0	676	3 US-08-438-862-3	Sequence 3, Appli
17	131.5	7.0	676	3 US-08-438-862-3	Sequence 3, Appli
18	131.5	7.0	676	3 US-08-438-862-3	Sequence 3, Appli
19	131.5	7.0	676	3 US-08-438-862-3	Sequence 3, Appli
20	131.5	7.0	676	3 US-08-438-862-3	Sequence 3, Appli
21	126	6.7	788	4 US-08-938-085A-27	Sequence 27, Appli
22	126	6.7	788	4 US-08-938-085A-27	Sequence 27, Appli
23	126	6.7	788	4 US-08-938-085A-27	Sequence 27, Appli
24	116	6.2	1251	5 PCT-US95-02251-3	Sequence 3, Appli
25	116	6.2	1251	5 PCT-US95-02251-3	Sequence 3, Appli
26	116	6.2	1252	2 US-08-316-650-3	Sequence 3, Appli
27	116	6.2	1253	3 US-08-479-722B-4	Sequence 4, Appli

28	110.5	5.9	1147	1 US-08-144-121-3	Sequence 3, Appli
29	110.5	5.9	1147	2 US-08-735-893-3	Sequence 3, Appli
30	110.5	5.9	1165	1 US-08-144-121-2	Sequence 2, Appli
31	110.5	5.9	1165	2 US-08-735-893-2	Sequence 2, Appli
32	110.5	5.9	2214	1 US-08-727-034-7	Sequence 7, Appli
33	110	5.9	2523	1 US-08-185-432-18	Sequence 18, Appli
34	110	5.9	2523	4 US-08-899-232-3	Sequence 3, Appli
35	108	5.7	299	3 US-09-188-930-192	Sequence 192, App
36	108	5.7	299	3 US-09-188-930-192	Sequence 192, App
37	108	5.7	299	4 US-09-312-283C-192	Sequence 192, App
38	108	5.7	299	4 US-09-312-283C-192	Sequence 192, App
39	108	5.7	1170	1 US-08-313-288B-20	Sequence 20, Appli
40	107.5	5.7	799	1 US-08-054-077C-2	Sequence 2, Appli
41	107.5	5.7	2556	1 US-08-185-432-17	Sequence 17, Appli
42	107.5	5.7	2556	4 US-08-899-232-2	Sequence 2, Appli
43	106.5	5.7	652	6 US-08-185-432-16	Sequence 16, Appli
44	106	5.6	2471	1 US-08-185-432-16	Sequence 16, Appli
45	106	5.6	2471	1 US-08-083-590A-19	Sequence 19, Appli

ALIGNMENTS

RESULT 1  
US-09-161-241-9  
; Sequence 9, Application US/09161241  
; Patent No. 6344541  
; GENERAL INFORMATION:  
; APPLICANT: Bass, Michael B  
; APPLICANT: Sullivan, John K  
; APPLICANT: Rhell, Lars E  
; APPLICANT: Wang, Daqiang  
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES  
; FILE REFERENCE: A-548  
; CURRENT APPLICATION NUMBER: US/09/161,241  
; CURRENT FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 350  
; TYPE: PRT  
; ORGANISM: Human  
US-09-161-241-9

Query Match	100.0%; Score 1880; DB 4; Length 350;
Best Local Similarity	100.0%; Pred. No. 1.6e-151; Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MQRIGATLILCLLAAAVPTAPAPATATAPVKGPPALSYPOEATLNMFEVEELMED 60
DB	1 MQRIGATLILCLLAAAVPTAPAPATATAPVKGPPALSYPOEATLNMFEVEELMED 60
QY	61 TQHKRSANVEEMAEBAKASSEVNLNLPSSYNENETDTQKNNTHVREIHKTN 120
DB	61 TQHKRSANVEEMAEBAKASSEVNLNLPSSYNENETDTQKNNTHVREIHKTN 120
QY	121 NOTGQVFESEVITVSGDEGRSHCEIIDEDCGSMTCOFASFOYTQPCPCGQMLCTR 180
DB	121 NOTGQVFESEVITVSGDEGRSHCEIIDEDCGSMTCOFASFOYTQPCPCGQMLCTR 180
QY	181 DSECCGDCQVGHCTKATRGSGNGTICNQRDCQGLCAQORGLIPFVCTPLPYEGTL 240
DB	181 DSECCGDCQVGHCTKATRGSGNGTICNQRDCQGLCAQORGLIPFVCTPLPYEGTL 240
QY	241 CHDPASRLDLITWELPFGALDRCPGASGLICQPHSHSLVYVCKPTFGSGRDQGEIIL 300
DB	241 CHDPASRLDLITWELPFGALDRCPGASGLICQPHSHSLVYVCKPTFGSGRDQGEIIL 300
QY	301 PREVPDEYVGSFMEVROELEDLERSLTENALGEPAAAAALGGEI 350
DB	301 PREVPDEYVGSFMEVROELEDLERSLTENALGEPAAAAALGGEI 350

```

RESULT 2
US-09-161-241-8
; Sequence 8, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Mouse
US-09-161-241-8

```

```

Query Match      84.5%; Score 1589; DB 4; Length 349;
Best Local Similarity 82.5%; Pred. No. 7,4e-127;
Matches 288; Conservative 26; Mismatches 33; Indels 2; Gaps 1;

```

```

QY 1 MORLGATLLCLLAAVPTAPAPATATSAVPKPGPALSYPOEATLNMFRVEELMD 60
DB 1 MORLGATLLCLLAAVPTAPAPATATSAVPKPGPALSYPOEATLNMFRVEELMD 60
QY 61 TORHLSAVERMEAEKAAASSEVNLANLPSTHNETNTDTYGNNTTTHVREIKTN 120
DB 61 TORHLSAVERMEAEKAAASSEVNLANLPSTHNETNTDTYGNNTTTHVREIKTN 120
QY 121 NOTGOWFSEVTIVTSVDEBGRSHCEITIDEDGSPSYCOFASFOYTCOPCRGRLCTR 180
DB 121 NOTGOWFSEVTIVTSVDEBGRSHCEITIDEDGSPSYCOFASFOYTCOPCRGRLCTR 180
QY 181 DSECCGQOLCVMGHCITMATRGSGNITCDNQRDCQGLCCAFORGLLPVCTPLPVEGEL 240
DB 181 DSECCGQOLCVMGHCITMATRGSGNITCDNQRDCQGLCCAFORGLLPVCTPLPVEGEL 240
QY 241 CHDPAASLLDITLWELRPPDALRCPASGLLCOPHSHSVYVCKPFPVSRDDEILL 300
DB 241 CHDPAASLLDITLWELRPPDALRCPASGLLCOPHSHSVYVCKPFPVSRDDEILL 300
QY 301 PREVPDEYVGSFMEYRQELIEDLERSLITEMALGEPAAAAALLGSEE 349
DB 301 PREVPDEYVGSFMEYRQELIEDLERSLITEMALGEPAAAAALLGSEE 349
QY 301 PREVPDEYVGSFMEYRQELIEDLERSLITEMALGEPAAAAALLGSEE 349
DB 301 PREVPDEYVGSFMEYRQELIEDLERSLITEMALGEPAAAAALLGSEE 349

```

```

RESULT 3
US-09-161-241-14
; Sequence 14, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Human
US-09-161-241-14

```

```

Query Match      11.4%; Score 214.5; DB 4; Length 224;
Best Local Similarity 26.5%; Pred. No. 1.2e-10;

```

```

Matches 57; Conservative 21; Mismatches 72; Indels 65; Gaps 7;
QY 124 GOWFSEVTIVTSVDEBGRSHCEITIDEDGSPSYCOFASFOYTCOPCRGRLCTR 181
DB 17 GALVLDNFNNISASDLHAKRGSGCLSDTONTKFCLOPREDKFPATCRGLRRRCORD 76
QY 182 SECCGQOLCVMGHCITMATRGSGNITCDNQRDCQGLCCAFORGLLPVCTPLPVEGEL 240
DB 77 AMCCPGTLCVNDVCTTMDATPIEROLDSDGTGHAEGTGHVQENQPRKRSIKKSQG 136
QY 200 TRGSNGTICDNQRDCQGLCCAFORGLLPVCTPLPVEGELC---HDPASRLDILTW 255
DB 137 RKGGEGESCLATPFGQGLCCA--RHFTKTKCKVLLGQVCSRGKMDTAQAEI---- 190
QY 256 LEPDGLDRCPASGLLCOF---HSHSLVYVCK 285
DB 191 ----FORCDDCGGLLCRSQLTNSRQHLRLVQC 219

```

```

RESULT 4
US-09-161-241-10
; Sequence 10, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human
US-09-161-241-10

```

```

Query Match      9.3%; Score 174.5; DB 4; Length 266;
Best Local Similarity 25.6%; Pred. No. 3.7e-07;
Matches 50; Conservative 18; Mismatches 60; Indels 67; Gaps 8;

```

```

QY 145 HECITIDEDGSPSYCOF---ASFQYTCOPCRGRLCTRDSGCCGQOLCVMGHC--- 195
DB 83 YPCAEDCEGTDYCYASPTRGDAGVQ-ICLACKRRRRCKRHAMCCPGNYCKXNGICVSS 141
QY 196 -----TKM-ATRGSGNITCDNQRDCQGLCC 220
DB 142 DONHFRGIEETTESFNDHSTLDGYSRRRTTSSKXHTTGQSGSYCLRSDDASGLCC 201
QY 221 AFQRLGFLPVCTPLPVEGELC---HDPASRLDILTWLEPDGLDRCPASGLLCC--- 273
DB 202 A--RHFMGKICKPVLKEGQVCTKRRKSHLEI-----FORCYCEBGLSCRIQK 249
QY 274 ---QPHSHSLVYVCK 285
DB 250 DHQASNSRLHTQC 264

```

```

RESULT 5
US-09-161-241-13
; Sequence 13, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241

```





C 82	33	1.3	1892	24	ABK62583	Rat sequence diffe
C 83	32	1.2	1891	21	AAA16384	Human colon cancer
C 84	32	1.2	680	20	AAV79011	Human secreted pro
C 85	32	1.2	710	22	AAH72514	Human cervical can
C 86	32	1.2	908	22	AAI96448	Human neuroblastom
C 87	32	1.2	917	22	AAO08474	Human secreted pro
C 88	32	1.2	1127	24	AA562815	CDNA sequence #602
C 89	32	1.2	1143	22	AAO08425	Human secreted pro
C 90	32	1.2	1430	21	AAFI6238	Human prostate can
C 91	32	1.2	1656	20	AAV60810	Human secreted pro
C 92	32	1.2	1656	22	AA552916	Human CDNA encodin
C 93	32	1.2	1656	24	ABV90885	Human polynucleoti
C 94	32	1.2	1787	24	ABQ55020	Human ovarian anti
C 95	32	1.2	3760	20	ABK35024	Human CDNA encodin
C 96	32	1.2	9551	20	AA222301	CDNA encoding a hu
C 97	32	1.2	30826	22	ABAO7345	Human pancreatic c
C 98	32	1.2	30826	22	AA532772	Human genomic DNA
C 99	31	1.2	83	19	AAV38810	Homo sapiens CESP
C 100	31	1.2	244	24	ABN94202	Gene #700 used to
C 101	31	1.2	390	22	AA188471	Human polynucleoti
C 102	31	1.2	589	23	ABK42784	Genomic sequence #
C 103	31	1.2	589	23	ABK42785	Genomic sequence #
C 104	31	1.2	765	21	AA059538	Human secreted pro
C 105	31	1.2	1014	21	AAAF21918	Human breast and o
C 106	31	1.2	1050	21	AA008838	Human secreted pro
C 107	31	1.2	1175	21	AA059061	Human secreted pro
C 108	31	1.2	1356	24	ABQ54823	Human ovarian anti
C 109	31	1.2	1517	24	ABL95739	Human angiogenesis
C 110	31	1.2	1517	24	ABL98250	Human PRO20044 CDN
C 111	31	1.2	1566	22	AAO08292	Human secreted pro
C 112	31	1.2	1566	25	AA050689	Human secreted pro
C 113	31	1.2	1568	25	ABZ71376	Secreted protein-e
C 114	31	1.2	1589	20	AAV97368	Human secreted pro
C 115	31	1.2	1880	24	ABQ55073	Human ovarian anti
C 116	31	1.2	1890	21	AAV34217	Human secreted pro
C 117	31	1.2	2051	19	AA059822	Human secreted pro
C 118	31	1.2	2053	22	AAO08198	Human secreted pro
C 119	31	1.2	2147	22	AA06930	CDNA encoding a hu
C 120	31	1.2	2380	21	AAV75137	CDNA encoding a mu
C 121	31	1.2	2381	19	AAV07911	Mouse cyclo-oxygen
C 122	31	1.2	2454	21	AA059728	CDNA encoding huma
C 123	31	1.2	3116	21	AA052568	Human secreted pro
C 124	31	1.2	3362	19	AAV29270	Nucleotide sequenc
C 125	31	1.2	3362	21	AA058320	Human beta catenin
C 126	31	1.2	3362	22	AA011164	Human beta-catenin
C 127	31	1.2	3362	24	ABK64700	Human CDNA diffe
C 128	31	1.2	3452	22	AA045206	CDNA encoding nove
C 129	31	1.2	3951	24	ABV93739	Human intracellular
C 130	31	1.2	4270	24	AB199812	Mouse ischaemic co
C 131	30	1.2	30	21	AA008863	PCR primer for hum
C 132	30	1.2	57	19	AAV27940	Human GAL3 CDNA t
C 133	30	1.2	57	24	AA035883	Human GAL3 CDNA t
C 134	30	1.2	120	24	AB163786	Breast cancer rela
C 135	30	1.2	120	24	AB163786	Human ovarian can
C 136	30	1.2	150	24	AB167440	Human ovarian can
C 137	30	1.2	150	24	AB168180	Human ovarian can
C 138	30	1.2	199	24	AB186482	Human ovarian can
C 139	30	1.2	204	24	AB186042	Human ovarian can
C 140	30	1.2	217	22	AA059037	CDNA encoding for
C 141	30	1.2	217	24	AB068177	CDNA encoding huma
C 142	30	1.2	220	22	AAI02613	Human reproductive
C 143	30	1.2	220	22	AAI02613	Human breast or ov
C 144	30	1.2	220	22	AAI02613	Rat metastatic tum
C 145	30	1.2	220	24	AB193053	Human secreted pro
C 146	30	1.2	263	22	AA008521	Human breast cance
C 147	30	1.2	297	22	AA020363	CDNA encoding for
C 148	30	1.2	297	22	AA020363	CDNA encoding huma
C 149	30	1.2	337	24	AA059114	CDNA encoding huma
C 150	30	1.2	337	24	ABV98816	Human pancreatic c
C 151	30	1.2	351	24	ABV98816	Human polynucleoti
C 152	30	1.2	398	22	AAI91636	Human polynucleoti
C 153	30	1.2	432	24	ABV98613	Human pancreatic c
C 154	30	1.2	454	24	ABN94920	Gene #1418 used to

228	30	1.2	1966	23	ABV22155	Human prostate exp	301	30	1.2	143068	24	ABL68124	Ovary cancer relat
229	30	1.2	1966	23	ABV24161	Human prostate exp	302	30	1.2	149412	21	AAI35151	Human adenosine re
230	30	1.2	1966	23	ABV24461	Human prostate exp	303	30	1.2	152740	21	AAI21273	Human low adenosin
231	30	1.2	1966	23	ABV25841	Human prostate exp	304	29	1.1	38	22	AAI60440	DNA oligonucleotid
232	30	1.2	1966	23	ABV27995	Human prostate exp	305	29	1.1	51	22	AAI28393	Human SNP oligonc
233	30	1.2	1971	21	AAA95063	Human secreted pro	306	29	1.1	51	22	AAI28394	Human SNP oligonc
234	30	1.2	2012	21	AACT7510	Human CRF3065	307	29	1.1	51	22	AAI31052	Human SNP oligonc
235	30	1.2	2021	21	AA541105	CDNA encoding nove	308	29	1.1	51	22	AAI31109	Human secreted pro
236	30	1.2	2059	22	AA502558	Human secreted pro	309	29	1.1	70	24	ABX14132	Human secreted pro
237	30	1.2	2070	19	AAV34194	Human secreted pro	310	29	1.1	107	21	AAI17591	Human GDP-mannose
238	30	1.2	2079	23	ABV24761	Human prostate exp	311	29	1.1	150	25	ABX26373	Human breast cance
239	30	1.2	2081	21	AAA39086	Human secreted pro	312	29	1.1	154	22	AAI23551	Human prostate exp
240	30	1.2	2126	24	AAH77186	Human oestrogen ag	313	29	1.1	165	20	AAV04929	Human prostate exp
241	30	1.2	2269	21	AAZ43684	A. Cryzae glucanin	314	29	1.1	166	20	AAV23763	Human prostate exp
242	30	1.2	2293	16	AB557346	CDNA encoding huma	315	29	1.1	167	24	ABL87719	Human prostate exp
243	30	1.2	2335	16	AA080216	Human proDRP-alpha	316	29	1.1	168	23	ABV58190	Human prostate exp
244	30	1.2	2439	22	AA526373	Human CDNA encodin	317	29	1.1	172	23	ABV58190	Human prostate exp
245	30	1.2	2489	25	ABX73714	Human novel polynu	318	29	1.1	173	22	AA560588	Human prostate exp
246	30	1.2	2504	22	AA525924	Human CDNA encodin	319	29	1.1	179	24	ABL6853	Human prostate exp
247	30	1.2	2504	25	ABX73265	Human novel polynu	320	29	1.1	181	23	ABV35200	Human prostate exp
248	30	1.2	2732	24	ABX35016	Human CDNA encodin	321	29	1.1	181	23	ABV44040	Human prostate exp
249	30	1.2	2770	18	AAI755035	Chick fringed B (lu	322	29	1.1	186	25	ABV18959	Human cancer agent
250	30	1.2	2801	22	AA526992	CDNA encoding nove	323	29	1.1	186	25	ABX61443	Human cancer agent
251	30	1.2	3059	8	AAI70566	Sequence encoding	324	29	1.1	189	22	AA560389	Human breast cance
252	30	1.2	3096	22	ABX82619	Human HBM gene reg	325	29	1.1	191	24	ABL37908	Human breast cance
253	30	1.2	3096	24	ABX22778	Human high bone ma	326	29	1.1	193	22	AAI14699	Human prostate exp
254	30	1.2	3096	25	ACC45360	Human HBM gene fra	327	29	1.1	196	23	ABV57324	Human prostate exp
255	30	1.2	3097	23	AA587573	DNA encoding novel	328	29	1.1	210	25	ABX45180	Human prostate exp
256	30	1.2	3098	21	AAA32459	CDNA encoding huma	329	29	1.1	214	22	ABV35244	Human prostate exp
257	30	1.2	3204	25	AB277317	Nucleotide sequenc	330	29	1.1	215	22	ABV58518	Human immune/haema
258	30	1.2	3673	21	AAA08994	Human WFS1 mutant	331	29	1.1	227	23	AAK70096	Human differential
259	30	1.2	3686	21	AAA08995	WFS1 variant CDNA	332	29	1.1	231	22	AAI55669	Human prostate exp
260	30	1.2	3688	21	AAA08995	Human WFS1 mutant	333	29	1.1	242	23	ABV34421	Human prostate exp
261	30	1.2	3688	21	AAA08995	Human WFS1 mutant	334	29	1.1	242	23	ABV43280	Human prostate exp
262	30	1.2	3688	21	AAA08995	Human WFS1 mutant	335	29	1.1	253	24	ABN94885	Human prostate exp
263	30	1.2	3688	21	AAA08995	Human WFS1 mutant	336	29	1.1	257	24	ABN96786	Human prostate exp
264	30	1.2	3688	21	AAA08998	Human WFS1 mutant	337	29	1.1	257	24	ABL66854	Human prostate exp
265	30	1.2	3688	21	AAA09000	Human WFS1 polymor	338	29	1.1	260	24	ABK29772	Human prostate exp
266	30	1.2	3688	21	AAA09001	Human WFS1 polymor	339	29	1.1	261	23	ABV56842	Human prostate exp
267	30	1.2	3688	21	AAA09002	Human WFS1 polymor	340	29	1.1	261	23	ABV56842	Human prostate exp
268	30	1.2	3688	21	AAA09003	Human WFS1 polymor	341	29	1.1	261	23	ABV57493	Human prostate exp
269	30	1.2	3688	21	AAA09004	Human WFS1 polymor	342	29	1.1	265	23	ABV57493	Human prostate exp
270	30	1.2	3688	21	AAA09005	Human WFS1 polymor	343	29	1.1	270	24	ABL86700	Human prostate exp
271	30	1.2	3688	21	AAA09006	Human WFS1 polymor	344	29	1.1	275	24	ABL86029	Human prostate exp
272	30	1.2	3688	21	AAA09007	Human WFS1 polymor	345	29	1.1	282	23	AAI16353	Human prostate exp
273	30	1.2	3688	21	AAA09008	Human WFS1 polymor	346	29	1.1	285	23	ABV49691	Human prostate exp
274	30	1.2	3688	21	AAA09009	Human WFS1 polymor	347	29	1.1	290	22	AAI25196	Human prostate exp
275	30	1.2	3688	21	AAA09010	Human WFS1 polymor	348	29	1.1	293	22	AAI25196	Human prostate exp
276	30	1.2	3688	21	AAA09011	Human WFS1 polymor	349	29	1.1	295	22	AAI10359	Human prostate exp
277	30	1.2	3695	22	AAK75039	Human WFS1 mutant	350	29	1.1	297	24	ABV98543	Human prostate exp
278	30	1.2	3805	22	AAK75039	Human immune/haema	351	29	1.1	297	24	ABL86125	Human prostate exp
279	30	1.2	4235	21	AAI00129	Human NIP2c long-1	352	29	1.1	301	21	ABL86108	Human prostate exp
280	30	1.2	4357	22	AAH44280	Human amyotrophic	353	29	1.1	302	21	AAI98533	Human prostate exp
281	30	1.2	4378	23	ABV22147	Human prostate exp	354	29	1.1	303	24	ABV98851	Human prostate exp
282	30	1.2	4589	11	AAQ06068	p150.95 alpha subu	355	29	1.1	307	24	ABL61191	Human prostate exp
283	30	1.2	4589	11	AAQ06068	DNA encoding murin	356	29	1.1	316	24	ABO55179	Human prostate exp
284	30	1.2	6901	23	AA595022	DNA encoding murin	357	29	1.1	319	23	ABV49114	Human prostate exp
285	30	1.2	6901	23	AA595022	DNA encoding murin	358	29	1.1	330	22	AAI15540	Human prostate exp
286	30	1.2	7119	23	AA595023	DNA encoding murin	359	29	1.1	335	23	ABV48738	Human prostate exp
287	30	1.2	7119	23	AA595023	DNA encoding murin	360	29	1.1	337	21	AACT4326	Human prostate exp
288	30	1.2	11006	22	AAK66281	Human immune/haema	361	29	1.1	340	23	ABV03377	Human prostate exp
289	30	1.2	14598	22	AAK79627	Human immune/haema	362	29	1.1	341	25	ABV12546	Human prostate exp
290	30	1.2	14598	22	AAK79627	Human immune/haema	363	29	1.1	341	25	ABV12546	Human prostate exp
291	30	1.2	30803	22	AAK68410	Human immune/haema	364	29	1.1	342	23	ABV12548	Human prostate exp
292	30	1.2	39119	25	ABZ74034	Secreted protein g	365	29	1.1	343	23	ABV12548	Human prostate exp
293	30	1.2	39119	25	ABZ74034	Human secreted pro	366	29	1.1	360	24	ABV13005	Human prostate exp
294	30	1.2	43593	24	ABN96830	Human cDNA differe	367	29	1.1	363	24	ABK44623	Human prostate exp
295	30	1.2	43593	24	ABN96830	Human cDNA differe	368	29	1.1	364	24	ABK44623	Human prostate exp
296	30	1.2	143068	21	AAI21105	Human low adenosin	369	29	1.1	366	23	ABV38897	Human prostate exp
297	30	1.2	143068	21	AAI21105	Human low adenosin	370	29	1.1	366	23	ABV38897	Human prostate exp
298	30	1.2	143068	21	AAA34983	Human adenosine re	371	29	1.1	371	22	ABO85465	Human prostate exp
299	30	1.2	143068	21	AAA35150	Human adenosine re	372	29	1.1	375	24	AAI10546	Human prostate exp
300	30	1.2	143068	24	ABT11034	Human breast cance	373	29	1.1	375	22	AAI17621	Human breast cance



Db 601 ACGAGACTGTGGCCACGATGTA CTGCCAGTTGCCAGCTTCCAGTACACCTGCCAGC 66

Oy ACAGGAGCAGTGGGCCCCAGCATGTAAGTGGCAGTTGGCCAGCTTCAGTACACCTCCAGC 660  
 Db 601 ACAGGAGCAGTGGGCCCCAGCATGTAAGTGGCAGTTGGCCAGCTTCAGTACACCTGGCAGC 660

```

QY 661 CATGCCGGGGCCAGAGAGTCTCTGCAACCCGGGACAGTGAAGTCTGTGAGAACCACTGT 720
Db 661 CATGCCGGGGCCAGAGAGTCTCTGCAACCCGGGACAGTGAAGTCTGTGAGAACCACTGT 720
QY 721 GTGTCTGGGGGTCACTGACCAAAATGGCCACAGAGGGGACAGCAATGGGACCATCTGTGACA 780
Db 721 GTGTCTGGGGGTCACTGACCAAAATGGCCACAGAGGGGACAGCAATGGGACCATCTGTGACA 780
QY 781 ACCAGAGGAACTGCGCAGCCGGGGCTGTGCTGTGCTCTTCCAGAGAGGCTGTGCTCCCTG 840
Db 781 ACCAGAGGAACTGCGCAGCCGGGGCTGTGCTGTGCTCTTCCAGAGAGGCTGTGCTCCCTG 840
QY 841 TGTGCAACACCCCTGCGCCGTGGAGGGGAGAGCTTTGACATGACCCCGGACAGCCGCTCTG 900
Db 841 TGTGCAACACCCCTGCGCCGTGGAGGGGAGAGCTTTGACATGACCCCGGACAGCCGCTCTG 900
QY 901 ACCTCATCACTGGGAGCTTGAAGCTGTATGAGAGCTTTGACCGATGCCCTTGTGCCAGTG 960
Db 901 ACCTCATCACTGGGAGCTTGAAGCTGTATGAGAGCTTTGACCGATGCCCTTGTGCCAGTG 960
QY 961 GCTCTCTCTGCGACACCCCAAGCCACAGCCTTGGTGTATGTGTGCAAGCCGACCTTGTG 1020
Db 961 GCTCTCTCTGCGACACCCCAAGCCACAGCCTTGGTGTATGTGTGCAAGCCGACCTTGTG 1020
QY 1021 GAGACCCGTGACCAAGATGGGGAGATCTGCTGCTGCCAGAGAGGTCCCGATGATATGAAG 1080
Db 1021 GAGACCCGTGACCAAGATGGGGAGATCTGCTGCTGCCAGAGAGGTCCCGATGATATGAAG 1080
QY 1081 TTGGCAGCTTCATGAGAGAGGTGCGCCAGAGCTGAGAGACTTGGAGAGAGAGCTTGACTG 1140
Db 1081 TTGGCAGCTTCATGAGAGAGGTGCGCCAGAGCTGAGAGAGCTTGGAGAGAGAGCTTGACTG 1140
QY 1141 AAGAGATGGGCGTGGGGAGAGCTGCGCTGCGCCGCTGCACTGCTGGAGGGAGAGAG 1200
Db 1141 AAGAGATGGGCGTGGGGAGAGCTGCGCTGCGCCGCTGCACTGCTGGAGGGAGAGAG 1200
QY 1201 TTTAGATCTGGACCAAGCTGTGGGTAGATGTGCATATGAAATAGCTAATTTATTTCCCA 1260
Db 1201 TTTAGATCTGGACCAAGCTGTGGGTAGATGTGCATATGAAATAGCTAATTTATTTCCCA 1260
QY 1261 GGTGTGTGCTTTAGGCGTGGGCTGACCAAGGCTTCTTCAATCTTTCCAGTAAGTT 1320
Db 1261 GGTGTGTGCTTTAGGCGTGGGCTGACCAAGGCTTCTTCAATCTTTCCAGTAAGTT 1320
QY 1321 TCCCTCTGCTTGAACAGCATGAGGTGTGTGCAATTTGTCACTGCCCAAGCTGTCT 1380
Db 1321 TCCCTCTGCTTGAACAGCATGAGGTGTGTGCAATTTGTCACTGCCCAAGCTGTCT 1380
QY 1381 CCAGGCTTCAAGTCTGGTGTGGAGAGTCAAGGCGGTTAACTGCAAGGAGAGGTT 1440
Db 1381 CCAGGCTTCAAGTCTGGTGTGGAGAGTCAAGGCGGTTAACTGCAAGGAGAGGTT 1440
QY 1441 GCCACCCCTGTCAAGATTATGGCTGTGCTCTTCAACAGTTGGCAGAGCCGCTTGT 1500
Db 1441 GCCACCCCTGTCAAGATTATGGCTGTGCTCTTCAACAGTTGGCAGAGCCGCTTGT 1500
QY 1501 TCTACATGGCTTTGATTAATTTTGGAGGGGAGAGATGAGAAACATGTGAGTCTCCCTC 1560
Db 1501 TCTACATGGCTTTGATTAATTTTGGAGGGGAGAGATGAGAAACATGTGAGTCTCCCTC 1560
QY 1561 TGATGTGTTTGGGGAATGTGAGAGAGTGCCTGTGTTTGCAAAACATCAACTGTGCAA 1620
Db 1561 TGATGTGTTTGGGGAATGTGAGAGAGTGCCTGTGTTTGCAAAACATCAACTGTGCAA 1620
QY 1621 AAAATGCAACAATGAATTTTCCAGCAGTCTTTTCCATGGGCAATAGTAAAGTGTGCTT 1680
Db 1621 AAAATGCAACAATGAATTTTCCAGCAGTCTTTTCCATGGGCAATAGTAAAGTGTGCTT 1680
QY 1681 CAGCTGTGACAGATGAATGTCTGTTCACCCCTGATACATGATGTTTATTCATCCAGCA 1740
Db 1681 CAGCTGTGACAGATGAATGTCTGTTCACCCCTGATACATGATGTTTATTCATCCAGCA 1740

```

```

QY 1741 GTGTGTCTCACTCTCTACTCTCTGTGTCAGAGGACAGATTTCATATCCAAATCAATCCC 1800
Db 1741 GTGTGTCTCACTCTCTACTCTCTGTGTCAGAGGACAGATTTCATATCCAAATCAATCCC 1800
QY 1801 TCTCTCAGCAGAGCTTGGAGAGGGGTCAATGTCTCTCTGCTCATCAGGATCTCAGAG 1860
Db 1801 TCTCTCAGCAGAGCTTGGAGAGGGGTCAATGTCTCTCTGCTCATCAGGATCTCAGAG 1860
QY 1861 GCTCAGAGACTGCAAGTCTTGTGCTCCCAATGACACACTAGTGAAGACAGAGAGTTTC 1920
Db 1861 GCTCAGAGACTGCAAGTCTTGTGCTCCCAATGACACACTAGTGAAGACAGAGAGTTTC 1920
QY 1921 ATCTGTGTGATCTCTAAGCTCAATGCTCTCTCACTACCCCAACACAGCTTGTGCCA 1980
Db 1921 ATCTGTGTGATCTCTAAGCTCAATGCTCTCTCACTACCCCAACACAGCTTGTGCCA 1980
QY 1981 CCAAAAAGTCTCCCAAAAAGAGAGAGATGGATTTTCTTGGAGGATGACATCTGGA 2040
Db 1981 CCAAAAAGTCTCCCAAAAAGAGAGAGATGGATTTTCTTGGAGGATGACATCTGGA 2040
QY 2041 ATTAAGTCAAACTAATCTCACAATCCCTCTAAGATAACTACTGTAGGACAGAGT 2100
Db 2041 ATTAAGTCAAACTAATCTCACAATCCCTCTAAGATAACTACTGTAGGACAGAGT 2100
QY 2101 GTTCTCACAGTGTGGGCGAGCCGTCTTCTAATGAGACAAATGATTTGACACTGTCCCT 2160
Db 2101 GTTCTCACAGTGTGGGCGAGCCGTCTTCTAATGAGACAAATGATTTGACACTGTCCCT 2160
QY 2161 CTTTGGCAGTTGATTAATCTTGAAGGTATATGCTGAGGCTGACATACAGTTAA 2220
Db 2161 CTTTGGCAGTTGATTAATCTTGAAGGTATATGCTGAGGCTGACATACAGTTAA 2220
QY 2221 CCTGCAAGAACAGTACTTAAAGTAAATGTAGGCGCAGAGTTATAATGAATTTGCCAAT 2280
Db 2221 CCTGCAAGAACAGTACTTAAAGTAAATGTAGGCGCAGAGTTATAATGAATTTGCCAAT 2280
QY 2281 CACTTAGAGAGCACTGAGAGCAATTAATCAACAGGTGAGAGAAATCAAACGAGAGGGC 2340
Db 2281 CACTTAGAGAGCACTGAGAGCAATTAATCAACAGGTGAGAGAAATCAAACGAGAGGGC 2340
QY 2341 TGTGTGAACAATGTGTGATATGAGCACTGCGAACTGGAACCTTACGCCACTCCACAA 2400
Db 2341 TGTGTGAACAATGTGTGATATGAGCACTGCGAACTGGAACCTTACGCCACTCCACAA 2400
QY 2401 TGAATTTTCAAGTGTCAATGACCTGTGCGCAACATGATATGATCAGAGTCTTAAAGTT 2460
Db 2401 TGAATTTTCAAGTGTCAATGACCTGTGCGCAACATGATATGATCAGAGTCTTAAAGTT 2460
QY 2461 TAAAGTTGACATGATGATTAAGCATGCTTTCTTGAAGTTTAAATATGATTAACAT 2520
Db 2461 TAAAGTTGACATGATGATTAAGCATGCTTTCTTGAAGTTTAAATATGATTAACAT 2520
QY 2521 AAGTTGATTTGAATCAAGATTAATCACTTCACTGCAAAAAAATTTTTTTTTTTTTTT 2580
Db 2521 AAGTTGATTTGAATCAAGATTAATCACTTCACTGCAAAAAAATTTTTTTTTTTTTTT 2580
QY 2581 AAAAAA 2586
Db 2581 AAAAAA 2586

```

```

RESULT 2
AA92061
ID AA92061 standard; cDNA; 2586 BP.
XX
XX AA92061;
XX AC
XX DT 15-MAY-2001 (first entry)
XX DE Human PRO295 cDNA.
XX KM Human; PRO protein; mapping; ss.
XX

```



OS Homo sapiens.  
 XX  
 XX WC200116318-A2.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 24-AUG-2000; 2000MO-US2328.  
 XX  
 XX 01-SEP-1999; 99MO-US20111.  
 PR 15-SEP-1999; 99MO-US21090.  
 PR 07-DEC-1999; 99US-0169495.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 11-JAN-2000; 2000MO-US04341.  
 PR 18-FEB-2000; 2000MO-US04342.  
 PR 22-FEB-2000; 2000MO-US04414.  
 PR 01-MAR-2000; 2000MO-US05601.  
 PR 03-MAR-2000; 2000US-0187202.  
 PR 25-APR-2000; 2000US-0199397.  
 PR 22-MAY-2000; 2000MO-US14042.  
 PR 05-JUN-2000; 2000US-0209832.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Baton DL, Filvaroff E, Gerritsen MB, Goddard A, Godowski PJ;  
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;  
 XX  
 XX WPI; 2001-183260/18.  
 DR P-PSDB; AAB87529.  
 XX  
 PT Eighty four nucleic acids encoding PRO polypeptides, useful in  
 PT molecular biology, including use as hybridization probes, and in  
 PT chromosome and gene mapping.  
 XX  
 BS Claim 2; Fig 7; 278pp; English.  
 CC The present sequence is the coding sequence for a human PRO polypeptide  
 CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO  
 CC antagonists or anti-PRO antibodies are useful for preparation of a  
 CC medicament useful in the treatment of a condition which is responsive to  
 CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO  
 CC protein may also be employed as molecular weight markers for protein  
 CC electrophoresis. The PRO coding sequence has applications in molecular  
 CC biology, including use as hybridisation probes, and in chromosome and  
 CC gene mapping.  
 CC  
 SQ Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;  
 Query Match 100.0%; Score 2586; DB 22; Length 2586;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGCGCGCTCCCGACCCCGCGCGCGCGCGCGCGCTCCCGCATCTGACCCCGAGC 60  
 DB 1 CGCGCGCTCCCGACCCCGCGCGCGCGCGCGCGCGCTCCCGCATCTGACCCCGAGC 60  
 QY 61 CGCGCGCGCTCCCGCGGAGAGAGAGATCCAGTCCCGCGCGCGCGCGCACTGGTCCA 120  
 DB 61 CGCGCGCGCTCCCGCGGAGAGAGAGATCCAGTCCCGCGCGCGCGCGCACTGGTCCA 120  
 QY 121 GTGCGGCGCGCGCGCGCGCGCGAGAGAGATGCAAGCGGCTTGCGGCGCACTGGTCTGT 180  
 DB 121 GTGCGGCGCGCGCGCGCGCGCGAGAGAGATGCAAGCGGCTTGCGGCGCACTGGTCTGT 180  
 QY 181 GCTGCTCTGCG 240  
 DB 181 GCTGCTCTGCG 240  
 QY 241 CTCGAGTGAAGCGCGCGCGCGCGCTCTCACTACCGCGAGAGAGAGCGCACTCATATGA 300  
 DB 241 CTCGAGTGAAGCGCGCGCGCGCGCTCTCACTACCGCGAGAGAGAGCGCACTCATATGA 300  
 QY 301 TGTTCGCGAGGTTGAGGAACCTGATGAGAGACGCGACCAATTTGGCGAGCGCGGTGG 360

DB 301 TGTTCGCGAGGTTGAGGAACCTGATGAGAGACGCGACCAATTTGGCGAGCGCGGTGG 360  
 QY 361 AAGAGATGAGGCGAGAGAGAGGCTGCTGCTAAAGCATCATCAGAAAGTGAACCTGGCAACT 420  
 DB 361 AAGAGATGAGGCGAGAGAGAGGCTGCTGCTAAAGCATCATCAGAAAGTGAACCTGGCAACT 420  
 QY 421 TACCTCCAGGCTATATCAATGAGACCAACAGACAGAGGTTGGAATTAATACATCC 480  
 DB 421 TACCTCCAGGCTATATCAATGAGACCAACAGACAGAGGTTGGAATTAATACATCC 480  
 QY 481 ATGTGCAACGAGAAATTCACAAAGATACCAACCAACCACTGAGCAATATGCTTTTCAG 540  
 DB 481 ATGTGCAACGAGAAATTCACAAAGATACCAACCAACCACTGAGCAATATGCTTTTCAG 540  
 QY 541 AGACAGTTATCAATCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
 DB 541 AGACAGTTATCAATCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
 QY 601 ACAGAGAGCTGTGGGCGCGAGAGATGTCTGACAGTTTGGCAGCTTCCAGTACACCTGCAGC 660  
 DB 601 ACAGAGAGCTGTGGGCGCGAGAGATGTCTGACAGTTTGGCAGCTTCCAGTACACCTGCAGC 660  
 QY 661 CATGCCGCGGCGCGAGAGATGCTCTGACACCGCGAGACGTAAGTGTGTGAGACACAGCTGT 720  
 DB 661 CATGCCGCGGCGCGAGAGATGCTCTGACACCGCGAGACGTAAGTGTGTGAGACACAGCTGT 720  
 QY 721 GTGTCTGCGGCTCACTGACACCAAAATGCGCACCGAGGCGAGAGAGAGAGAGAGAGAGAG 780  
 DB 721 GTGTCTGCGGCTCACTGACACCAAAATGCGCACCGAGGCGAGAGAGAGAGAGAGAGAGAG 780  
 QY 781 ACCAGAGGAGCTGCCAGCGCGGCTGTGTGCTTCCAGAGAGAGCTGTGTCTCTG 840  
 DB 781 ACCAGAGGAGCTGCCAGCGCGGCTGTGTGCTTCCAGAGAGAGCTGTGTCTCTG 840  
 QY 841 TGTGCAACACCCCTGCGCGGTGAGAGGCGAGAGCTTTGGCATGACCCGCGCGGCTTCGG 900  
 DB 841 TGTGCAACACCCCTGCGCGGTGAGAGGCGAGAGCTTTGGCATGACCCGCGCGGCTTCGG 900  
 QY 901 ACCCTATCACTGAGAGAGTGAAGCTGTATGAGAGCTTGGACCGATGCCCTTGTGCGAGTG 960  
 DB 901 ACCCTATCACTGAGAGAGTGAAGCTGTATGAGAGCTTGGACCGATGCCCTTGTGCGAGTG 960  
 QY 961 GCTCTCTGCGAGCG 1020  
 DB 961 GCTCTCTGCGAGCG 1020  
 QY 1021 GGAGCGGTGACCAAGATGAGAGAGATCTGCTGCGCGAGAGAGTCCCGATGATATGAG 1080  
 DB 1021 GGAGCGGTGACCAAGATGAGAGAGATCTGCTGCGCGAGAGAGTCCCGATGATATGAG 1080  
 QY 1081 TTGGGAGCTTCAATGAGAGAGGTGCGCGAGAGCTGAGAGAGCTTGGAGAGAGCTGACTG 1140  
 DB 1081 TTGGGAGCTTCAATGAGAGAGGTGCGCGAGAGCTGAGAGAGCTTGGAGAGAGCTGACTG 1140  
 QY 1141 AAGAGATGAGCGCTGAGGAGAGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200  
 DB 1141 AAGAGATGAGCGCTGAGGAGAGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200  
 QY 1201 TTTAGATCTGGAACAGAGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCA 1260  
 DB 1201 TTTAGATCTGGAACAGAGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCA 1260  
 QY 1261 GGTGTGTGCTTAAAGGCGGTGAGCGAGGCTTCTTCCATCACTCTTCCAGTAAGTT 1320  
 DB 1261 GGTGTGTGCTTAAAGGCGGTGAGCGAGGCTTCTTCCATCACTCTTCCAGTAAGTT 1320  
 QY 1321 TCCCTCTGAGCTTGAACAGATAGAGTGTGTGCTTCACTTGTTCAGTCCCGCGAGCGTGTCT 1380  
 DB 1321 TCCCTCTGAGCTTGAACAGATAGAGTGTGTGCTTCACTTGTTCAGTCCCGCGAGCGTGTCT 1380  
 QY 1381 CAGAGCTTACAGCTGTGTGTGAGAGAGTGAAGGAGGTTAACTGACAGAGAGAGTT 1440

Db 1381 CCAGGCTTCAACAGTCTGCTGCTGGAGAGTCAAGGAGGGTTAACTCGAGAGCAAGTTT 1440  
 Qy 1441 GCCACCCCTGTCAGATTAATTTGGCTGCTTGGCTCTACACAGTTGGCAGACAGCCGTTTG 1500  
 Db 1441 GCCACCCCTGTCAGATTAATTTGGCTGCTTGGCTCTACACAGTTGGCAGACAGCCGTTTG 1500  
 Qy 1501 TCTACATGAGCTTTGAATTTGTTGAGGAGAGAGTGAACAATGTGAGTCTCCCTC 1560  
 Db 1501 TCTACATGAGCTTTGAATTTGTTGAGGAGAGAGTGAACAATGTGAGTCTCCCTC 1560  
 Qy 1561 TGATTTGTTTGGGAAATGTGAGAAAGAGTCCCTGCTTTGGCAAAATCACTGAGCA 1620  
 Db 1561 TGATTTGTTTGGGAAATGTGAGAAAGAGTCCCTGCTTTGGCAAAATCACTGAGCA 1620  
 Qy 1621 AAATGCAACAAATGAATTTTCCAGCAGTCTTTCCATGAGGATAGGTAGCTGTGCTT 1680  
 Db 1621 AAATGCAACAAATGAATTTTCCAGCAGTCTTTCCATGAGGATAGGTAGGTGCTGCTT 1680  
 Qy 1681 CAGCTGTTGAGATGAATGTTCTGTTCACTCCCTGATTAATGTTTATTCATCCAGCA 1740  
 Db 1681 CAGCTGTTGAGATGAATGTTCTGTTCACTCCCTGATTAATGTTTATTCATCCAGCA 1740  
 Qy 1741 GTGTTGCTCAGCTCTTACCTCTGTCAGAGGAGCAGATTTTCAATCCAGATCAATCCC 1800  
 Db 1741 GTGTTGCTCAGCTCTTACCTCTGTCAGAGGAGCAGATTTTCAATCCAGATCAATCCC 1800  
 Qy 1801 TCTCTCAGCAGAGCTGGGAGGAGGAGTCTGTTCTCTGTCATCAGGAGATCTCAGAG 1860  
 Db 1801 TCTCTCAGCAGAGCTGGGAGGAGGAGTCTGTTCTCTGTCATCAGGAGATCTCAGAG 1860  
 Qy 1861 GCTCAGAGACTGCAAGCTGCTTCCCAAGTCAACAGCTAATGAGAACCAAGCAGTTTC 1920  
 Db 1861 GCTCAGAGACTGCAAGCTGCTTCCCAAGTCAACAGCTAATGAGAACCAAGCAGTTTC 1920  
 Qy 1921 ATCTGTTGTAATCTCTAAGCTCAGTGCCTCTCCACATCCCAACAGCCTTGTGAGCA 1980  
 Db 1921 ATCTGTTGTAATCTCTAAGCTCAGTGCCTCTCCACATCCCAACAGCCTTGTGAGCA 1980  
 Qy 1981 CCAAAAGTCTCCCCAAAAGAGAGAGATGGATTTTTCTTGGAGCATGCATCTGGA 2040  
 Db 1981 CCAAAAGTCTCCCCAAAAGAGAGAGATGGATTTTTCTTGGAGCATGCATCTGGA 2040  
 Qy 2041 AATTAAGGCAACTAATTTCTACATCCCTCTAAAGTAATCTCTGTTAGGAACAGAGT 2100  
 Db 2041 AATTAAGGCAACTAATTTCTACATCCCTCTAAAGTAATCTCTGTTAGGAACAGAGT 2100  
 Qy 2101 GTTCTCAGAGTGTGGGAGGAGCCGCTCTTAATGAGAACATGATTTGACATGTCCT 2160  
 Db 2101 GTTCTCAGAGTGTGGGAGGAGCCGCTCTTAATGAGAACATGATTTGACATGTCCT 2160  
 Qy 2161 CTTTGGCAGTGTGATTAATCTTTGAAAGTAAATGATGAGGTGATTAACAGTTA 2220  
 Db 2161 CTTTGGCAGTGTGATTAATCTTTGAAAGTAAATGATGAGGTGATTAACAGTTA 2220  
 Qy 2221 CCTGCAAGAACAGTACTTAAGTAAATGAGGAGGAGTAAATGAAATGTTGCAAAAT 2280  
 Db 2221 CCTGCAAGAACAGTACTTAAGTAAATGAGGAGGAGTAAATGAAATGTTGCAAAAT 2280  
 Qy 2281 CACTTAGCAGCACTGAAGACAAATTAATCAACAGTGAAGAAATCAAAACGAGCAGGCG 2340  
 Db 2281 CACTTAGCAGCACTGAAGACAAATTAATCAACAGTGAAGAAATCAAAACGAGCAGGCG 2340  
 Qy 2341 TGTGTGAAGAACAGTGTGATATATGCACTGAGAACCTGTAAGCCACTCCACAA 2400  
 Db 2341 TGTGTGAAGAACAGTGTGATATATGCACTGAGAACCTGTAAGCCACTCCACAA 2400  
 Qy 2401 TGAATGTTTCAAGGTGTATGAGAGCTGTTGCCACCATGATTTATTCACAGTTCTTAAAGT 2460  
 Db 2401 TGAATGTTTCAAGGTGTATGAGAGCTGTTGCCACCATGATTTATTCACAGTTCTTAAAGT 2460  
 Qy 2461 TAAAGTTGACATATGATATAGCAATGCTTTCTTTGAGTTTAAATATGATTAACAT 2520  
 Db 2461 TAAAGTTGACATATGATATAGCAATGCTTTCTTTGAGTTTAAATATGATTAACAT 2520

Qy 2521 AAGTTGATTTAGAAATCAACATTAATCACTCACTGCAAAAAAAAAAAAAAAAAAAAA 2580  
 Db 2521 AAGTTGATTTAGAAATCAACATTAATCACTCACTGCAAAAAAAAAAAAAAAAAAAAA 2580  
 Qy 2581 AAAAAA 2586  
 Db 2581 AAAAAA 2586  
 RESULT 3  
 AAF72413  
 ID AAF72413 standard; cDNA; 2586 BP.  
 XX  
 AC AAF72413;  
 XX  
 DT 24-APR-2001 (first entry)  
 XX  
 DE Human PRO295 cDNA.  
 XX  
 KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;  
 KW antiparkinsonian neurotropic; neuroprotective; vulnerary; cardiant;  
 KW antiangiogenic; vasotropic; antischmatic; antitumoric; cancer;  
 KW antiautistic; antilethality; antidiabetic; antiviral; diabetes;  
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;  
 KW lechaemia; inflammation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 EN WO200104311-A1.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 22-FEB-2000; 2000MO-US04414.  
 XX  
 PR 07-JUL-1999; 99US-0143048.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 08-SEP-1999; 99MO-US20594.  
 PR 13-SEP-1999; 99MO-US20944.  
 PR 15-SEP-1999; 99MO-US21090.  
 PR 15-SEP-1999; 99MO-US21547.  
 PR 05-OCT-1999; 99MO-US23089.  
 PR 29-NOV-1999; 99MO-US28214.  
 PR 30-NOV-1999; 99MO-US28313.  
 PR 16-DEC-1999; 99MO-US30095.  
 PR 20-DEC-1999; 99MO-US30911.  
 PR 20-DEC-1999; 99MO-US30999.  
 PR 05-JAN-2000; 99MO-US00219.  
 XX  
 PA (GENTH) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Grimaldi CJ, Gurney AJ, Hillan KJ, Kijavlin IJ;  
 PI Mather JP, Pan U, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WZ;  
 XX  
 DR MPI, 2001-081051/09.  
 DR F-PSDB; AAB80252.  
 XX  
 PT Sixty one nucleic acids encoding PRO polypeptides which are useful in  
 PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung  
 PT squamous cell carcinoma) and neurodegenerative diseases (e.g.  
 PT Alzheimer's disease) -  
 XX  
 PS Claim 2; Fig 83; 393pp; English.  
 XX  
 CC The present sequence is one of sixty one nucleic acids encoding novel  
 CC secreted and transmembrane PRO polypeptides. The PRO polypeptides are  
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung  
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.  
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,

CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.  
 CC endometrial bleeding angiogenesis, ischaemias such as coronary  
 CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,  
 CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and  
 CC diabetes and retinal disorders such as retinitis pigmentosa.  
 CC The PRO nucleic acids have applications in molecular biology, including  
 CC use as hybridization probes, and in chromosome and gene mapping.

xx Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;

Query Match 100.0%; Score 2586; DB 22; Length 2586;

Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGCTCCCGGACCCGCGGCGCCGACCGGCGGCTCCCGCATCTGACCCCGAGC 60  
 Db 1 CGCGCGCTCCCGGACCCGCGGCGCCGACCGGCGGCTCCCGCATCTGACCCCGAGC 60  
 QY 61 CGCGCGGCTCCCGGCGGAGCGAGATCCAGTCCGCGCCGCGAGCGCAACTCGTCCA 120  
 Db 61 CGCGCGGCTCCCGGCGGAGCGAGATCCAGTCCGCGCCGCGAGCGCAACTCGTCCA 120  
 QY 121 GTCCGGGCGGCGGCTGCGCGGCGCAGAGCGAGATGCAAGCGGCTTGAGGCGCACTGCTGT 180  
 Db 121 GTCCGGGCGGCGGCTGCGCGGCGCAGAGCGAGATGCAAGCGGCTTGAGGCGCACTGCTGT 180  
 QY 181 GCTGCTCTGAGCGGCGGCTGCCCGAGCGCCCGCGCGCTCCGAGCGGCGACTCGG 240  
 Db 181 GCTGCTCTGAGCGGCGGCTGCCCGAGCGCCCGCGCGCTCCGAGCGGCGACTCGG 240  
 QY 241 CTCCAGTCAAGCCCGGCGGCTCTCAAGTACCCGCGAGAGAGCGCACTCTCATATAGA 300  
 Db 241 CTCCAGTCAAGCCCGGCGGCTCTCAAGTACCCGCGAGAGAGCGCACTCTCATATAGA 300  
 QY 301 TGTTCGCGAGGTTGAGGAACTGATGAGGACAGCGACCAATTCGCGAGCGGCTGG 360  
 Db 301 TGTTCGCGAGGTTGAGGAACTGATGAGGACAGCGACCAATTCGCGAGCGGCTGG 360  
 QY 361 AAGAGATGAGGCGAGAAAGCTGCTAAAGCATCATCAAGTGAACCTGGCAACT 420  
 Db 361 AAGAGATGAGGCGAGAAAGCTGCTAAAGCATCATCAAGTGAACCTGGCAACT 420  
 QY 421 TACCTCCGAGTATACATGAGACCAAGACAGACGAAAGTGGAAATATATCCATCC 480  
 Db 421 TACCTCCGAGTATACATGAGACCAAGACAGACGAAAGTGGAAATATATCCATCC 480  
 QY 481 ATGTGACCGGAAATTCACAAGATTAACAACAACAGACTGACCAATGCTCTTTTCA 540  
 Db 481 ATGTGACCGGAAATTCACAAGATTAACAACAACAGACTGACCAATGCTCTTTTCA 540  
 QY 541 AGACAGTTATCATCTGTGGGAGACGAAAGGACGAGAGGACGAGATGATCATCG 600  
 Db 541 AGACAGTTATCATCTGTGGGAGACGAAAGGACGAGAGGACGAGATGATCATCG 600  
 QY 601 ACGAGAGCTGTGGGCGCAGCATGTACTGCACTTTCAGCTTCAGTACACTGCGACG 660  
 Db 601 ACGAGAGCTGTGGGCGCAGCATGTACTGCACTTTCAGCTTCAGTACACTGCGACG 660  
 QY 661 CATGCCGGGCGCAGAGATGCTGTGACCCCGGACAGTGAAGTGTGTGGAAACCAAGTGT 720  
 Db 661 CATGCCGGGCGCAGAGATGCTGTGACCCCGGACAGTGAAGTGTGTGGAAACCAAGTGT 720  
 QY 721 GTGTCTGGGGTCACTGCAACAAATGCGCACAGGGGCGAGCAATGAGCACTGTGTACA 780  
 Db 721 GTGTCTGGGGTCACTGCAACAAATGCGCACAGGGGCGAGCAATGAGCACTGTGTACA 780  
 QY 781 ACCAGAGGAGCTGCGACCGGGGCTGTGCTGTGCTTCCAGAGAGGCTGTGTTCCCTG 840  
 Db 781 ACCAGAGGAGCTGCGACCGGGGCTGTGCTGTGCTTCCAGAGAGGCTGTGTTCCCTG 840  
 QY 841 TGTGCAACCCCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900  
 Db 841 TGTGCAACCCCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900

QY 901 ACCTCATCACTTGGAGAGCTAGAGCTGATGAGAGCTTGGACCGATGCTTGTGCTAGT 960  
 Db 901 ACCTCATCACTTGGAGAGCTAGAGCTGATGAGAGCTTGGACCGATGCTTGTGCTAGT 960  
 QY 961 GCTTCCTCGGAGCGCCACAGCCACAGGCTGTGATGTGTGCAAGCGGACCTTGTG 1020  
 Db 961 GCTTCCTCGGAGCGCCACAGCCACAGGCTGTGATGTGTGCAAGCGGACCTTGTG 1020  
 QY 1021 GAGGCGGTGACCAAGATGGGAGATCTGTGCTCCAGAGAGGCTCCGATGATGAG 1080  
 Db 1021 GAGGCGGTGACCAAGATGGGAGATCTGTGCTCCAGAGAGGCTCCGATGATGAG 1080  
 QY 1081 TTGGCAGCTTCATGAGAGAGGCGGCGCAGAGCTGAGAGGAGGAGGAGGAGGAGG 1140  
 Db 1081 TTGGCAGCTTCATGAGAGAGGCGGCGCAGAGCTGAGAGGAGGAGGAGGAGGAGG 1140  
 QY 1141 AAGAGATGAGCGCTGGGAGAGCTGCGGCTCCGCGCTGCACTGTGGAGGGGAGAGA 1200  
 Db 1141 AAGAGATGAGCGCTGGGAGAGCTGCGGCTCCGCGCTGCACTGTGGAGGGGAGAGA 1200  
 QY 1201 TTTAGATCTGAGACAGGCTGTGGATGATGATGATGATGATGATGATGATGATGAT 1260  
 Db 1201 TTTAGATCTGAGACAGGCTGTGGATGATGATGATGATGATGATGATGATGATGAT 1260  
 QY 1261 GGTGTGCTTGAAGCGGTGAGGCTGACACAGGCTTCTTCTACATCTTCTTCCAGTAA 1320  
 Db 1261 GGTGTGCTTGAAGCGGTGAGGCTGACACAGGCTTCTTCTACATCTTCTTCCAGTAA 1320  
 QY 1321 TCCCTCTGCTTGAAGCGGTGAGGCTGACACAGGCTTCTTCTACATCTTCTTCCAGTAA 1380  
 Db 1321 TCCCTCTGCTTGAAGCGGTGAGGCTGACACAGGCTTCTTCTACATCTTCTTCCAGTAA 1380  
 QY 1381 CCAGGCTTCAAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1440  
 Db 1381 CCAGGCTTCAAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1440  
 QY 1441 GCGACCCCTGTCAGATTAATGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1500  
 Db 1441 GCGACCCCTGTCAGATTAATGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1500  
 QY 1501 TCTACATGCTTGAATTAATGTTGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1560  
 Db 1501 TCTACATGCTTGAATTAATGTTGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560  
 QY 1561 TGAATGTTTGGGAAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620  
 Db 1561 TGAATGTTTGGGAAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620  
 QY 1621 AATGCAACAATGAATTTTCAAGAGAGTCTTTCATGAGGAGTAAAGTGTGCTT 1680  
 Db 1621 AATGCAACAATGAATTTTCAAGAGAGTCTTTCATGAGGAGTAAAGTGTGCTT 1680  
 QY 1681 CAGCTGTGCAAGATGAATGTTCTGTTCACTGATTAACATGTTTATATTCACAGA 1740  
 Db 1681 CAGCTGTGCAAGATGAATGTTCTGTTCACTGATTAACATGTTTATATTCACAGA 1740  
 QY 1741 GTGTGCTGAGCTTCACTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800  
 Db 1741 GTGTGCTGAGCTTCACTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800  
 QY 1801 TCTCTGAGCAGGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860  
 Db 1801 TCTCTGAGCAGGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860  
 QY 1861 GCTCAGAGCTGAGAGCTTGGCCCAAGTCAACAGCTAGTGAAGACCAAGAGCACTTTC 1920  
 Db 1861 GCTCAGAGCTGAGAGCTTGGCCCAAGTCAACAGCTAGTGAAGACCAAGAGCACTTTC 1920  
 QY 1921 ATCTGTTGATGATCTAAGCTAGTGTCTCTCACTACACCAACCAAGCTTGTGCA 1980  
 Db 1921 ATCTGTTGATGATCTAAGCTAGTGTCTCTCACTACACCAACCAAGCTTGTGCA 1980





Db 1921 AACTGTTGACTCTTAAGCTAGTCTCTCTCCACTACCCACACAGCCCTGGTGCA 1980  
Qy 1981 CCAAAAGTCTCCCAAGAGAGAAATGGATTTTCTTGAGGAGTGCACATCTGGA 2040  
Db 1981 CCAAAAGTCTCCCAAGAGAGAAATGGATTTTCTTGAGGAGTGCACATCTGGA 2040  
Qy 2041 ATTAAGTCAAACTAATTTCTCATCTCTCTAAAGTAACTACTGTTAGAACAGCACT 2100  
Db 2041 ATTAAGTCAAACTAATTTCTCATCTCTCTAAAGTAACTACTGTTAGAACAGCACT 2100  
Qy 2101 GTTCTCAAGTGTGGGCGAGCCCTCTTCTTAATGAAGAATTAATTAAGTCTCTCT 2160  
Db 2101 GTTCTCAAGTGTGGGCGAGCCCTCTTCTTAATGAAGAATTAATTAAGTCTCTCT 2160  
Qy 2161 CTTTGCAAGTGTAGTATGTAATCTTTGAAAGTATATGACTGAGCGTACAGGTTAA 2220  
Db 2161 CTTTGCAAGTGTAGTATGTAATCTTTGAAAGTATATGACTGAGCGTACAGGTTAA 2220  
Qy 2221 CTTGCAAGAACTAGTATGTAATGTAAGGAGGAGGATTAATGAATTTGCAAAAT 2280  
Db 2221 CTTGCAAGAACTAGTATGTAATGTAAGGAGGAGGATTAATGAATTTGCAAAAT 2280  
Qy 2281 CACTAGCAGCACTAGTACATTAATCAACAGCTGAGAAATCAACAGCAGGAGG 2340  
Db 2281 CACTAGCAGCACTAGTACATTAATCAACAGCTGAGAAATCAACAGCAGGAGG 2340  
Qy 2341 TGTGTGAACATGTTGTAATATGCACTGCGAAGCTGTAAGCTCTTCCGCACTCAAA 2400  
Db 2341 TGTGTGAACATGTTGTAATATGCACTGCGAAGCTGTAAGCTCTTCCGCACTCAAA 2400  
Qy 2401 TGAATGTTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460  
Db 2401 TGAATGTTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460  
Qy 2461 TAAAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
Db 2461 TAAAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
Qy 2521 AAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580  
Db 2521 AAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580  
Qy 2581 AAAAAA 2586  
Db 2581 AAAAAA 2586  
RESULT 5  
ABL95585  
ID ABL95585 standard; cDNA; 2586 BP.  
XX ABL95585;  
AC  
XX 19-JUL-2002 (first entry)  
DT  
XX  
XX Human angiogenesis related cDNA PRO295 SEQ ID NO: 49.  
DE  
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiac; cyclostatic; antiangiogenic; hypotensive; vllnerary;  
KW antiarteriosclerotic; gene; se.  
XX Homo sapiens.  
OS  
XX WO200208284-A2.  
PN  
XX 31-JAN-2002.  
PD  
XX 09-JUL-2001; 2001WO-US21735.  
PT  
XX 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.

PR 25-JUL-2000; 2000US-220624P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23338.  
PR 07-SEP-2000; 2000US-230978P.  
PR 15-SEP-2000; 2000US-000000P.  
PR 18-SEP-2000; 2000US-064610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001US-0802706.  
PR 09-MAR-2001; 2001US-0808689.  
PR 14-MAR-2001; 2001US-0816744.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 01-JUN-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 28-JUN-2001; 2001WO-US19692.  
PR 28-JUN-2001; 2001WO-US00000.  
XX (GETH ) GENENTECH INC.  
PA (BAKE ) BAKER K P.  
PA (FERR ) FERRARA N.  
PA (GERB ) GERBER H.  
PA (GERR ) GERRITSEN M E.  
PA (GODD ) GODDARD A.  
PA (GODO ) GODOWSKI P J.  
PA (GURN ) GURNEY A L.  
PA (HILL ) HILLAN K J.  
PA (MARS ) MARSTERS S A.  
PA (PANO ) PAN J.  
PA (PAON ) PAONI N F.  
PA (STEP ) STEPHAN J F.  
PA (WATA ) WATANABE C K.  
PA (WILL ) WILLIAMS P M.  
PA (WOOD ) WOOD W I.  
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
PI MPI: 2002-171999/22.  
XX P-PSDB; ABB5447.  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
XX infarction), endothelial or angiogenic disorders in a mammal -  
XX Claim 1; Fig 49; 567pp; English.  
XX The present invention provides the protein and coding sequences of human  
CC PRO proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
CC hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound





```

Db      2041 ATTAAGTCAAACTAATTCATCCCTCTTAAAGTAAGTAAGTCTTGAAGACGACGT 2100
QY      2101 GTTCTCAGAGTGTGGGAGAGCCGCTCTTAATGAAGCAATGATTTGACATGTCCT 2160
Db      2101 GTTCTCAGAGTGTGGGAGAGCCGCTCTTAAATGAAGCAATGATTTGACATGTCCT 2160
QY      2161 CTTTGGCAGTTGCACTTAACTTGAAGGTATGACTAGGCTACATACAGGTTAA 2220
Db      2161 CTTTGGCAGTTGCACTTAACTTGAAGGTATGACTAGGCTACATACAGGTTAA 2220
QY      2221 CTTGAGAAACAGTACTTAAATGTAAGGCGAGGATTAATAAGTAATTGCAAAAT 2280
Db      2221 CTTGAGAAACAGTACTTAAATGTAAGGCGAGGATTAATAAGTAATTGCAAAAT 2280
QY      2281 CACTTACGACGACACTGAAACAAATTAACAACCTGGAGAAATCAACGAGAGGGGC 2340
Db      2281 CACTTACGACGACACTGAAACAAATTAACAACCTGGAGAAATCAACGAGAGGGGC 2340
QY      2341 TGTGTGAACATGTTGTATATGCGACTGCGAACAAGTCTTACGCCACTCCACAAA 2400
Db      2341 TGTGTGAACATGTTGTATATGCGACTGCGAACAAGTCTTACGCCACTCCACAAA 2400
QY      2401 TGAATGTTTCAAGTGTATGACATGTTGCGACCATGATTCATCCAGAGTTCTTAAATT 2460
Db      2401 TGAATGTTTCAAGTGTATGACATGTTGCGACCATGATTCATCCAGAGTTCTTAAATT 2460
QY      2461 TAAAGTTGACATGATTTGTATAGAGATGCTTCTTGAAGTTTAAATGATTAACAT 2520
Db      2461 TAAAGTTGACATGATTTGTATAGAGATGCTTCTTGAAGTTTAAATGATTAACAT 2520
QY      2521 AAGTTGCATTTAGAAATCAAGCATTAATCACTTCAATGCAAAAAA 2580
Db      2521 AAGTTGCATTTAGAAATCAAGCATTAATCACTTCAATGCAAAAAA 2580
QY      2581 AAAAAA 2586
Db      2581 AAAAAA 2586

```

RESULT 6  
ABL88096  
ID ABL88096 standard; cDNA; 2586 BP.  
AC ABL88096;  
DT 16-MAY-2002 (first entry)  
DE Human PRO295 cDNA sequence SEQ ID NO:49.  
XX Human; angiogenesis; cardiact; cytostatic; antiangiogenic; hypotensive;  
XX Humoral; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
XX age-related macular degeneration; arterial restenosis; angina;  
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
XX wound healing; chromosome mapping; gene mapping; gene; ss.  
XX Homo sapiens.  
XX OS  
XX WO200200690-A2.  
XX PD 03-JAN-2002.  
XX PF 20-JUN-2001; 2001WO-US19692.  
XX PR 23-JUN-2000; 2000US-213637P.  
XX PR 20-JUL-2000; 2000US-219556P.  
XX PR 25-JUL-2000; 2000US-220624P.  
XX PR 28-JUL-2000; 2000US-220664P.  
XX PR 02-AUG-2000; 2000US-222695P.  
XX PR 17-AUG-2000; 2000US-0643657.

```

PR      23-AUG-2000; 2000WO-US23522.  
PR      24-AUG-2000; 2000WO-US23338.  
PR      07-SEP-2000; 2000US-230978P.  
PR      18-SEP-2000; 2000US-0664610.  
PR      18-SEP-2000; 2000US-0665350.  
PR      24-OCT-2000; 2000US-242922P.  
PR      08-NOV-2000; 2000US-0709238.  
PR      08-NOV-2000; 2000WO-US30952.  
PR      10-NOV-2000; 2000WO-US30873.  
PR      01-DEC-2000; 2000WO-US32678.  
PR      20-DEC-2000; 2000US-0744259.  
PR      20-DEC-2000; 2000WO-US34956.  
PR      22-JAN-2001; 2001US-0767609.  
PR      28-FEB-2001; 2001US-0796498.  
PR      28-FEB-2001; 2001WO-US06520.  
PR      01-MAR-2001; 2001WO-US06666.  
PR      09-MAR-2001; 2001US-0802706.  
PR      14-MAR-2001; 2001US-0808689.  
PR      22-MAR-2001; 2001US-0816744.  
PR      05-APR-2001; 2001US-0828366.  
PR      10-MAY-2001; 2001US-0854208.  
PR      10-MAY-2001; 2001US-0854280.  
PR      25-MAY-2001; 2001US-0866028.  
PR      25-MAY-2001; 2001WO-US17092.  
PR      25-MAY-2001; 2001WO-US17092.  
PR      30-MAY-2001; 2001US-0870574.  
PR      30-MAY-2001; 2001WO-US17443.  
PR      01-JUN-2001; 2001WO-US17800.  

XX      (GETH ) GENENTECH INC.  
XX      Baker KP, Ferrara N, Gerber H, Gertsen MB, Goddard A,  
XX      Godlewski PJ, Guirney AL, Hillan KJ, Marsters SA, Pan J,  
XX      Stephen JF, Watanabe CK, Williams PM, Wood WI, Ye W,  
XX      WPI: 2002-090516/12.  
XX      P-PSDB; ABB84841.  
XX      One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
XX      useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
XX      infarction), endothelial or angiogenic disorders in a mammal -  
XX      Claim 2; Fig 49; 565pp; English.  
XX      ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
XX      ABB85003. The PRO proteins and polynucleotides have cardiact, cytostatic,  
XX      antiangiogenic, hypotensive, vulnereary and antiarteriosclerotic  
XX      activities, and can be used in gene therapy. The PRO polynucleotides,  
XX      proteins, agonists and antagonists are useful for treating or diagnosing  
XX      a cardiovascular, endothelial or angiogenic disorder in a mammal,  
XX      e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
XX      degeneration, atherosclerosis, hypertension, arterial restenosis,  
XX      rheumatoid arthritis, angina, myocardial infarction, thrombophlebitis,  
XX      lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
XX      carcinoma), and wound healing. The PRO polynucleotides have applications  
XX      in molecular biology, including use as hybridisation probes, and in  
XX      chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
XX      probes used in the exemplification of the present invention.  

XX      Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;

```

```

Query Match      100.0%; Score 2586; DB 24; Length 2586;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2586; Conservative 0;
QY      1 CGCGCGCTCCCGGACCGCGCGCCCGCCACCGCGCGCTCCGCACTGACCCCGGACG 60
Db      1 CGCGCGCTCCCGGACCGCGCGCCCGCCACCGCGCGCTCCGCACTGACCCCGGACG 60
QY      61 CCGCGCGCTCCCGGCGGAGACGACATTCAGTCCGCGCGGAGCGCACTCGGTCCA 120
Db      61 CCGCGCGCTCCCGGCGGAGCGAGACATTCAGTCCGCGCGGAGCGCACTCGGTCCA 120

```



DB 2281 CACTAGCAGCACTGAGACATTAATCAACAGCTGAGAAAAATCAACGACGAGGCG 2340  
QY 2341 TGTGTGAACACTGTTGTATATATGCGACTGCGAACTGTAATCTTACGCCATCTCCACAA 2400  
DB 2341 TGTGTGAACACTGTTGTATATATGCGACTGCGAACTGTAATCTTACGCCATCTCCACAA 2400  
QY 2401 TGATGTTTTCAGTGTGCTGAGCTGTGCGACCATGTATTCATCCAGAGTTCTTAAAGT 2460  
DB 2401 TGATGTTTTCAGTGTGCTGAGCTGTGCGACCATGTATTCATCCAGAGTTCTTAAAGT 2460  
QY 2461 TAAAGTGCACATATTTGTATATAGCATGCTTTCTTTGAGTTTAAATATATATTAACAT 2520  
DB 2461 TAAAGTGCACATATTTGTATATAGCATGCTTTCTTTGAGTTTAAATATATTAACAT 2520  
QY 2521 AAGTTGCATTTAGAAATCAAGCATTAATCACTTCACTGCGAAAAA 2580  
DB 2521 AAGTTGCATTTAGAAATCAAGCATTAATCACTTCACTGCGAAAAA 2580  
QY 2581 AAAAAA 2586  
DB 2581 AAAAAA 2586  
  
RESULT 7  
ACAS5002  
ID ACAS5002 standard; cDNA; 2586 BP.  
AC  
ACAS5002;  
XX  
DT 05-JUN-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO295 cDNA.  
XX  
XX Human; secreted and transmembrane protein; gene therapy; psoriasis;  
XX enterocolitis; gastrointestinal ulceration; skin disease;  
XX keratinocyte differentiation; epithelial cancer; Alzheimer's disease;  
XX squamous cell carcinoma; Parkinson's disease; inflammatory disease;  
XX amyotrophic lateral sclerosis; rheumatoid arthritis; asthma;  
XX multiple sclerosis; organ failure; atherosclerosis; cardiac injury;  
XX infertility; birth defect; premature aging; AIDS; cancer;  
XX diabetic complication; wound repair; tissue re-growth; gene; ss.  
OS Homo sapiens.  
PN US2003017463-A1.  
XX  
XX 23-JAN-2003.  
PD  
XX  
XX 11-JUL-2001; 2001US-0903640.  
XX  
PR 10-SEP-1998; 98WO-US18824.  
PR 14-SEP-1998; 98WO-US19177.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 01-DEC-1998; 98WO-US25108.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30939.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.

PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 17-SEP-1997; 97US-059113P.  
PR 17-SEP-1997; 97US-059113P.  
PR 17-SEP-1997; 97US-059117P.  
PR 17-SEP-1997; 97US-059119P.  
PR 17-SEP-1997; 97US-059121P.  
PR 17-SEP-1997; 97US-059122P.  
PR 17-SEP-1997; 97US-059184P.  
PR 18-SEP-1997; 97US-059263P.  
PR 18-SEP-1997; 97US-059266P.  
PR 15-OCT-1997; 97US-062125P.  
PR 17-OCT-1997; 97US-062285P.  
PR 17-OCT-1997; 97US-062287P.  
PR 21-OCT-1997; 97US-063486P.  
PR 24-OCT-1997; 97US-062814P.  
PR 24-OCT-1997; 97US-062816P.  
PR 24-OCT-1997; 97US-063045P.  
PR 24-OCT-1997; 97US-063120P.  
PR 24-OCT-1997; 97US-063121P.  
PR 24-OCT-1997; 97US-063127P.  
PR 24-OCT-1997; 97US-063128P.  
PR 27-OCT-1997; 97US-063327P.  
PR 27-OCT-1997; 97US-063329P.  
PR 28-OCT-1997; 97US-063541P.  
PR 28-OCT-1997; 97US-063542P.  
PR 28-OCT-1997; 97US-063544P.  
PR 28-OCT-1997; 97US-063549P.  
PR 28-OCT-1997; 97US-063550P.  
PR 28-OCT-1997; 97US-063564P.  
PR 29-OCT-1997; 97US-063435P.  
PR 29-OCT-1997; 97US-063704P.  
PR 29-OCT-1997; 97US-063722P.  
PR 29-OCT-1997; 97US-063734P.  
PR 29-OCT-1997; 97US-063735P.  
PR 29-OCT-1997; 97US-063738P.  
PR 29-OCT-1997; 97US-064255P.  
PR 29-OCT-1997; 97US-064256P.  
PR 31-OCT-1997; 97US-064103P.  
PR 03-NOV-1997; 97US-064248P.  
PR 07-NOV-1997; 97US-064809P.  
PR 12-NOV-1997; 97US-065186P.  
PR 17-NOV-1997; 97US-065846P.  
PR 18-NOV-1997; 97US-065893P.  
PR 21-NOV-1997; 97US-066120P.  
PR 21-NOV-1997; 97US-066364P.  
PR 24-NOV-1997; 97US-066453P.  
PR 24-NOV-1997; 97US-066466P.  
PR 24-NOV-1997; 97US-066511P.  
PR 24-NOV-1997; 97US-066770P.  
PR 24-NOV-1997; 97US-066772P.  
PR 25-NOV-1997; 97US-066840P.  
PR 12-DEC-1997; 97US-069425P.  
PR 04-JUN-1998; 98US-098026P.  
PR 10-SEP-1998; 98US-098036P.  
PR 14-SEP-1998; 98US-100262P.  
PR 17-SEP-1998; 98US-100858P.  
PR 13-OCT-1998; 98US-104080P.  
PR 20-NOV-1998; 98US-109304P.  
PR 22-DEC-1998; 98US-113296P.  
PR 07-JUL-1999; 99US-143048P.  
PR 26-JUL-1999; 99US-145698P.  
PR 28-JUL-1999; 99US-146222P.  
PR 18-SEP-2000; 2000US-0665350.  
  
(GENTH ) GENENTECH INC.  
XX  
XX Ashkenazi A, Botstein D, Desnuyers L, Eaton DL, Ferrara N,  
PI Flivarov E, Fong S, Gerder H, Gerlitsen ME, Goddard A;

PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini II;  
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
PI Williams PM, Wood WI;  
DR WPI: 2003-341586/32.  
P-PSDB: ABU69662.

XX New PRO polypeptides and nucleic acid molecules, useful in diagnosing  
FT or treating inflammatory diseases, organ failure, atherosclerosis,  
PT cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or  
PT Parkinson's disease -

PS Claim 2; Fig 83; 473pp; English.

XX The invention describes sixty one nucleic acids encoding PRO polypeptides  
CC (secreted and transmembrane). The PRO polypeptides and nucleic acids are  
CC useful in diagnosing or treating enterocolitis, gastrointestinal  
CC ulceration, skin diseases associated with abnormal keratinocyte  
CC differentiation, e.g. psoriasis or epithelial cancers such as squamous  
CC cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic  
CC lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis,  
CC asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac  
CC injury, infertility, birth defects, premature aging, AIDS, cancer,  
CC diabetic complications, or mutations in general. The polypeptides are  
CC also useful for wound repair and associated therapies concerned with  
CC re-growth of tissue. The PRO polypeptides and nucleic acid molecules  
CC are also useful in gene therapy, and as molecular weight markers for  
CC protein electrophoresis purposes. The anti-PRO antibodies may be used  
CC in diagnostic assays for PRO, or for the affinity purification of PRO  
CC from recombinant cell culture or natural sources. This sequence  
CC encodes a novel human PRO polypeptide.

XX Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;

XX Query Match 100.0%; Score 2586; DB 25; Length 2586;  
XX Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGCCGCGTCCCGACCCCGGCGCCGACCGCGCGCTCCGCGATCTGACCCCGAGC 60  
1 CGCCGCGTCCCGACCCCGGCGCCGACCGCGCGCTCCGCGATCTGACCCCGAGC 60  
61 CGCGGCGCTCCCGGCGGAGAGAGATCAATGTCGCGCGCGCGCACTGGTCCA 120  
61 CGCGGCGCTCCCGGCGGAGAGAGATCAATGTCGCGCGCGCGCACTGGTCCA 120  
121 GTCCGCGCGCGCGCTGCGGCGGAGAGAGATCAATGTCGCGCGCGCACTGGT 180  
121 GTCCGCGCGCGCGCTGCGGCGGAGAGAGATCAATGTCGCGCGCGCACTGGT 180  
181 GCTTCGCTGCGCGCGCGCTGCGGCGGAGAGAGATCAATGTCGCGCGCGCACT 240  
181 GCTTCGCTGCGCGCGCGCTGCGGCGGAGAGAGATCAATGTCGCGCGCGCACT 240  
241 CTCGCGTCAAGCGCGCGCGCGCTGCGGCGGAGAGAGATCAATGTCGCGCGCG 300  
241 CTCGCGTCAAGCGCGCGCGCGCTGCGGCGGAGAGAGATCAATGTCGCGCGCG 300  
301 TGTTCGCGGAGGTGAAGAACTGATGAGAGACGCGAGCAAAATTCGCGCGCGGTG 360  
301 TGTTCGCGGAGGTGAAGAACTGATGAGAGACGCGAGCAAAATTCGCGCGCGGTG 360  
361 AAGAGATGAGGCGAGAGAGAGTGTGCTGAAGCATCATCAAGATGAACCTGGCAACT 420  
361 AAGAGATGAGGCGAGAGAGAGTGTGCTGAAGCATCATCAAGATGAACCTGGCAACT 420  
421 TACCTCCAGCTATCAATGAGACCAACAGACAGAGAGAGTGGAAATATACATCC 480  
421 TACCTCCAGCTATCAATGAGACCAACAGACAGAGAGAGTGGAAATATACATCC 480  
481 ATGTGACCGAGAAATTCACAAATTAACCAACAGAGAGTGGAAATATATACATCC 540  
481 ATGTGACCGAGAAATTCACAAATTAACCAACAGAGAGTGGAAATATATACATCC 540

541 AAGACGTTATCAATCTGTGGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
541 AAGACGTTATCAATCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
601 AAG 660  
601 AAG 660  
661 CATGCGCGGCGAG 720  
661 CATGCGCGGCGAG 720  
721 GTGTCTGGGAGTCACTGACCAAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
721 GTGTCTGGGAGTCACTGACCAAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
781 ACCAG 840  
781 ACCAG 840  
841 TGTGACACCCCTGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
841 TGTGACACCCCTGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
901 ACCTCATCACTGAG 960  
901 ACCTCATCACTGAG 960  
961 GCTCTCTTCCAG 1020  
961 GCTCTCTTCCAG 1020  
1021 GAG 1080  
1021 GAG 1080  
1081 TGGCAGCTTCATGAG 1140  
1081 TGGCAGCTTCATGAG 1140  
1141 AAGAGATGAG 1200  
1141 AAGAGATGAG 1200  
1201 TTTAGATCTGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260  
1201 TTTAGATCTGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260  
1261 GGTGTGTGCTTGAAG 1320  
1261 GGTGTGTGCTTGAAG 1320  
1321 TCCCTCTGAG 1380  
1321 TCCCTCTGAG 1380  
1381 CAGAGCTTCAAG 1440  
1381 CAGAGCTTCAAG 1440  
1381 CAGAGCTTCAAG 1440  
1381 CAGAGCTTCAAG 1440  
1441 GCCACCTCTGAG 1500  
1441 GCCACCTCTGAG 1500  
1501 TTTAGATCTGAG 1560  
1501 TTTAGATCTGAG 1560  
1561 TGAATGCTTTTGGAG 1620  
1561 TGAATGCTTTTGGAG 1620

```

QY 1621 AAATGCAAAATGATTTTCCAGCAGTCTTTCCATGGGCAATAGGTAGTGTGCTT 1680
DB 1621 AAATGCAAAATGATTTTCCAGCAGTCTTTCCATGGGCAATAGGTAGTGTGCTT 1680
QY 1681 CAGCTGTGAGATGAAATGTTCTGTTCACCTGECATTAATGTTTATTCATCCAGCA 1740
DB 1681 CAGCTGTGAGATGAAATGTTCTGTTCACCTGECATTAATGTTTATTCATCCAGCA 1740
QY 1741 GTGTGCTCAGCTCTTACCTCTGTGCGCAGGAGACATTTTCATATCCAAATGATTTCC 1800
DB 1741 GTGTGCTCAGCTCTTACCTCTGTGCGCAGGAGACATTTTCATATCCAAATGATTTCC 1800
QY 1801 TCTCTCAGCAGCTGCGGAGGAGGAGTCAATGTTCTCTGTCATCAGGATCTCAGAG 1860
DB 1801 TCTCTCAGCAGCTGCGGAGGAGGAGTCAATGTTCTCTGTCATCAGGATCTCAGAG 1860
QY 1861 GCTCAGAGACTGCAAGCTGCTTCCCAAGTCAACAGCTAGTGAAGCCAGACAGTTTC 1920
DB 1861 GCTCAGAGACTGCAAGCTGCTTCCCAAGTCAACAGCTAGTGAAGCCAGACAGTTTC 1920
QY 1921 ATCTGTTGTGACTCTTAAGCTCAGTGTCTCTCCACTACCCCAACAGCCTTGTCCTCA 1980
DB 1921 ATCTGTTGTGACTCTTAAGCTCAGTGTCTCTCCACTACCCCAACAGCCTTGTCCTCA 1980
QY 1981 CCAAAAGTGTCTCCCAAAAGGAGAGAAATGGGATTTTCTTGAGGATGCAATCTGGA 2040
DB 1981 CCAAAAGTGTCTCCCAAAAGGAGAGAAATGGGATTTTCTTGAGGATGCAATCTGGA 2040
QY 2041 ATTAAGGCAACTAATTTCTCAGATCCCTCTAAAGTAACTACTGTTAGAAACAGAGT 2100
DB 2041 ATTAAGGCAACTAATTTCTCAGATCCCTCTAAAGTAACTACTGTTAGAAACAGAGT 2100
QY 2101 GTTCTCAAGTGTGGGGGAGCGCTCTTCTAATGAAGACAAATGATTTGAACACTGTCTCT 2160
DB 2101 GTTCTCAAGTGTGGGGGAGCGCTCTTCTAATGAAGACAAATGATTTGAACACTGTCTCT 2160
QY 2161 CTTTGCGAGTGTGACTTGTATCTTGAAGGTATATGACAGGCTGAGCATACAGGTTAA 2220
DB 2161 CTTTGCGAGTGTGACTTGTATCTTGAAGGTATATGACAGGCTGAGCATACAGGTTAA 2220
QY 2221 CCTGCAAGAACAGTACTTAAAGTAAATTTGAGGCGAGGATTAATAAATTTGCAAAAT 2280
DB 2221 CCTGCAAGAACAGTACTTAAAGTAAATTTGAGGCGAGGATTAATAAATTTGCAAAAT 2280
QY 2281 CACTTAGAGAGCACTGAAGAAATTAATCAACAGCTGAGAAATCAAAACGAGGAGGCT 2340
DB 2281 CACTTAGAGAGCACTGAAGAAATTAATCAACAGCTGAGAAATCAAAACGAGGAGGCT 2340
QY 2341 TGTGTGAACAATGTTGTATATGAGCACTGCGAACACTGAACCTGTAGCCACTCCAA 2400
DB 2341 TGTGTGAACAATGTTGTATATGAGCACTGCGAACACTGAACCTGTAGCCACTCCAA 2400
QY 2401 TGATGTTTTCAGGCTCATGCACTGTGCGCACTATATTAATCAAGATTTTAAAGT 2460
DB 2401 TGATGTTTTCAGGCTCATGCACTGTGCGCACTATATTAATCAAGATTTTAAAGT 2460
QY 2461 TAAAGTTGCAATGATTTGATTAAGCATGCTTTCTTGAGTTTAAATTAATTAATTAACAT 2520
DB 2461 TAAAGTTGCAATGATTTGATTAAGCATGCTTTCTTGAGTTTAAATTAATTAATTAACAT 2520
QY 2521 AAGTTGCACTTAAGAAATCAAGCAATTAATCACTTCACTGCAAAAAAATTTTTAAAAA 2580
DB 2521 AAGTTGCACTTAAGAAATCAAGCAATTAATCACTTCACTGCAAAAAAATTTTTAAAAA 2580
QY 2581 AAAAAA 2586
DB 2581 AAAAAA 2586

```

RESULT 8  
ACAS8487  
ID ACAS8487 standard; cDNA; 2586 BP.  
XX

```

AC ACAS8487;
XX 10-JUN-2003 (first entry)
DE cDNA encoding human PRO polypeptide #41.
XX Human; secreted and transmembrane protein; PRO polypeptide; cancer;
XX Alzheimer's disease; ischemia; cytostatic; nootropic; vasotropic;
XX neuroprotective; gene; ss.
OS Homo sapiens.
XX US2002192659-A1.
XX 19-DEC-2002.
XX 10-JUL-2001; 2001US-0902853.
XX 10-SEP-1998; 98WO-US18824.
XX 14-SEP-1998; 98WO-US19177.
XX 16-SEP-1998; 98WO-US19330.
XX 17-SEP-1998; 98WO-US19437.
XX 01-DEC-1998; 98WO-US25108.
XX 08-SEP-1999; 99WO-US20594.
XX 13-SEP-1999; 99WO-US20944.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 05-OCT-1999; 99WO-US23089.
XX 01-DEC-1999; 99WO-US28301.
XX 02-DEC-1999; 99WO-US28564.
XX 16-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30911.
XX 20-DEC-1999; 99WO-US30999.
XX 05-JAN-2000; 2000WO-US00219.
XX 11-FEB-2000; 2000WO-US03565.
XX 22-FEB-2000; 2000WO-US04414.
XX 28-JUL-2000; 2000WO-US20710.
XX 24-AUG-2000; 2000WO-US23328.
XX 17-SEP-1997; 97US-059113P.
XX 17-SEP-1997; 97US-059115P.
XX 17-SEP-1997; 97US-059117P.
XX 18-SEP-1997; 97US-059266P.
XX 15-OCT-1997; 97US-062125P.
XX 17-OCT-1997; 97US-062285P.
XX 17-OCT-1997; 97US-062287P.
XX 21-OCT-1997; 97US-063486P.
XX 24-OCT-1997; 97US-062814P.
XX 24-OCT-1997; 97US-062816P.
XX (GENTH ) GENENTECH INC.
XX Ashkenasi A, Borstein D, Desnoyers L, Eaton DL, Ferrara N;
XX Filveroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Grimaldi JC, Gurney AL, Hillian KJ, Kijavlin IJ;
XX Mather JP, Pan U, Paoni NF, Roy MA, Stewart TA, Tumas D;
XX Williams PM, Wood WL;
XX WPI; 2003-361832/34.
XX P-PDSB; ABUT1485.
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
XX PRO168, useful in molecular biology, chromosome and gene mapping, in
XX generating antisense RNA and DNA, and in gene therapy.
XX Claim 2; Fig 83; 474pp; English.
XX The present invention relates to the isolation of novel human secreted
XX and transmembrane proteins (PRO polypeptides), and the polynucleotide
XX sequences encoding them. The polynucleotide sequences are useful in
XX molecular biology, as hybridisation probes, in chromosome and gene
XX mapping, in generating antisense RNA and DNA, and in gene therapy. The
XX polynucleotide sequences may also be used in preparing PRO polypeptides

```



CC by recombinant techniques, and in generating either transgenic animals  
CC or knock-out animals which, in turn, are useful in the development and  
CC screening of therapeutically useful reagents. The PRO polypeptides or  
CC their antibodies are useful in preparing a medication for treating a  
CC condition responsive to the polypeptide or antibody, such as cancer,  
CC Alzheimer's disease or ischaemia, and in various diagnostic assays.  
CC The present sequence encodes a human PRO polypeptide of the invention.

XX Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;

Query Match 100.0%; Score 2586; DB 25; Length 2586;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
1 CGCCGCGCTCCCGACCCCGCGCCCGCCACCGCGCCCTCCCGCATCTGACCCCGAGC 60
1 CGCGCGCTCCCGACCCCGCGCCCGCCACCGCGCCCTCCCGCATCTGACCCCGAGC 60
61 CCGGCGGCTCCCGCGCGGAGAGAGAGATCCAGTCCGCGCCGCGCAACTGCTGCTCA 120
61 CCGGCGGCTCCCGCGCGGAGAGAGAGATCCAGTCCGCGCCGCGCAACTGCTGCTCA 120
121 GTCCGCGCGCGCGCTGCGCGGCGAGAGAGATGAGAGAGAGCTTGCGGCGCACTGCTG 180
121 GTCCGCGCGCGCGCTGCGCGGCGAGAGAGAGATGAGAGAGAGCTTGCGGCGCACTGCTG 180
181 GCTTGTCTGCGCGCGCGCTGCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
181 GCTTGTCTGCGCGCGCGCTGCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
241 CTCGAGTAAAGCGCGCGCGCGCTGCTGAGTAAAGTAAAGTAAAGTAAAGTAAAGT 300
241 CTCGAGTAAAGCGCGCGCGCGCTGCTGAGTAAAGTAAAGTAAAGTAAAGTAAAGT 300
301 TGTTCGCGAGAGTGAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
301 TGTTCGCGAGAGTGAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
361 AAGAGATGAGAGAGAGAGAGAGAGTGTGCTAAAGTAAAGTAAAGTAAAGTAAAGT 420
361 AAGAGATGAGAGAGAGAGAGAGTGTGCTAAAGTAAAGTAAAGTAAAGTAAAGT 420
421 TACCTCCCGAGTATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
421 TACCTCCCGAGTATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
481 ATGTGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
481 ATGTGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
541 AGACAGTATATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
541 AGACAGTATATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
601 ACGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
601 ACGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
661 CATGCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
661 CATGCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
721 GTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
721 GTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
781 ACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
781 ACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
841 TGTGACACACCCCTGCGCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
841 TGTGACACACCCCTGCGCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
```

```
901 ACCATCATCCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
901 ACCATCATCCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
961 GCTTCTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
961 GCTTCTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
1021 GAGAGCGGTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
1021 GAGAGCGGTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
1081 TTGGCAGCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
1081 TTGGCAGCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
1141 AAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
1141 AAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
1201 TTAGATCTGAGACAGAGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATCC 1260
1201 TTAGATCTGAGACAGAGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATCC 1260
1261 GGTGTGTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
1261 GGTGTGTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
1321 TCCCTCTGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
1321 TCCCTCTGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
1381 CAGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
1381 CAGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
1441 GCCAGCCCTGTCAGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
1441 GCCAGCCCTGTCAGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
1501 TCTACATGAGCTTGAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
1501 TCTACATGAGCTTGAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
1561 TGAATGAGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
1561 TGAATGAGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
1621 AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
1621 AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
1681 CAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
1681 CAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
1681 CAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
1681 CAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
1741 GTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
1741 GTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
1801 TCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
1801 TCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
1801 TCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
1801 TCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
1861 GCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
1861 GCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
1921 ATCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
1921 ATCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
```



QY	61	CCGCGCGACCTCCCGCGGGGAGGAGAGATCCAGTCCGCGCCGCGAGCCGACATCGGTCCA	120
Db	61	CCGCGCGACCTCCCGCGGGGAGGAGAGATCCAGTCCGCGCCGCGAGCCGACATCGGTCCA	120
QY	121	GTCCGCGCGCGCGCTCCGCGCGCGAGACCGAGATGACGCGGCTTGGGCGCACCTGCTGT	180
Db	121	GTCCGCGCGCGCGCTCCGCGCGCGAGACCGAGATGACGCGGCTTGGGCGCACCTGCTGT	180
QY	181	GCTGCTGTGTGGCGCGCGCGGTCCCCACGCGCCCGCGCGCGCTCCGAGGGGACCTCGG	240
Db	181	GCTGCTGTGTGGCGCGCGCGGTCCCCACGCGCCCGCGCGCGCTCCGAGGGGACCTCGG	240
QY	241	CTCCAGTCAAGCCCGCGCCCGCTCAGCTTACCCGAGAGAGGCGCACCTCAATAGAGA	300
Db	241	CTCCAGTCAAGCCCGCGCCCGCTCAGCTTACCCGAGAGAGGCGCACCTCAATAGAGA	300
QY	301	TGTTCCGCGAGGTTGAGAGACTGATGAGAGACACCGACGACAAATTGGCGCGCGCGTGG	360
Db	301	TGTTCCGCGAGGTTGAGAGACTGATGAGAGACACCGACGACAAATTGGCGCGCGCGTGG	360
QY	361	AAGAGATGAGAGGCGAGAAAGCTGCTGCTAAAGCATCATCAAGAGAACTGGGAGACT	420
Db	361	AAGAGATGAGAGGCGAGAAAGCTGCTGCTAAAGCATCATCAAGAGAACTGGGAGACT	420
QY	421	TACCTTCCAGCTATCACAATGAGCAACACAGACGAGAGGTTGAAATAATACATCC	480
Db	421	TACCTTCCAGCTATCACAATGAGCAACACAGACGAGAGGTTGAAATAATACATCC	480
QY	481	ATGTACACCGAGAAATTTACAGAGATACCAACACAGACTGAGAAATGTCTTTTCA	540
Db	481	ATGTACACCGAGAAATTTACAGAGATACCAACACAGACTGAGAAATGTCTTTTCA	540
QY	541	AGACAGTTATCACATCTGTGGGAGACGAAGAGGAGAGAGGACGACGAGTGCATCATCG	600
Db	541	AGACAGTTATCACATCTGTGGGAGACGAAGAGGAGAGAGGACGACGAGTGCATCATCG	600
QY	601	ACGAGAGACTGTGGGGGCCAGCATGTACTGCACATTTGGCCAGCTTCCAGTACACTGCGCAGC	660
Db	601	ACGAGAGACTGTGGGGGCCAGCATGTACTGCACATTTGGCCAGCTTCCAGTACACTGCGCAGC	660
QY	661	CATGCGCGGGCCAGAGAGTGTCTACACCGGGGACAGTAGTGCTGTGAGAGACGACGCT	720
Db	661	CATGCGCGGGCCAGAGAGTGTCTACACCGGGGACAGTAGTGCTGTGAGAGACGACGCT	720
QY	721	GTGTCTGGGGTCACTGCAACCAATATGCGCACCGGGGACGACATGCGGACCACTGTGACA	780
Db	721	GTGTCTGGGGTCACTGCAACCAATATGCGCACCGGGGACGACATGCGGACCACTGTGACA	780
QY	781	ACCAAGAGGAGCTGCGCAGCGCGGGGCTGTGTGCTTCCAGAGAGGCTGCTGTCCCTG	840
Db	781	ACCAAGAGGAGCTGCGCAGCGCGGGGCTGTGTGCTTCCAGAGAGGCTGCTGTCCCTG	840
QY	841	TGTGCACACCCCTGCGCTGCGTGAAGGGCGAGCTTGTCCATGACCCCGCGACCGCGCTTCTGG	900
Db	841	TGTGCACACCCCTGCGCTGCGTGAAGGGCGAGCTTGTCCATGACCCCGCGACCGCGCTTCTGG	900
QY	901	ACCTCATTAACCTTGGGAGAGCTTAGAGCTTATGAGAGCTTGGACCGAGTCCCTTGTGTGCACTG	960
Db	901	ACCTCATTAACCTTGGGAGAGCTTAGAGAGCTTATGAGAGCTTGGACCGAGTCCCTTGTGTGCACTG	960
QY	961	GCTTCTCTTGCAGCGCCACAGCCACACCTGATATGTGTGACAGCGGACCTTCTGTGG	1020
Db	961	GCTTCTCTTGCAGCGCCACAGCCACACCTGATATGTGTGACAGCGGACCTTCTGTGG	1020
QY	1021	GGAGCCGTTGACCAAGATGGGAGATCTCTGCTCCAGAGAGGCTCCCATATGATAGAG	1080
Db	1021	GGAGCCGTTGACCAAGATGGGAGATCTCTGCTCCAGAGAGGCTCCCATATGATAGAG	1080
QY	1081	TTGGCAGCTTATGAGAGAGGTGCGCCAGAGACTGAGAGACTTGGAGAGAGGACCTGACTG	1140
Db	1081	TTGGCAGCTTATGAGAGAGGTGCGCCAGAGACTGAGAGACTTGGAGAGAGGACCTGACTG	1140
QY	1141	AAGAGATGCGCTGGGGAGACCTTGGCGCTGCGCGCTGCACTGCTGGAGGGGAGAGAGA	1200

Db	1141	AAGAGATGGCCCTGGGGAGGCTGGGCTGGCCGCGCACTGCTGGAGAGGGAAGA	1200
Qy	1201	TTTGAATCTGACACAGGCTGTGGAGATGTGCATAGAAATAGCTAATTATTTCCCA	1260
Db	1201	TTTGAATCTGACACAGGCTGTGGAGATGTGCATAGAAATAGCTAATTATTTCCCA	1260
Qy	1261	GGTGTGTCTTTAGGCGTGGGCTGACCAAGGCTTCTTCCATACCTTCTTCCAGTAAGTT	1320
Db	1261	GGTGTGTCTTTAGGCGTGGGCTGACCAAGGCTTCTTCCATACCTTCTTCCAGTAAGTT	1320
Qy	1321	TCCCTCTGGCTTGACAGCATAGAGGTGTGTGCATTTGTTCAAGTCCCCAGGCGTGTCT	1380
Db	1321	TCCCTCTGGCTTGACAGCATAGAGGTGTGTGCATTTGTTCAAGTCCCCAGGCGTGTCT	1380
Qy	1381	CCAGGCTTCAACAGTCTGGTGTCTGGGAGAGTCAGGCAAGGTTAACTGACAGACAGTTT	1440
Db	1381	CCAGGCTTCAACAGTCTGGTGTCTGGGAGAGTCAGGCAAGGTTAACTGACAGACAGTTT	1440
Qy	1441	GCAACCCCTGTCAGATTAATGAGCGTCTTGGCTCTCAACAGTTGGACAGACGCGTTGT	1500
Db	1441	GCAACCCCTGTCAGATTAATGAGCGTCTTGGCTCTCAACAGTTGGACAGACGCGTTGT	1500
Qy	1501	TCTACATGGCTTGAATAATGTGTTGAGGGAGAGATGAAACATATGAGAGTCTCCCTC	1560
Db	1501	TCTACATGGCTTGAATAATGTGTTGAGGGAGAGATGAAACATATGAGAGTCTCCCTC	1560
Qy	1561	TGATTTGGTTTGGGGAAATGTGAGAAAGATGCGCCTGTTTGCAACATCAACTGGCA	1620
Db	1561	TGATTTGGTTTGGGGAAATGTGAGAAAGATGCGCCTGTTTGCAACATCAACTGGCA	1620
Qy	1621	AAATGCAACAATGAATTTTCCACGCAAGTTCTTTCACATGGGCAATAGGTAAGCTGGCCTT	1680
Db	1621	AAATGCAACAATGAATTTTCCACGCAAGTTCTTTCACATGGGCAATAGGTAAGCTGGCCTT	1680
Qy	1681	CAGCTGTTCAGATGAATAATGTTCTGTTCACCCCTGCAATTCATGTGTTAATTCATCCAGA	1740
Db	1681	CAGCTGTTCAGATGAATAATGTTCTGTTCACCCCTGCAATTCATGTGTTAATTCATCCAGA	1740
Qy	1741	GTTGTGCTCAGACTCTCACTGCTGTCGACAGGAGACATTTTCAATTCACATCAATTTCCC	1800
Db	1741	GTTGTGCTCAGACTCTCACTGCTGTCGACAGGAGACATTTTCAATTCACATCAATTTCCC	1800
Qy	1801	TCTCTCAGACAGGCTGGGAGGGGGTCAATGTTCTCTCTGTCATCAGGATCTCAGAG	1860
Db	1801	TCTCTCAGACAGGCTGGGAGGGGGTCAATGTTCTCTCTGTCATCAGGATCTCAGAG	1860
Qy	1861	GCTCAGAGACTGCAAGGCTGTGGCCCAAGTCACACAGCTAGTAAAGCCAGAGACGTTTC	1920
Db	1861	GCTCAGAGACTGCAAGGCTGTGGCCCAAGTCACACAGCTAGTAAAGCCAGAGACGTTTC	1920
Qy	1921	ATCTGTGTGTGACTCTAAGCTCAAGTGTCTCTCTCCATCACCCACACAGGCTTGTGTCCA	1980
Db	1921	ATCTGTGTGTGACTCTAAGCTCAAGTGTCTCTCTCCATCACCCACACAGGCTTGTGTCCA	1980
Qy	1981	CCAAAAGTGTCTCCCAAAAAGGAGAGATGGGATTTTTCTTGAGGATCAACATCTGGA	2040
Db	1981	CCAAAAGTGTCTCCCAAAAAGGAGAGATGGGATTTTTCTTGAGGATCAACATCTGGA	2040
Qy	2041	ATTAAAGTCAAACCTAATTTCTCAATCCCTCTAAAGAACTACTGTGTAAGAACAGAGT	2100
Db	2041	ATTAAAGTCAAACCTAATTTCTCAATCCCTCTAAAGAACTACTGTGTAAGAACAGAGT	2100
Qy	2101	GTTCTCACAAGTGTGGGAGCGCTCTTCTTAATGAAACATGATATTTGACACTGTCCCT	2160
Db	2101	GTTCTCACAAGTGTGGGAGCGCTCTTCTTAATGAAACATGATATTTGACACTGTCCCT	2160
Qy	2161	CTTTGAGAGTTCATTTAGTAATTTGAAAGGTATATGACTGAGCGTATACAGGTTAA	2220
Db	2161	CTTTGAGAGTTCATTTAGTAATTTGAAAGGTATATGACTGAGCGTATACAGGTTAA	2220
Qy	2221	CTTGACAGAAACAGTACTTAGGTAAATGTGAGGCGAGAGATTATTAATGAATTTGCAAAAT	2280
Db	2221	CTTGACAGAAACAGTACTTAGGTAAATGTGAGGCGAGAGATTATTAATGAATTTGCAAAAT	2280



CC nucleic acid sequence identity to a nucleotide sequence encoding one of  
CC 61 secreted/transportable polypeptides, or PRO polypeptides or encoding a  
CC PRO protein extracellular domain. Also included are a vector comprising a  
CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO  
CC polypeptide (by culturing the host cell for the expression of the PRO  
CC polypeptide, and recovering the PRO polypeptide from the cell culture),  
CC an isolated PRO polypeptide (having at least 80% sequence identity  
CC to: (a) an amino acid sequence selected from the 61 PRO proteins;  
CC (b) an amino acid sequence encoded by a nucleic acid molecule deposited  
CC with an ATCC number (detailed in the specification); or (c) an  
CC extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking  
CC its associated signal peptide), a chimeric molecule comprising a PRO  
CC polypeptide of fused to a heterologous amino acid sequence, an anti-PRO  
CC antibody, detecting a PRO245 or PRO1868 in a sample suspected of  
CC containing a PRO245 or PRO1868 and modulating at least one biological  
CC expression of a cell expressing a PRO245 or PRO1868. Nucleic acids which  
CC activity of a cell expressing a PRO245 or PRO1868. Nucleic acids which  
CC encode PRO can be used to generate either transgenic animals or knock-out  
CC animals which may be used in the development and screening of  
CC therapeutically useful reagents. The nucleic acids may also be used in  
CC gene therapy, in chromosome identification, as chromosome markers, or in  
CC generating probes. The PRO polypeptides are useful as molecular markers  
CC for protein electrophoresis, and the isolated nucleic acids may be used  
CC for recombinantly expressing those markers. The PRO polypeptides and  
CC nucleic acids may also be used in tissue typing. Anti-PRO antibodies  
CC are useful in diagnostic assays for PRO, and in affinity purification  
CC of PRO from recombinant cell culture or natural sources. The  
CC present sequence encodes a PRO protein.

Sequence 2586 BP; 631 A; 679 C; 703 G; 573 T; 0 other;

Query Match 100.0%; Score 2586; DB 25; Length 2586;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGCGCTCCCGCAGCCGCGCCGCGCCGCTCCCGCATTCGACCGCGAGC 60  
DB 1 CGCCGCGCTCCCGCAGCCGCGCCGCGCCGCTCCCGCATTCGACCGCGAGC 60  
QY 61 CCGCGCGCTCCCGCAGCCGCGCCGCGCCGCTCCCGCATTCGACCGCGAGC 120  
DB 61 CCGCGCGCTCCCGCAGCCGCGCCGCGCCGCTCCCGCATTCGACCGCGAGC 120  
QY 121 GTCGCGCGCGCGCTCCCGCAGCCGCGCCGCGCTCCCGCATTCGACCGCGAGC 180  
DB 121 GTCGCGCGCGCGCTCCCGCAGCCGCGCCGCGCTCCCGCATTCGACCGCGAGC 180  
QY 181 GCTGCTGCTGCGCGCGCTCCCGCAGCCGCGCCGCGCTCCCGCATTCGACCGCGAGC 240  
DB 181 GCTGCTGCTGCGCGCGCTCCCGCAGCCGCGCCGCGCTCCCGCATTCGACCGCGAGC 240  
QY 241 CTCGCGCGCGCGCGCTCCCGCAGCCGCGCCGCGCTCCCGCATTCGACCGCGAGC 300  
DB 241 CTCGCGCGCGCGCGCTCCCGCAGCCGCGCCGCGCTCCCGCATTCGACCGCGAGC 300  
QY 301 TGTTCGCGCGCGCGCTCCCGCAGCCGCGCCGCGCTCCCGCATTCGACCGCGAGC 360  
DB 301 TGTTCGCGCGCGCGCTCCCGCAGCCGCGCCGCGCTCCCGCATTCGACCGCGAGC 360  
QY 361 AAGAGATGAGGCGAGAAAGCTGCTGCTAAAGCATTCAGAACTGGAAGTGAAGTGAAGT 420  
DB 361 AAGAGATGAGGCGAGAAAGCTGCTGCTAAAGCATTCAGAACTGGAAGTGAAGTGAAGT 420  
QY 421 TACCTCCGAGCTATGACATGAGCAACACAGACAGAAAGTGAAGTGAAGTGAAGTGAAGT 480  
DB 421 TACCTCCGAGCTATGACATGAGCAACACAGACAGAAAGTGAAGTGAAGTGAAGTGAAGT 480  
QY 481 ATGTGACCGGAGAAATTCAGAAATTAACCAACAGATGAGCAAAATGCTTTTTCAG 540  
DB 481 ATGTGACCGGAGAAATTCAGAAATTAACCAACAGATGAGCAAAATGCTTTTTCAG 540  
QY 541 AGACAGTTATCATCTGTGGAGAGCAAGAAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600  
DB 541 AGACAGTTATCATCTGTGGAGAGCAAGAAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600

DB 541 AGACAGTTATCATCTGTGGAGAGCAAGAAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600  
QY 601 ACAGAGACTGTGGGCGCCAGCATGTAATCTGCAAGTTTCCAGCTTCCAGTACCTGCGACG 660  
DB 601 ACAGAGACTGTGGGCGCCAGCATGTAATCTGCAAGTTTCCAGCTTCCAGTACCTGCGACG 660  
QY 661 CATGCCGGGCGCAGAGATGCTCTGACCCGGGACAGTGAAGTGTGGAGACAGCTGT 720  
DB 661 CATGCCGGGCGCAGAGATGCTCTGACCCGGGACAGTGAAGTGTGGAGACAGCTGT 720  
QY 721 GTGTCTGGGCTCACTGACCAAAATGCGACAGGGGCGAGCAATGAGACCATCTGTGACA 780  
DB 721 GTGTCTGGGCTCACTGACCAAAATGCGACAGGGGCGAGCAATGAGACCATCTGTGACA 780  
QY 781 ACAGAGAGGAGCTCGACCGGGGCTGTGTGTGCTTCCAGAGAGGCGCTGTTCCTG 840  
DB 781 ACAGAGAGGAGCTCGACCGGGGCTGTGTGTGCTTCCAGAGAGGCGCTGTTCCTG 840  
QY 841 TGTGCAACCCCTGCGCGGTGAGAGGCGAGCTTGCATGACCCCGCAGCCGCTTCTG 900  
DB 841 TGTGCAACCCCTGCGCGGTGAGAGGCGAGCTTGCATGACCCCGCAGCCGCTTCTG 900  
QY 901 ACCTCATCACTGGGAGCTGAGAGCTTGAAGCTTGAACCGATCCCTGTGCGACAGT 960  
DB 901 ACCTCATCACTGGGAGCTGAGAGCTTGAAGCTTGAACCGATCCCTGTGCGACAGT 960  
QY 961 GCTCTCTGCGCAGCCCGCAGCAGCAGCAGCTGTGTGTGTGCAAGCGACCTTGTG 1020  
DB 961 GCTCTCTGCGCAGCCCGCAGCAGCAGCAGCTGTGTGTGTGCAAGCGACCTTGTG 1020  
QY 1021 GAGACCGGTACCAAGATGGGAGATCTGTGCTCCGAGAGGTCCTCCGATGATGAAG 1080  
DB 1021 GAGACCGGTACCAAGATGGGAGATCTGTGCTCCGAGAGGTCCTCCGATGATGAAG 1080  
QY 1081 TTGGAGCTTCATGAGAGAGTGTGCGCAGAGCTGAGAGACCTGAGAGAGAGCTGACTG 1140  
DB 1081 TTGGAGCTTCATGAGAGAGTGTGCGCAGAGCTGAGAGACCTGAGAGAGAGCTGACTG 1140  
QY 1141 AAGAGATGCGCTGCGGAGAGCTGCGGCTGCGCTGCACTGCTGAGAGGAGAGAGAG 1200  
DB 1141 AAGAGATGCGCTGCGGAGAGCTGCGGCTGCGCTGCACTGCTGAGAGGAGAGAGAG 1200  
QY 1201 TTTAGATCTGGAACAGAGCTGTGGATGTGCAATGAAATAGTAAATTTATTTCCCA 1260  
DB 1201 TTTAGATCTGGAACAGAGCTGTGGATGTGCAATGAAATAGTAAATTTATTTCCCA 1260  
QY 1261 GGTGTGTCTTAAAGCGTGGGCTGACAGGCTTCTTCTAATCTTCTTCCAGTAAGT 1320  
DB 1261 GGTGTGTCTTAAAGCGTGGGCTGACAGGCTTCTTCTAATCTTCTTCCAGTAAGT 1320  
QY 1321 TCCGCTCTGCTTGAAGAGATGAGTGTGTGATTTGTCAGCTCCCGCAGGCTGTCT 1380  
DB 1321 TCCGCTCTGCTTGAAGAGATGAGTGTGTGATTTGTCAGCTCCCGCAGGCTGTCT 1380  
QY 1381 CAGGCTTCACTGTGTGCTTGGAGAGTCAAGAGGCTTAACTGACAGAGAGAGT 1440  
DB 1381 CAGGCTTCACTGTGTGCTTGGAGAGTCAAGAGGCTTAACTGACAGAGAGAGT 1440  
QY 1441 GCGACCCGCTGCAAGATTTGCTGCTTGTGCTTCAAGATTTGCTGCTGCTGCTGCT 1500  
DB 1441 GCGACCCGCTGCAAGATTTGCTGCTTGTGCTTCAAGATTTGCTGCTGCTGCTGCT 1500  
QY 1501 TCTACATGCTTGTATGATTTGTGAGGAGAGAGATGAGAAACAATGTGAGTCTCTC 1560  
DB 1501 TCTACATGCTTGTATGATTTGTGAGGAGAGAGATGAGAAACAATGTGAGTCTCTC 1560  
QY 1561 TGAATGCTTTGGGAGAAATGTGAGAGAGTCCCTGCTTTCGAAACATCAACCTGCGCA 1620  
DB 1561 TGAATGCTTTGGGAGAAATGTGAGAGAGTCCCTGCTTTCGAAACATCAACCTGCGCA 1620  
QY 1621 AAATGCAACAATGATTTTTCAGAGCTTCTTTCATGGGATAGTAAAGCTGTGCTT 1680  
DB 1621 AAATGCAACAATGATTTTTCAGAGCTTCTTTCATGGGATAGTAAAGCTGTGCTT 1680





Db 241 CTCGATGAAGCCCGGCTCTGAGTACCCGAGAGAGAGCCACCTTCAATGAGA 300  
Qy 301 TGTTCGCGAGGTTGAGGAATGATGANGACAAGCAGACAAATTGGCAGCGCGTGG 360  
Db 301 TGTTCGCGAGGTTGAGGAATGATGANGACAAGCAGACAAATTGGCAGCGCGTGG 360  
Qy 361 AAGAGATGAGGCAAGAAGGCTGCTTAAGCATCATCAGAAAGTGAACCTGGCAACT 420  
Db 361 AAGAGATGAGGCAAGAAGGCTGCTTAAGCATCATCAGAAAGTGAACCTGGCAACT 420  
Qy 421 TAACCTCCAGCTATCAATGAGAACCAACAGACAGAGGTTGAAATATATCAATCC 480  
Db 421 TAACCTCCAGCTATCAATGAGAACCAACAGACAGAGGTTGAAATATATCAATCC 480  
Qy 481 ATGTGCACCGAAGAAATTCAAGATTAACCAACAGACTGAGCAATGGTCTTTTCAG 540  
Db 481 ATGTGCACCGAAGAAATTCAAGATTAACCAACAGACTGAGCAATGGTCTTTTCAG 540  
Qy 541 AGACAGTTATACATCTGTGGAGACGAAGAGCAGAGAGCCAGAGTGCATCATCG 600  
Db 541 AGACAGTTATACATCTGTGGAGACGAAGAGCAGAGAGCCAGAGTGCATCATCG 600  
Qy 601 ACGAGAGCTGTGGGCGCCAGCATGTACTGCGAGTTTGCAGCTTCCAGTACCTGCGACG 660  
Db 601 ACGAGAGCTGTGGGCGCCAGCATGTACTGCGAGTTTGCAGCTTCCAGTACCTGCGACG 660  
Qy 661 CATGCGGCGGCGAGAGATGCTCTGCAACCCGAGACGTGATGCTGTGAGAACCAAGCTGT 720  
Db 661 CATGCGGCGGCGAGAGATGCTCTGCAACCCGAGACGTGATGCTGTGAGAACCAAGCTGT 720  
Qy 721 GTGTCTGGGGTCTGACACCAAAATGSCACCAAGGGGCGAGCAATGGGACCATCTGTGACA 780  
Db 721 GTGTCTGGGGTCTGACACCAAAATGSCACCAAGGGGCGAGCAATGGGACCATCTGTGACA 780  
Qy 781 ACCAGAGGAGCTGCGACGCGGGGCTGTGCTGTGCTTCAAGAGGGCTGTGTTCCCTG 840  
Db 781 ACCAGAGGAGCTGCGACGCGGGGCTGTGCTGTGCTTCAAGAGGGCTGTGTTCCCTG 840  
Qy 841 TGTGACACCCCTGCGGCTGAGAGGAGCGAAGCTTTCAGATGACCCGCGCAGCGGCTTTCG 900  
Db 841 TGTGACACCCCTGCGGCTGAGAGGAGCGAAGCTTTCAGATGACCCGCGCAGCGGCTTTCG 900  
Qy 901 AACTCATACCTTGAAGTATAGCTGTGATGAGCTTGAACCGATGCGCTTGTGGCAGTG 960  
Db 901 AACTCATACCTTGAAGTATAGCTGTGATGAGCTTGAACCGATGCGCTTGTGGCAGTG 960  
Qy 961 GCTTCCTTGCAGGCCCAAGCAGCAGCTGTGTGTATGTGTGCAAGCCGACTTTCGTGG 1020  
Db 961 GCTTCCTTGCAGGCCCAAGCAGCAGCTGTGTGTATGTGTGCAAGCCGACTTTCGTGG 1020  
Qy 1021 GGAAGCCCTGACCAAGATGGGAGATCTGTGCTGCCAGAGAGTCCCGATGATGATGAAG 1080  
Db 1021 GGAAGCCCTGACCAAGATGGGAGATCTGTGCTGCCAGAGAGTCCCGATGATGATGAAG 1080  
Qy 1081 TTGGAGCTTATGAGAGGAGTGGCCAGAGACTGTGAGAGACCTTGAGAGAGAGCCTGACTG 1140  
Db 1081 TTGGAGCTTATGAGAGGAGTGGCCAGAGACTGTGAGAGACCTTGAGAGAGAGCCTGACTG 1140  
Qy 1141 AAGAGATGGCGCTGGGGAGGCTTGGCGCTGCGCGCTGCACTGCTGAGAGGGAGAGA 1200  
Db 1141 AAGAGATGGCGCTGGGGAGGCTTGGCGCTGCGCGCTGCACTGCTGAGAGGGAGAGA 1200  
Qy 1201 TTTAGATCTGAGACGAGCTGTGGGATGTGCAATAGAAATAGCTATATTTATTTCCCA 1260  
Db 1201 TTTAGATCTGAGACGAGCTGTGGGATGTGCAATAGAAATAGCTATATTTATTTCCCA 1260  
Qy 1261 GGTGTGTCTTTAGGCGTGGCTGACAGAGCTTCTTCTCATCATCTTCTTCCCAATGAGTT 1320  
Db 1261 GGTGTGTCTTTAGGCGTGGCTGACAGAGCTTCTTCTCATCATCTTCTTCCCAATGAGTT 1320  
Qy 1321 TCCCTCTGAGCTTGAAGCATGAGGTTGTGCAATTTGTCAGCTCCCGCAGGCTGTCT 1380  
Db 1321 TCCCTCTGAGCTTGAAGCATGAGGTTGTGCAATTTGTCAGCTCCCGCAGGCTGTCT 1380  
Qy 1381 CCAGGCTTCAAGTCTGTGCTTGGAGAGTCAAGCAGGCTTAACTGACAGAGCATGTT 1440  
Db 1381 CCAGGCTTCAAGTCTGTGCTTGGAGAGTCAAGCAGGCTTAACTGACAGAGCATGTT 1440  
Qy 1441 GCGACCCCTGTCAGATTAATGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
Db 1441 GCGACCCCTGTCAGATTAATGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
Qy 1501 TCTACATGAGCTTGAATTAATGTTGAGAGGAGAGATGAGAACAATGTGAGTCTCCCTC 1560  
Db 1501 TCTACATGAGCTTGAATTAATGTTGAGAGGAGAGATGAGAACAATGTGAGTCTCCCTC 1560  
Qy 1561 TGAATGTTTGGGGAAATGAGAGAGAGTCCCTGCTTGCATTAACATCAACCTGGGCA 1620  
Db 1561 TGAATGTTTGGGGAAATGAGAGAGAGTCCCTGCTTGCATTAACATCAACCTGGGCA 1620  
Qy 1621 AATGCAACAAATGAATTTTTCACGAGTCTTTCATAGGATAGTAAAGCTGTGCTT 1680  
Db 1621 AATGCAACAAATGAATTTTTCACGAGTCTTTCATAGGATAGTAAAGCTGTGCTT 1680  
Qy 1681 CAGCTGTGAGATGAATGTTCTGTGACCTGTGATTAATGATGTTTATTCACAGA 1740  
Db 1681 CAGCTGTGAGATGAATGTTCTGTGACCTGTGATTAATGATGTTTATTCACAGA 1740  
Qy 1741 GGTGTGCTAGCTCTTCACTCTGTGCGCAGGGGAGATTTTCATTCACAAATTCCTC 1800  
Db 1741 GGTGTGCTAGCTCTTCACTCTGTGCGCAGGGGAGATTTTCATTCACAAATTCCTC 1800  
Qy 1801 TCTCTAGACACAGCTGGGAGAGGGGTCTTGTCTCTCTCTCTCATCAGGATCTCAGAG 1860  
Db 1801 TCTCTAGACACAGCTGGGAGAGGGGTCTTGTCTCTCTCTCTCATCAGGATCTCAGAG 1860  
Qy 1861 GCTCAGAGACTCAAGCTCTTGCACAGTCAAGCTAAGTGAAGACCAAGAGAGTTC 1920  
Db 1861 GCTCAGAGACTCAAGCTCTTGCACAGTCAAGCTAAGTGAAGACCAAGAGAGTTC 1920  
Qy 1921 ATCTGTTGTGACTTAAGCTCAATGCTCTTCACTAACCCCAACAGCTTGTGCTCA 1980  
Db 1921 ATCTGTTGTGACTTAAGCTCAATGCTCTTCACTAACCCCAACAGCTTGTGCTCA 1980  
Qy 1981 CCAAAAGTCTCCCAAAAGAGAGAGATGGGATTTTCTTGAAGGATGACATCTGGA 2040  
Db 1981 CCAAAAGTCTCCCAAAAGAGAGAGATGGGATTTTCTTGAAGGATGACATCTGGA 2040  
Qy 2041 ATTAAGTCAAACTAATCTCATCTCCCTCTAAGATGAATCTAAGTGAAGACAGCT 2100  
Db 2041 ATTAAGTCAAACTAATCTCATCTCCCTCTAAGATGAATCTAAGTGAAGACAGCT 2100  
Qy 2101 GTTTCACAGTGGGGAGCGGCTCTTCTAATGAAGCAATGATATGACCTGCTCT 2160  
Db 2101 GTTTCACAGTGGGGAGCGGCTCTTCTAATGAAGCAATGATATGACCTGCTCT 2160  
Qy 2161 CTTTGCAGTTGCAATTAATCTTGAAGATATGACTGAGCTGAGATACAGTTTA 2220  
Db 2161 CTTTGCAGTTGCAATTAATCTTGAAGATATGACTGAGCTGAGATACAGTTTA 2220  
Qy 2221 CTTGCAAGAACGTAATTAATGATGAGGCGAGATTAATTAATGAATTTGCAAAAT 2280  
Db 2221 CTTGCAAGAACGTAATTAATGATGAGGCGAGATTAATTAATGAATTTGCAAAAT 2280  
Qy 2281 CACTTGAAGCACTGAAGACATTAATCAACCACTGAGAGAAATCAACCGAGAGAGG 2340  
Db 2281 CACTTGAAGCACTGAAGACATTAATCAACCACTGAGAGAAATCAACCGAGAGAGG 2340  
Qy 2341 TGTGTGAACATGTTGTAATGCGACTGCGAACACTGAATCTTACGCACTTCAAAA 2400  
Db 2341 TGTGTGAACATGTTGTAATGCGACTGCGAACACTGAATCTTACGCACTTCAAAA 2400  
Qy 2401 TGAATGTTTCAAGTGTGACAGTGTGCAACATGATATTCACAGATTTCTTAAAGTT 2460  
Db 2401 TGAATGTTTCAAGTGTGACAGTGTGCAACATGATATTCACAGATTTCTTAAAGTT 2460



```

Db      1141 AAGAGATGGCGCTGGGGGAGCGTGGCTGCCGCGCTGCACGTGCGGGAGGGAAG 1200
Qy      1201 TTTTGAATCTGAGACCAAGCTGTGGGTAGATGTGCAATAGAAATAGCTTAATTTTCCCA 1260
Db      1201 TTTTGAATCTGAGACCAAGCTGTGGGTAGATGTGCAATAGAAATAGCTTAATTTTCCCA 1260
Qy      1261 GGTGTGTGCTTTAGCGCTGGGCTGACCAAGGCTTCTTCTCAATCTTCTTCCAGTAAGTT 1320
Db      1261 GGTGTGTGCTTTAGCGCTGGGCTGACCAAGGCTTCTTCTCAATCTTCTTCCAGTAAGTT 1320
Qy      1321 TCCCTCTGTGCTTACAGCATGAGGTGTGTGCAATTTGTTCAGTCTCCCAAGGCTGTCT 1380
Db      1321 TCCCTCTGTGCTTACAGCATGAGGTGTGTGCAATTTGTTCAGTCTCCCAAGGCTGTCT 1380
Qy      1381 CCAGGCTTACAGCATGCTGTGCTTGGAGAGTCAAGGCTTAACTGACAGACAGTTT 1440
Db      1381 CCAGGCTTACAGCATGCTGTGCTTGGAGAGTCAAGGCTTAACTGACAGACAGTTT 1440
Qy      1441 GCCACCCCTGTGCAGATTATTGGCTGCTTGCCTTACCAAGTTGGCAGACAGCCGTTGT 1500
Db      1441 GCCACCCCTGTGCAGATTATTGGCTGCTTGCCTTACCAAGTTGGCAGACAGCCGTTGT 1500
Qy      1501 TCTPACATGCTTATGATTAATGTTTGAAGGGAGAGATGAAACATGTGAGTCTCCCTC 1560
Db      1501 TCTPACATGCTTATGATTAATGTTTGAAGGGAGAGATGAAACATGTGAGTCTCCCTC 1560
Qy      1561 TGATTGCTTTTGGGAAAATGTGAGAAAGAGTCCCTGCTTGCACCAATCACTGAGCAA 1620
Db      1561 TGATTGCTTTTGGGAAAATGTGAGAAAGAGTCCCTGCTTGCACCAATCACTGAGCAA 1620
Qy      1621 AAATGCAACAAATTAATTTTCCAGCAGTCTTCCATGGGCAATAGCTAGCTGTGCTT 1680
Db      1621 AAATGCAACAAATTAATTTTCCAGCAGTCTTCCATGGGCAATAGCTAGCTGTGCTT 1680
Qy      1681 CAGCTGTGTCAGATGAATATGTTCTGTTCAACCTGCACTTACATGTTATTATCCAGCA 1740
Db      1681 CAGCTGTGTCAGATGAATATGTTCTGTTCAACCTGCACTTACATGTTATTATCCAGCA 1740
Qy      1741 GTGTGTGCTCAGCTCTTACCTCTGTGCCAGGAGACATTTTCATATCCAAATCAATCCC 1800
Db      1741 GTGTGTGCTCAGCTCTTACCTCTGTGCCAGGAGACATTTTCATATCCAAATCAATCCC 1800
Qy      1801 TCTCTCAGCAGCGCTGGGAGGAGGATCATGTTCTCTCCTGTCATCAGGATCTCAGAG 1860
Db      1801 TCTCTCAGCAGCGCTGGGAGGAGGATCATGTTCTCTCCTGTCATCAGGATCTCAGAG 1860
Qy      1861 GCTCAGAGACTGCAAGCTGTGCTGCCAAGTCAACAGCTAGTGAAGACAGAGAGTTTC 1920
Db      1861 GCTCAGAGACTGCAAGCTGTGCTGCCAAGTCAACAGCTAGTGAAGACAGAGAGTTTC 1920
Qy      1921 ATCTGTGTTGACTCTAAGCTCAGTGTCTCTCTCCACTACCCACACAGCCTTGTGCTCA 1980
Db      1921 ATCTGTGTTGACTCTAAGCTCAGTGTCTCTCTCCACTACCCACACAGCCTTGTGCTCA 1980
Qy      1991 CCAAAAAGTCTCCCAAAAAGAGAGATGGATTTTCTTGAAGCATGACATCTTGA 2040
Db      1991 CCAAAAAGTCTCCCAAAAAGAGAGATGGATTTTCTTGAAGCATGACATCTTGA 2040
Qy      2041 ATTAAAGTCAAACTAATCTCACAATCCCTCTAAAGTAACTAATCTGTTAGGACAGAGT 2100
Db      2041 ATTAAAGTCAAACTAATCTCACAATCCCTCTAAAGTAACTAATCTGTTAGGACAGAGT 2100
Qy      2101 GTTCTCAGAGTGTGGGAGCGCTCTTCTTAATGAAGCAATGATTTGACATGCTCCCT 2160
Db      2101 GTTCTCAGAGTGTGGGAGCGCTCTTCTTAATGAAGCAATGATTTGACATGCTCCCT 2160
Qy      2161 CTTTGGCAGTGTGCAATTAATCTTGAAGGATATAGCTAGCGGTGACATACAGTTAA 2220
Db      2161 CTTTGGCAGTGTGCAATTAATCTTGAAGGATATAGCTAGCGGTGACATACAGTTAA 2220
Qy      2221 CCTGCAAGAAAGTACTTAGTAAATGTGAGGCGAGATTAATAATGAATTTGCAAAAT 2280

```

```

Db      2221 CCTGCAAGAAAGTACTTAGTAAATGTGAGGCGAGATTAATAATGAATTTGCAAAAT 2280
Qy      2281 CACTTAGAGCAACATGAGACAAATTAATCAACGATGAGAAATCAACCGAGAGAGGC 2340
Db      2281 CACTTAGAGCAACATGAGACAAATTAATCAACGATGAGAAATCAACCGAGAGAGGC 2340
Qy      2341 TGTGTGAACATGTTGTAATATGCACTGCGAACACTGAACTTACGCCACTCCAGAA 2400
Db      2341 TGTGTGAACATGTTGTAATATGCACTGCGAACACTGAACTTACGCCACTCCAGAA 2400
Qy      2401 TGTATTTTTCAGGTGTCATGACGTGTGCGCAACATGATTAATCAGAGTCTTAAAGTT 2460
Db      2401 TGTATTTTTCAGGTGTCATGACGTGTGCGCAACATGATTAATCAGAGTCTTAAAGTT 2460
Qy      2461 TAAAGTTGACATGATGTATATAGCATGCTTCTTGAAGTTTAAATTAATATTAACAT 2520
Db      2461 TAAAGTTGACATGATGTATATAGCATGCTTCTTGAAGTTTAAATTAATATTAACAT 2520
Qy      2521 AAGTTGCAATTTGAATATCAAGATTAATCACTCAACTGCAAAAATTAATTAATTAAT 2580
Db      2521 AAGTTGCAATTTGAATATCAAGATTAATCACTCAACTGCAAAAATTAATTAATTAAT 2580
Qy      2581 AAAAAA 2586
Db      2581 AAAAAA 2586

RESULT 13
ACAO5532
ID ACAA05532 standard; cDNA; 2586 BP.
XX
AC ACAA05532;
XX
DT 29-MAY-2003 (first entry)
DE
XX cDNA encoding human secreted protein PRO295.
XX
KW Human; gene therapy; mucosal lesion; ulcer; enterocolitis; skin disease;
KW psoriasis; cancer; lung cancer; colon cancer; nerve cell disease;
KW Alzheimer's disease; Parkinson's disease; Usher syndrome; angiogenesis;
KW atrophla areata; inflammatory disease; asthma; rheumatoid arthritis;
KW lechaemia; ss; gene.
XX
OS Homo sapiens.
XX
PN US2003023054-A1.
XX
PD 30-JUN-2003.
XX
PF 16-JUL-2001; 2001US-0906742.
XX
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 01-DEC-1998; 98WO-US25108.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30919.
PR 05-JAN-2000; 2000WO-US00219.
PR 11-FEB-2000; 2000WO-US03565.
PR 24-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.

```

PR	02-MAR-2000;	2000MO-US05841.
PR	20-MAR-2000;	2000MO-US07377.
PR	30-MAR-2000;	2000MO-US08439.
PR	22-MAY-2000;	2000MO-US14042.
PR	02-JUN-2000;	2000MO-US15264.
PR	28-JUL-2000;	2000MO-US20710.
PR	24-AUG-2000;	2000MO-US23328.
PR	17-SEP-1997;	97US-059113P.
PR	17-SEP-1997;	97US-059117P.
PR	17-SEP-1997;	97US-059119P.
PR	17-SEP-1997;	97US-059121P.
PR	17-SEP-1997;	97US-059123P.
PR	17-SEP-1997;	97US-059184P.
PR	18-SEP-1997;	97US-059263P.
PR	18-SEP-1997;	97US-059266P.
PR	15-OCT-1997;	97US-062125P.
PR	17-OCT-1997;	97US-062285P.
PR	17-OCT-1997;	97US-062287P.
PR	21-OCT-1997;	97US-063486P.
PR	24-OCT-1997;	97US-063814P.
PR	24-OCT-1997;	97US-063816P.
PR	24-OCT-1997;	97US-063045P.
PR	24-OCT-1997;	97US-063120P.
PR	24-OCT-1997;	97US-063121P.
PR	24-OCT-1997;	97US-063127P.
PR	24-OCT-1997;	97US-063128P.
PR	27-OCT-1997;	97US-063327P.
PR	27-OCT-1997;	97US-063329P.
PR	26-OCT-1997;	97US-063541P.
PR	26-OCT-1997;	97US-063542P.
PR	28-OCT-1997;	97US-063544P.
PR	28-OCT-1997;	97US-063549P.
PR	28-OCT-1997;	97US-063550P.
PR	28-OCT-1997;	97US-063564P.
PR	29-OCT-1997;	97US-064335P.
PR	29-OCT-1997;	97US-063704P.
PR	29-OCT-1997;	97US-063732P.
PR	29-OCT-1997;	97US-063734P.
PR	29-OCT-1997;	97US-063735P.
PR	29-OCT-1997;	97US-063738P.
PR	29-OCT-1997;	97US-064215P.
PR	31-OCT-1997;	97US-063870P.
PR	31-OCT-1997;	97US-064103P.
PR	03-NOV-1997;	97US-064248P.
PR	07-NOV-1997;	97US-064809P.
PR	12-NOV-1997;	97US-065186P.
PR	17-NOV-1997;	97US-065846P.
PR	18-NOV-1997;	97US-065933P.
PR	21-NOV-1997;	97US-066120P.
PR	21-NOV-1997;	97US-066164P.
PR	24-NOV-1997;	97US-066453P.
PR	24-NOV-1997;	97US-066466P.
PR	24-NOV-1997;	97US-066511P.
PR	24-NOV-1997;	97US-066770P.
PR	24-NOV-1997;	97US-066772P.
PR	25-NOV-1997;	97US-066840P.
PR	12-DEC-1997;	97US-069425P.
PR	04-JUN-1998;	98US-098026P.
PR	10-SEP-1998;	98US-099803P.
PR	14-SEP-1998;	98US-100262P.
PR	17-SEP-1998;	98US-100858P.
PR	13-OCT-1998;	98US-104080P.
PR	20-NOV-1998;	98US-109304P.
PR	22-DEC-1998;	98US-113296P.
PR	07-JUL-1999;	99US-143048P.
PR	26-JUL-1999;	99US-145698P.
PR	28-JUL-1999;	99US-146222P.
PR	18-SEP-2000;	2000US-0665350.
XX		
PA	(GETH )	GEOMETECH INC.
XX		
PI	Ashtkenazi A,	Botstein D, Desnoyers L, Eaton DL, Ferrara N

WP1: 2003-331485/31.  
 P-PSDB: AB067385.  
 Williams PF, Wood WI;  
 Matther JP, Pan J, Paoni NF, Roy MA, Stewart TH, Tamas D,  
 Goddard PJ, Grimaldi JC, Gunney AL, Hillan KJ, Klibin IJ,  
 Filarszoff E, Fong S, Gao W, Geber H, Gerritsen ME, Goddard A,  
 Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g.  
 PRO345 or PRO1868, useful in chromosome and gene mapping, in generating  
 antisense RNA and DNA, and in treating cancer and Alzheimer's disease -  
 Example 36; Fig 83; 48pp; English.

The inventors related to sixty one nucleic acids encoding PRO polypeptides (secreted and transmembrane). The polynucleotide is useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polynucleotide may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptide or the antibody is used in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as mucosal lesions e.g. ulcers and enterocolitis, skin disease e.g. psoriasis, cancer e.g. lung cancer and colon cancer, nerve cell disease e.g. Alzheimer's disease and Parkinson's disease, Usher syndrome, reticophia areata, angiogenesis, inflammatory disease e.g. asthma and rheumatoid arthritis, ischaemia, and in various diagnostic assays. The present sequence represents an cDNA which encodes a PRO polypeptide.

Query Match	100.0%;	Score 2586;	DB 25;	Length 2586;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2586;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

QY	541	AGACAGTTATCACTCTGTGGGAAACAAAGAAAGGACAAAGAGCACAGATGCATCTCG	600
Db	541	AGACAGTTATCACTCTGTGGGAAACAAAGAAAGGACAAAGAGCACAGATGCATCTCG	600
QY	601	ACGAGACGTGTGGGCCGACGATGTACTGCCAGTTTGCAGCTTCCAGTACACCTGCCAGC	660
Db	601	ACGAGGACGTGTGGGCCGACGATGTACTGCCAGTTTGCAGCTTCCAGTACACCTGCCAGC	660
QY	661	CATGCCGGGGCCAAAGAAATGCTCTGCACCCGGGACAGTAGAGTGTGTGTGGAGAACAGCTGT	720
Db	661	CATGCCGGGGCCAAAGAAATGCTCTGCACCCGGGACAGTAGAGTGTGTGTGGAGAACAGCTGT	720
QY	721	GTGTCTGGGGTCACTGACACCAAAATGGCCACCAAGGGGACGCAATGGAGCACTGTGTACA	780
Db	721	GTGTCTGGGGTCACTGACACCAAAATGGCCACCAAGGGGACGCAATGGAGCACTGTGTACA	780
QY	781	ACCGAGAGGAATGCCACAGCCGGGGCTGTGTCTGTGCTTTCAGAAAGAGCTGTGTTCCTGT	840
Db	781	ACCGAGAGGAATGCCACAGCCGGGGCTGTGTCTGTGCTTTCAGAAAGAGCTGTGTTCCTGT	840
QY	841	TGTACACACCCCTGACCCGTGAGAGGGACGAGCTTTCAGATGACCCCGACAGCCGGCTTCTGG	900
Db	841	TGTACACACCCCTGACCCGTGAGAGGGACGAGCTTTCAGATGACCCCGACAGCCGGCTTCTGG	900
QY	901	ACCTCATCACTGGAGAGCTAAGCTGATAGAGACCTTTGACCGATGCCCTTTGTGCCAGTG	960
Db	901	ACCTCATCACTGGAGAGCTAAGCTGATAGAGACCTTTGACCGATGCCCTTTGTGCCAGTG	960
QY	961	GGCTCTCTGTGCACCCGCCACAGCCACAGACCTGTGTATGTGTGTAAGGCCACCTTGCATGG	1020
Db	961	GGCTCTCTGTGCACCCGCCACAGACCTGTGTGTATGTGTGTAAGGCCACCTTGCATGG	1020
QY	1021	GGAGCCGTGACCAAGATGGGGAGATCTGTCTGTCCACAGAGAGTCCCGATGATATGAG	1080
Db	1021	GGAGCCGTGACCAAGATGGGGAGATCTGTCTGTCCACAGAGAGTCCCGATGATATGAG	1080
QY	1081	TTGGCAGCTTATAGAGAGATGTGCGCCAGAGCTGTGAGAGACCTGTGAGAGAGCCTTGACTG	1140
Db	1081	TTGGCAGCTTATAGAGAGATGTGCGCCAGAGCTGTGAGAGACCTGTGAGAGAGCCTTGACTG	1140
QY	1141	AAGAGATGGCCCTGGGGAGGCTGTGGCGTGGCCGCGCTGCACCTGTGGAGAGGGAAAGAA	1200
Db	1141	AAGAGATGGCGCTGGGGAGGCTGTGGCGTGGCGCGCTGCACCTGTGGAGAGGGAAAGAA	1200
QY	1201	TTTATGATTTGGACCAAGCGCTGTGGGTATGTGCATAATAGATAATTATTTTCCCA	1260
Db	1201	TTTATGATTTGGACCAAGCGCTGTGGGTATGTGCATAATAGATAATTATTTTCCCA	1260
QY	1261	GGTGTGTCTTAAAGCGTGGGCTGACCAAGGCTTCTTCTAATCATCTTCTCCAGATAGTT	1320
Db	1261	GGTGTGTCTTAAAGCGTGGGCTGACCAAGGCTTCTTCTAATCATCTTCTCCAGATAGTT	1320
QY	1321	TCCCTCTGGGCTTGAACAGATGAGGTGTGTGCATTGTTCAGCTCCCCGAGGCTGTCT	1380
Db	1321	TCCCTCTGGGCTTGAACAGATGAGGTGTGTGCATTGTTCAGCTCCCCGAGGCTGTCT	1380
QY	1381	CCAGGCTTCAAGTCTGTGTGTGGGAAAGTCAAGGACAGGTTAAATCTGACAGAGAGTTT	1440
Db	1381	CCAGGCTTCAAGTGTGTGTGTGGGAAAGTCAAGGAGGTTAAATCTGACAGAGAGAGTTT	1440
QY	1441	GCCACCCCTGTCCAGATTAATTTGGCTTTTGCTTCTTACAGTTGGCAGACAGCCGTTTGT	1500
Db	1441	GCCACCCCTGTCCAGATTAATTTGGCTTTTGCTTCTTACAGTTGGCAGACAGCCGTTTGT	1500
QY	1501	TCATACATGGCTTTGATTAATTGTTTGAGGGGAGAGATGGAAACAATGTGAGATCTCCCTC	1560
Db	1501	TCATACATGGCTTTGATTAATTGTTTGAGGGGAGAGATGGAAACAATGTGAGATCTCCCTC	1560
QY	1561	TGATTTGTTTTGGGAAATGTGAAAGATGACCTGCTTTTGCAAAATCAACTGACGCAA	1620
Db	1561	TGATTTGTTTTGGGAAATGTGAAAGATGACCTGCTTTTGCAAAATCAACTGACGCAA	1620
QY	1621	AAATGCAACAAATGAATTTTCCACGCAAGTCTTTTCCATGAGGCATAGTAACTGTGCTT	1680

D	b	1621	AAATGGACAAGAAATGAAATTTTCCAGGAGTTCTTTTCATGGGCAATAGTAAGCTGTGCTT	1680
Q	y	1681	CAGCTGTGGCAATGAAATGTTCTGTTCACCCCTGCAATTAATGTGTTATTCATCCAGCA	1740
D	b	1681	CACCTGTTGGAGATGAAATGTTCTGTTCACCCCTGCAATTAATGTGTTATTCATCCAGCA	1740
Q	y	1741	GTGTGGCTGAGCTCCATCTCTGTGGCAGGGGAGCAATTTCAATCAACATCAATTTCC	1800
D	b	1741	GTGTGGCTGAGCTCCATCTCTGTGGCAGGGGAGCAATTTCAATCAACATCAATTTCC	1800
Q	y	1801	TCTCTGAGCAAGCTTGGGAGGGGGTCAATTGTTCTCTCTGTCATAGGGATCTCAGAG	1860
D	b	1801	TCTCTGAGCAAGCTTGGGAGGGGGTCAATTGTTCTCTCTGTCATAGGGATCTCAGAG	1860
Q	y	1861	GGTCAGAGACTGGAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACAGAGCAATTTC	1920
D	b	1861	GGTCAGAGACTGGAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACAGAGCAATTTC	1920
Q	y	1921	ATCTGTTGTGACTCTTAAGCTCAGTGTCTCTCCACTACCCACACAGCCTTGTGTCCA	1980
D	b	1921	ATCTGTTGTGACTCTTAAGCTCAGTGTCTCTCCACTACCCACACAGCCTTGTGTCCA	1980
Q	y	1981	CCAAAAGTGTCCCCCAAAAGGAAAGGAAATGGGATTTTCTTGAGGATGACACTGGGA	2040
D	b	1981	CCAAAAGTGTCCCCCAAAAGGAAAGGAAATGGGATTTTCTTGAGGATGACACTGGGA	2040
Q	y	2041	ATTAAAGTCAAACTAATTCACATCCCTCTAAAGTAACCTAGTAGGAACAGCAGT	2100
D	b	2041	ATTAAAGTCAAACTAATTCACATCCCTCTAAAGTAACCTAGTAGGAACAGCAGT	2100
Q	y	2101	GTTCTCAAGTGTGGGGCAGCCGCTCTCTTAAGGAACATGATATTGACACTGTCCCT	2160
D	b	2101	GTTCTCAAGTGTGGGGCAGCCGCTCTCTTAAGGAACATGATATTGACACTGTCCCT	2160
Q	y	2161	CTTTGGAGATGTGACTTAGTAATCTTGAAGATATATGACTGAGCGTAGCATACAGTTAA	2220
D	b	2161	CTTTGGAGATGTGACTTAGTAATCTTGAAGATATATGACTGAGCGTAGCATACAGTTAA	2220
Q	y	2221	CCTGACAGAAACAGTACTTAAGGTAATTGTAGGGCGAGGATTTATTAATGAAATTTCGAAAT	2280
D	b	2221	CCTGACAGAAACAGTACTTAAGGTAATTGTAGGGCGAGGATTTATTAATGAAATTTCGAAAT	2280
Q	y	2281	CACCTAGCAGCACTGTAAGCAATTAATCAACACAGTGAAGAAATCAAAACGAGCAGGGC	2340
D	b	2281	CACCTAGCAGCACTGTAAGCAATTAATCAACACAGTGAAGAAATCAAAACGAGCAGGGC	2340
Q	y	2341	TGTGTGAACAATGGTTGTAAATATGCGACTGGAACACTGAACTGTACGCCACTCCAAA	2400
D	b	2341	TGTGTGAACAATGGTTGTAAATATGCGACTGGAACACTGAACTGTACGCCACTCCAAA	2400
Q	y	2401	TGAAGTTTCAAGGTCATGATGTAAGCAAGCTTCTTTGAGTTTAAATTATGTATTAACAT	2460
D	b	2401	TGAAGTTTCAAGGTCATGATGTAAGCAAGCTTCTTTGAGTTTAAATTATGTATTAACAT	2460
Q	y	2461	TAAAGTTGCACTGATGTAATTAAGCAAGCTTCTTTGAGTTTAAATTATGTATTAACAT	2520
D	b	2461	TAAAGTTGCACTGATGTAATTAAGCAAGCTTCTTTGAGTTTAAATTATGTATTAACAT	2520
Q	y	2521	AAAGTTGATTTAGAAATCAAGCATTAATCACTTAATCGCAAAAAAATTTTTTTTTTTT	2580
D	b	2521	AAAGTTGATTTAGAAATCAAGCATTAATCACTTAATCGCAAAAAAATTTTTTTTTTTT	2580
Q	y	2581	AAAAAA 2586	
D	b	2581	AAAAAA 2586	
RESULT 14				
ABX96211				
ID ABX96211 standard; cDNA; 2586 BP.				
XX ABX96211;				
AC				





Db	61	CCGGCGGCGCTCCCGGCGGAGCGAGATCCAGTCCCGCGCGCAACTGGTGCA	120
Qy	121	GTGCGGCGCGCGCTGCGGCGCGAGACCGGAGATGACCGGCTTGGGCGCACTGCTGT	180
Db	121	GTGCGGCGCGCGGCTGCGGCGCGAGACCGGAGATGACGCGGCTTGGGCGCACTGCTGT	180
Qy	181	GCTGCTGCTGCTGCGGCGCGGCTCCCGAGCGCCCCCGCGCCCGCTCGAGCGCGACTCGG	240
Db	181	GCTGCTGCTGCTGCGGCGCGGCTCCCGAGCGCCCCCGCGCCCGCTCGAGCGCGACTCGG	240
Qy	241	CTCCAGTCAAGCCCGGCGCGGCTCTGAGCTAACCGCGAGAGGAGCGCACTCGTAATAGA	300
Db	241	CTCCAGTCAAGCCCGGCGCGGCTCTGAGCTAACCGCGAGAGGAGCGCACTCGTAATAGA	300
Qy	301	TGTTCCGCGAGTTGAGGAACTGATGAGAGCACGCGACGCAAAATTGCGAGCGCGGTGG	360
Db	301	TGTTCCGCGAGTTGAGGAACTGATGAGAGCACGCGACGCAAAATTGCGAGCGCGGTGG	360
Qy	361	AAGGATGAGGAGCGAGAGAGCTGCTGTAAGCATATAGAAAGTGAACCTGGCAACT	420
Db	361	AAGGATGAGGAGCGAGAGAGCTGCTGTAAGCATATAGAAAGTGAACCTGGCAACT	420
Qy	421	TACCTCCAGCTATCAGAAATGAGACCAACAGACGAAAGTTGGAATPATACATCC	480
Db	421	TACCTCCAGCTATCAGAAATGAGACCAACAGACGAAAGTTGGAATPATACATCC	480
Qy	481	ATGTGCACCGAATAATTCACAAATTAACCAACAACGAGCTGGAACAATGCTCTTTGAG	540
Db	481	ATGTGCACCGAATAATTCACAAATTAACCAACAACGAGCTGGAACAATGCTCTTTGAG	540
Qy	541	AGAAGATTATACATCTGTGGGAGACGAAAGGCGAAGAGGACGAGAGTGCATATCG	600
Db	541	AGAAGATTATACATCTGTGGGAGACGAAAGGCGAAGAGGACGAGAGTGCATATCG	600
Qy	601	ACGAGGACTGTGGGCCCGACATGTAAGTCCAGTTGCCAGTTCCAGTACACTGCCAGC	660
Db	601	ACGAGGACTGTGGGCCCGACATGTAAGTCCAGTTGCCAGTTCCAGTACACTGCCAGC	660
Qy	661	CATGCGGAGGCGCAAGAGATGCTCTGACCCGGGACAGTGAATGCTGTGGAGACCAAGCTGT	720
Db	661	CATGCGGAGGCGCAAGAGATGCTCTGACCCGGGACAGTGAATGCTGTGGAGACCAAGCTGT	720
Qy	721	GTGTCTGGGATCACTGCACAAAATGCGCACAGAGGCGACGCAATGGAGCAATCTGTACA	780
Db	721	GTGTCTGGGATCACTGCACAAAATGCGCACAGAGGCGACGCAATGGAGCAATCTGTACA	780
Qy	781	ACGAGAGGAGATGCGCAGCCGGGGCTGTGCTGTGCTTCCANAGAGCTGTGTTCCCTG	840
Db	781	ACGAGAGGAGATGCGCAGCCGGGGCTGTGCTGTGCTTCCANAGAGCTGTGTTCCCTG	840
Qy	841	TGTGCACACCCCTGCGCTGTGAGGGCGAGCTTGTGCATGACCCCGCGACGCGGCTTGTGG	900
Db	841	TGTGCACACCCCTGCGCTGTGAGGGCGAGCTTGTGCATGACCCCGCGACGCGGCTTGTGG	900
Qy	901	ACCTCATTAAGCTGAGAGCTTAGAGCTGATGAGAGCTTGAACCGATGCCCCCTGTGTCCAGTG	960
Db	901	ACCTCATTAAGCTGAGAGCTTAGAGCTGATGAGAGCTTGAACCGATGCCCCCTGTGTCCAGTG	960
Qy	961	GCTGCTCTGCGAGGCCACAGCAACAGCTGTGTATGTGTGAAGCGGCACTTCTGTGG	1020
Db	961	GCTGCTCTGCGAGGCCACAGCAACAGCTGTGTATGTGTGAAGCGGCACTTCTGTGG	1020
Qy	1021	GGAAGCGGTGACCAAGATGGGAGATCTGTGCTGCCAGAGAGTCCCGGATGATATGAG	1080
Db	1021	GGAAGCGGTGACCAAGATGGGAGATCTGTGCTGCCAGAGAGTCCCGGATGATATGAG	1080
Qy	1081	TTGGCAGTTTATGAGAGAGGTGCGCGAGAGCTGTGAGAACTTGAAGAGAGCCTTGACTG	1140
Db	1081	TTGGCAGTTTATGAGAGAGGTGCGCGAGAGCTGTGAGAACTTGAAGAGAGCCTTGACTG	1140
Qy	1141	AAGAGATGCGCTGGGAGAGCCTTGGGCTGCGCGCGTGCATCTGTGGAGGAGGAAAGA	1200

D	b	1141	AAGAATGCGCGTGGGGGAGCCTTCGCGCTGCCCGCGCTGCACCTGCTGGAGGGGAGAGA	1200
Q	y	1201	TTTAGATCTGAGCCAGGCTGTGGGTAGATGCAATGAATAGCTAATTTATTTCCCA	1260
D	b	1201	TTTAGATCTGAGCCAGGCTGTGGGTAGATGCAATGAATAGCTAATTTATTTCCCA	1260
Q	y	1261	GGTGTGCTTTTAGCGCTGGGCTGACCAAGCCTTCTCCACATCTCTTCCAGTAAGT	1320
D	b	1261	GGTGTGCTTTTAGCGCTGGGCTGACCAAGCCTTCTCCACATCTCTTCCAGTAAGT	1320
Q	y	1321	TCCCTCTGCGCTTGACAGCATGAGTGTGTGCAATTTGTCAGCTCCCGCAGCTGTCT	1380
D	b	1321	TCCCTCTGCGCTTGACAGCATGAGTGTGTGCAATTTGTCAGCTCCCGCAGCTGTCT	1380
Q	y	1381	CCAGGCTTCACAGCTGTGTGCTTGGAGAGTCAAGCGGTTAACTGCAAGACATTT	1440
D	b	1381	CCAGGCTTCACAGCTGTGTGCTTGGAGAGTCAAGCGGTTAACTGCAAGACATTT	1440
Q	y	1441	GCCACCCCTGTCAGATTTATTTGCTGTTTGGCTCTACAGTTGGCAGACAGCCGTTGT	1500
D	b	1441	GCCACCCCTGTCAGATTTATTTGCTGTTTGGCTCTACAGTTGGCAGACAGCCGTTGT	1500
Q	y	1501	TCTACATGCGCTTGATTAATGTTTGAAGGGAGAGATGAAACATGTGAGTCTCCCTC	1560
D	b	1501	TCTACATGCGCTTGATTAATGTTTGAAGGGAGAGATGAAACATGTGAGTCTCCCTC	1560
Q	y	1561	TGATTTGTTTTGGGGAAATGTGAGGAATGCGCTTTCGCAACATGACCTGGCAA	1620
D	b	1561	TGATTTGTTTTGGGGAAATGTGAGGAATGCGCTTTCGCAACATGACCTGGCAA	1620
Q	y	1621	AAATGCAACAAATGAATTTTCCAGCAGTTCTTTCATGSGCATGGAAGCTGTGCTT	1680
D	b	1621	AAATGCAACAAATGAATTTTCCAGCAGTTCTTTCATGSGCATGGAAGCTGTGCTT	1680
Q	y	1681	CAGCTGTTGCAGATGAATGTTCTGTTCAACCTGACATTAATGTTTATTCACAGCA	1740
D	b	1681	CAGCTGTTGCAGATGAATGTTCTGTTCAACCTGACATTAATGTTTATTCACAGCA	1740
Q	y	1741	GTTGTGTCAGACTCTACCTCTGTGCCAGGACAGCATTTTCATATCCAGATCAATCCC	1800
D	b	1741	GTTGTGTCAGACTCTACCTCTGTGCCAGGACAGCATTTTCATATCCAGATCAATCCC	1800
Q	y	1801	TCTCTCAGCACAGCTTGCGGGAGGGGGATCTTGTCTCTCTGTCATACAGGATCTCAGAG	1860
D	b	1801	TCTCTCAGCACAGCTTGCGGGAGGGGGATCTTGTCTCTCTGTCATACAGGATCTCAGAG	1860
Q	y	1861	GCTCAGAGACTGCAGAGCTGTGCGCCCAAGTACACACTAGTGAAGACCAAGACAGTTTC	1920
D	b	1861	GCTCAGAGACTGCAGAGCTGTGCGCCCAAGTACACACTAGTGAAGACCAAGACAGTTTC	1920
Q	y	1921	ATCTGTTGTGACTCTAAGCTCAGTGTCTTCTCCACTACCCCAACAGCCTTGTGTCCA	1980
D	b	1921	ATCTGTTGTGACTCTAAGCTCAGTGTCTTCTCCACTACCCCAACAGCCTTGTGTCCA	1980
Q	y	1981	CCAAAGTGCCTCCCAAAAGGAGAGAAATGGATTTTCTGAGGATGCAACATCTGGA	2040
D	b	1981	CCAAAGTGCCTCCCAAAAGGAGAGAAATGGATTTTCTGAGGATGCAACATCTGGA	2040
Q	y	2041	ATTAAAGTCAAACTAATTTCTCACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGT	2100
D	b	2041	ATTAAAGTCAAACTAATTTCTCACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGT	2100
Q	y	2101	GTTCTCAGAGTGTGGGACGCGCTCTCTAATGAAGACATGATTTGAACACTGTCCCT	2160
D	b	2101	GTTCTCAGAGTGTGGGACGCGCTCTCTAATGAAGACATGATTTGAACACTGTCCCT	2160
Q	y	2161	CTTTGCGAGTTGACTTAAGTAACTTTGAAAGGTATATGACTAGCGGTAGCAATACAGTTAA	2220
D	b	2161	CTTTGCGAGTTGACTTAAGTAACTTTGAAAGGTATATGACTAGCGGTAGCAATACAGTTAA	2220
Q	y	2221	CCTGACAGAAACAGTACTTAAGTAACTTTGAGGCGCAGAGATTTAATGAAATTTGCCAAAT	2280
D	b	2221	CCTGACAGAAACAGTACTTAAGTAACTTTGAGGCGCAGAGATTTAATGAAATTTGCCAAAT	2280



Db 1 CGCCGCGCTCCCGACCCGCGGCCGCCACCGCGCCGCTCCGCGATCTGCACCCGCAAC 60  
Qy 61 CCGCGCGCTCCCGCGGAGACGAGATCCAGTCCGCGCCCGAGGCGAACTCGGCTCA 120  
Db 61 CCGCGCGCTCCCGCGGAGACGAGATCCAGTCCGCGCCCGAGGCGAACTCGGCTCA 120  
Qy 121 GTCGCGGCGCGCGCTGCGCGGCGCAGAGCGAGATGCAGCGCGCTTGCGGCGCACTCTGCTGT 180  
Db 121 GTCGCGGCGCGCGCTGCGCGGCGCAGAGCGAGATGCAGCGCGCTTGCGGCGCACTCTGCTGT 180  
Qy 181 GCTGCTGCTGCTGCGCGCGCTGCTCCCAAGCGCGCGCGCGCGCTGCTCCCAAGCGCGCACTCTGCG 240  
Db 181 GCTGCTGCTGCTGCGCGCGCTGCTCCCAAGCGCGCGCGCGCGCTGCTCCCAAGCGCGCACTCTGCG 240  
Qy 241 CTCGCGTCAAGCCCGCGCGCGCTCTCAGCTTACCGCGCAGAGAGAGCGCACTCTCATAGA 300  
Db 241 CTCGCGTCAAGCCCGCGCGCGCTCTCAGCTTACCGCGCAGAGAGAGCGCACTCTCATAGA 300  
Qy 301 TGTTCGCGAGGTTGAGGAACTGATGAGGACAGCGCAGCAAAATGCGCAGCGCGGTGG 360  
Db 301 TGTTCGCGAGGTTGAGGAACTGATGAGGACAGCGCAGCAAAATGCGCAGCGCGGTGG 360  
Qy 361 AAGAGATGAGGCGAGAGAGAGCTGCTGCTAAAGCATCATGAAAGTGAACCTGGCAACT 420  
Db 361 AAGAGATGAGGCGAGAGAGAGCTGCTGCTAAAGCATCATGAAAGTGAACCTGGCAACT 420  
Qy 421 TACCTCCGAGCTTACATGAGACCAACAGACACGAGAGTTGAAATTAATACATCC 480  
Db 421 TACCTCCGAGCTTACATGAGACCAACAGACACGAGAGTTGAAATTAATACATCC 480  
Qy 481 ATGTGACCGGAGAAATTCAGAAATTAACCAACAGACAGCTGAGCAATGCTTTTCAG 540  
Db 481 ATGTGACCGGAGAAATTCAGAAATTAACCAACAGACAGCTGAGCAATGCTTTTCAG 540  
Qy 541 AGACAGTATACATCTGTGGAGAGCAGAGAGGAGAGAGGACAGAGCTGATCATCG 600  
Db 541 AGACAGTATACATCTGTGGAGAGCAGAGAGGAGAGAGGACAGAGCTGATCATCG 600  
Qy 601 ACGAGAGCTGTGGGCGCCAGCATGTACTGCGAGTTTGCGAGCTTCCAGTACACCTGCCAGC 660  
Db 601 ACGAGAGCTGTGGGCGCCAGCATGTACTGCGAGTTTGCGAGCTTCCAGTACACCTGCCAGC 660  
Qy 661 CATGCGCGGCGCAGAGATGCTCTGCAACCCGCGAGAGTGAAGTGTGTGAGAACAGCTGT 720  
Db 661 CATGCGCGGCGCAGAGATGCTCTGCAACCCGCGAGAGTGAAGTGTGTGAGAACAGCTGT 720  
Qy 721 GTGCTGTGGGCTGCTGCAACCAAAATGCGCACCAAGGCGAGCAATGAGCACTCTGTGCA 780  
Db 721 GTGCTGTGGGCTGCTGCAACCAAAATGCGCACCAAGGCGAGCAATGAGCACTCTGTGCA 780  
Qy 781 ACCAGAGGAGCTGCGAGCGCGGCGTGTGCTGCTTCCAGAGAGGCTGCTGTCCCTG 840  
Db 781 ACCAGAGGAGCTGCGAGCGCGGCGTGTGCTGCTTCCAGAGAGGCTGCTGTCCCTG 840  
Qy 841 TGTGCAACCCCTGCGCGGAGGCGAGCTTTCGATGACCCGCGAGCGGCTTTCG 900  
Db 841 TGTGCAACCCCTGCGCGGAGGCGAGCTTTCGATGACCCGCGAGCGGCTTTCG 900  
Qy 901 ACCGTATACCTGCGAGAGCTGAGGCTGAGAGCTTGTGACCGATGCTTGTGCAAG 960  
Db 901 ACCGTATACCTGCGAGAGCTGAGGCTGAGAGCTTGTGACCGATGCTTGTGCAAG 960  
Qy 961 GCTCTCTTCCAGGCGCCACAGCCACAGCTGTGTATGTGTGCAAGCGGCTTTCG 1020  
Db 961 GCTCTCTTCCAGGCGCCACAGCCACAGCTGTGTATGTGTGCAAGCGGCTTTCG 1020  
Qy 1021 GGAAGCGCTGACCAAAATGCGGAGATCTGTGCTCCAGAGAGGTCCCATGATGAG 1080  
Db 1021 GGAAGCGCTGACCAAAATGCGGAGATCTGTGCTCCAGAGAGGTCCCATGATGAG 1080  
Qy 1081 TTGGCAGCTTTCATGAGAGGAGTGTGCGCAGAGAGCTGAGAGAGCTGAGAGAGCTGACTG 1140  
Db 1081 TTGGCAGCTTTCATGAGAGGAGTGTGCGCAGAGAGCTGAGAGAGCTGAGAGAGCTGACTG 1140

Qy 1141 AAGAGATGAGCGCTGTGGGAGAGCTGTGCGGCTGCGCGCTGCTGCACTGTGAGAGAGGAGAGA 1200  
Db 1141 AAGAGATGAGCGCTGTGGGAGAGCTGTGCGGCTGCGCGCTGCTGCACTGTGAGAGAGGAGAGA 1200  
Qy 1201 TTTAGATCTGAGACCAAGCTGTGGGATGATGTGCAATGAGAAATAGCTAATTTTCCCA 1260  
Db 1201 TTTAGATCTGAGACCAAGCTGTGGGATGATGTGCAATGAGAAATAGCTAATTTTCCCA 1260  
Qy 1261 GGTGTGTGCTTTAAGGAGTGGGAGCAAGGCTTCTCCAGACTCTTCTTCCAGTAAGTT 1320  
Db 1261 GGTGTGTGCTTTAAGGAGTGGGAGCAAGGCTTCTCCAGACTCTTCTTCCAGTAAGTT 1320  
Qy 1321 TCCCTCTGAGCTTGAACAGCATGAGTGTGTGCTGCTTACATTTGTCAGCTCCCGAGCGTGTCT 1380  
Db 1321 TCCCTCTGAGCTTGAACAGCATGAGTGTGTGCTGCTTACATTTGTCAGCTCCCGAGCGTGTCT 1380  
Qy 1381 CCAAGCTTCAAGCTGTGCTGTGGGAGAGTGAAGAGAGGCTTAACTGAGAGAGAGTT 1440  
Db 1381 CCAAGCTTCAAGCTGTGCTGTGGGAGAGTGAAGAGAGGCTTAACTGAGAGAGAGTT 1440  
Qy 1441 GCCACCCCTGTCCAGATTAATGCGCTTGTGCTTACAGATTGCGACAGCGGTTGT 1500  
Db 1441 GCCACCCCTGTCCAGATTAATGCGCTTGTGCTTACAGATTGCGACAGCGGTTGT 1500  
Qy 1501 TCTACATGCTTGTATTAATTTGTTGAGGAGAGAGATGAGAAATGTTGAGACTCTCCCTC 1560  
Db 1501 TCTACATGCTTGTATTAATTTGTTGAGGAGAGAGATGAGAAATGTTGAGACTCTCCCTC 1560  
Qy 1561 TGAATGTTTGGGAGAAATGTGAGAGAGAGTCCCTGCTTCCAAACATCAACTGCGAA 1620  
Db 1561 TGAATGTTTGGGAGAAATGTGAGAGAGAGTCCCTGCTTCCAAACATCAACTGCGAA 1620  
Qy 1621 AAATGCAAAATGAATTTTCCACGCGATTCTTCCATGCGCATGAGTGTGCTT 1680  
Db 1621 AAATGCAAAATGAATTTTCCACGCGATTCTTCCATGCGCATGAGTGTGCTT 1680  
Qy 1681 CAGCTGTGAGATGAATGTTCTGTTCAACCTGATTCATGATGTTTATTCATCAGCA 1740  
Db 1681 CAGCTGTGAGATGAATGTTCTGTTCAACCTGATTCATGATGTTTATTCATCAGCA 1740  
Qy 1741 GTGTGCTCAGCTCTTACCTGTGTGCGCAGGCGAGCATTTTCATATCCAAATGATCC 1800  
Db 1741 GTGTGCTCAGCTCTTACCTGTGTGCGCAGGCGAGCATTTTCATATCCAAATGATCC 1800  
Qy 1801 TCTCTGAGCAGGCTGTGGAGAGGAGTCAATGTTCTCTGTGCTCATGAGGATCTCAG 1860  
Db 1801 TCTCTGAGCAGGCTGTGGAGAGGAGTCAATGTTCTCTGTGCTCATGAGGATCTCAG 1860  
Qy 1861 GCTCAGAGACTGCAAGCTCTTGCCTCAAGTCAACAGTATGAGAGCAGAGCAGTTTC 1920  
Db 1861 GCTCAGAGACTGCAAGCTCTTGCCTCAAGTCAACAGTATGAGAGCAGAGCAGTTTC 1920  
Qy 1921 ATCTGTGTGATCTTAAGCTCAGTCTCTCTCACTACCCCAACAGCCTTGTGCGCA 1980  
Db 1921 ATCTGTGTGATCTTAAGCTCAGTCTCTCTCACTACCCCAACAGCCTTGTGCGCA 1980  
Qy 1981 CCAAAAGTGTCCCAAAAGAGAGAGATGGAATTTTCTTGAAGCATGCACTGTGA 2040  
Db 1981 CCAAAAGTGTCCCAAAAGAGAGAGATGGAATTTTCTTGAAGCATGCACTGTGA 2040  
Qy 2041 ATTAAGTCAAAATTAATTTCTCATCTCTTAAAGTAATTAAGTGAAGAGCACT 2100  
Db 2041 ATTAAGTCAAAATTAATTTCTCATCTCTTAAAGTAATTAAGTGAAGAGCACT 2100  
Qy 2101 GTTCTCAGAGTGTGGGAGAGCGCTCTTCTAATGAGACATATGATCACTGTCCCT 2160  
Db 2101 GTTCTCAGAGTGTGGGAGAGCGCTCTTCTAATGAGACATATGATCACTGTCCCT 2160  
Qy 2161 CTTTGGCAGTTGATTAATTAATTTGAAAGGATTAATGACTGAGCGTATGAGATTAAGGTTAA 2220  
Db 2161 CTTTGGCAGTTGATTAATTAATTTGAAAGGATTAATGACTGAGCGTATGAGATTAAGGTTAA 2220

QY	2221	CCTGCAGAAACGCTACTTAAAGTAATTTGAGGCGAGATTTAAATGAAATTTGCAGAAAT	2280
Db	2221	CCTGCAGAAACGCTACTTAAAGTAATTTGAGGCGAGATTTAAATGAAATTTGCAGAAAT	2280
QY	2281	CAGTTAGCAGCACTGAGAGACAACTTATCAACCGTGGAGAAATCAAAACCGAGCAGGCG	2340
Db	2281	CAGTTAGCAGCACTGAGAGACAACTTATCAACCGTGGAGAAATCAAAACCGAGCAGGCG	2340
QY	2341	TGTGTGAAACATGGTTTAAATATGCGACTGCGAAACACTGAACTCTAGCGCACTCCAGAA	2400
Db	2341	TGTGTGAAACATGGTTTAAATATGCGACTGCGAAACACTGAACTCTAGCGCACTCCAGAA	2400
QY	2401	TGATGTTTCAAGTGTCAATGACCTGTTCGACCACTGATTCATCCAGATTCCTTAAAGT	2460
Db	2401	TGATGTTTCAAGTGTCAATGACCTGTTCGACCACTGATTCATCCAGATTCCTTAAAGT	2460
QY	2461	TAAAGTTGCACATGATTTGATTAAGCAGTCCTTCTTTGAGTTTAAATATGATTAACAT	2520
Db	2461	TAAAGTTGCACATGATTTGATTAAGCAGTCCTTCTTTGAGTTTAAATATGATTAACAT	2520
QY	2521	AAGTTGCATTTAGAAATCAAGCATTAACCTTCACTGCAAAAAAATTTTAAAAAATTTT	2580
Db	2521	AAGTTGCATTTAGAAATCAAGCATTAACCTTCACTGCAAAAAAATTTTAAAAAATTTT	2580
QY	2581	AAAAAA 2586	
Db	2581	AAAAAA 2586	
RESULT 16			
AAH45490	ID	AAH45490 standard; DNA; 2660 bp.	
AAH45490;	AC		
10-SEP-2001	DT	(first entry)	
Human reduced expression in immortalised cells DNA sequence SEQ ID 3.	XX		
REIC; reduced expression in immortalised cells; cancer; tumour;	XX		
proliferation inhibitor; viral infection; human; ds.	XX		
Homo sapiens.	OS		
Location/Qualifiers	XX		
226..1278	FT		
/*tag= a	FT		
/product= "REIC"	FT		
/note="Reduced expression in immortalised cells protein"	FT		
WO200138528-A1.	PN		
31-MAY-2001.	PD		
30-AUG-2000; 2000WO-JP05879.	PE		
19-NOV-1999; 99JP-0330604.	PR		
(HISM ) HISAMITSU PHARM CO LTD.	PA		
Namba M, Tsuji T;	PI		
WPI; 2001-367688/38.	DR		
P-PSDB; AAG62468.	DR		
Cell proliferation inhibiting protein REIC and polynucleotide encoding	XX		
it for diagnosis and therapy of cancer and as an antiviral agent -	XX		
Claim 2; Page 57-59; 66pp; Japanese.	XX		
This invention relates to a protein designated REIC (reduced expression	CC		
in immortalised cells) which inhibits proliferation. REIC shows reduced	CC		
or suppressed expression in immortalised cells such as cancer cells. The	CC		

Query Match	Best Local Similarity	Score	DB	Length
Matches 2560; Conservative	92.0%; Pred. No. 0; Mismatches 0; Indels 2; Gaps 1	2380;	DB 22;	2660;
1	CGCGCGCTCCCGAACCCCGGCGCCCGCCACCGCGCGCTCCCGCATGTGACCCCGCAGC	60		
74	CGCGCGCTCCCGAACCCCGGCGCCCGCCACCGCGCGCTCCCGCATGTGACCCCGCAGC	133		
61	CGCGCGCGCTCCCGCGCGGAGCGAGCATGCAGTCCGCGCGCGCGCAATCCGCTCA	120		
134	CGCGCGCGCTCCCGCGCGGAGCGAGCATGCAGTCCGCGCGCGCGCAATCCGCTCA	193		
121	GTCGGGGGCGCGCGCTGCGCGCGGAGAGCGAGATGCAACGGCTGGGGCGACCCGCTGT	180		
194	GTCGGGGGCGCGCGCTGCGCGCGGAGAGCGAGATGCAACGGCTGGGGCGACCCGCTGT	253		
181	GCGTCTCTGTGGCGCGCGCGGTCCCGACGCGCCCGCGCGCTTCGACGCGGACCTCGG	240		
254	GCGTCTCTGTGGCGCGCGCGGTCCCGACGCGCCCGCGCGCTTCGACGCGGACCTCGG	313		
241	CTCCAGTCAAGCCCGCGCGCGCTCTCAAGCTACCCGACAGAGAGGCCACCCCTCATAGGA	300		
314	CTCCAGTCAAGCCCGCGCGCGCTCTCAAGCTACCCGACAGAGAGGCCACCCCTCATAGGA	373		
301	TGTTCCGCGAGGTTGAGGAATCGATGAGAGGACGACGACACCAATTTGGCAGCGCGTGG	360		
374	TGTTCCGCGAGGTTGAGGAATCGATGAGAGGACGACGACACCAATTTGGCAGCGGTTGG	433		
361	AAAGATGAGGCGAGAGAAAGTGTCTGTAAAGCATCATCAGAAATGAACCTGGCAACT	420		
434	AAAGATGAGGCGAGAGAAAGTGTCTGTAAAGCATCATCAGAAATGAACCTGGCAACT	493		
421	TACCTCCAGCATATCAATGATGACCAACACAGACAGAGAGGTTGAAATATATACATCC	480		
494	TACCTCCAGCATATCAATGATGACCAACACAGACAGAGAGGTTGAAATATATACATCC	553		
481	ATGTGACCGAGAAATTCACAGATATACCAACACAGACTGGAATAATGTCTTTTCAG	540		
554	ATGTGACCGAGAAATTCACAGATATACCAACACAGACTGGAATAATGTCTTTTCAG	613		
541	AACAGTTATCAATCTGTGGGAGCGAAGAGGAGGACAGGACAGATGATCATGCG	600		
614	AACAGTTATCAATCTGTGGGAGCGAAGAGGAGGACAGGACAGATGATCATGCG	673		
601	ACGAGGACTGTGGGCGCAGCATGTACTGTCCAGTTTCCAGCTTCAGTACACTGCGACG	660		
674	ACGAGGACTGTGGGCGCAGCATGTACTGTCCAGTTTCCAGCTTCAGTACACTGCGACG	733		
661	CATGCCGGGGCGAGAGATGTCTTGACACCCGGGACAGTAGTGCTGTGGAGACACACTGT	720		
734	CATGCCGGGGCGAGAGATGTCTTGACACCCGGGACAGTAGTGCTGTGGAGACACACTGT	793		
721	GATGCTGGGGGTCACTGACCAATAATGGCACACAGGGGCGAGCATGGGACCATCTGTGAC	780		
794	GATGCTGGGGGTCACTGACCAATAATGGCACACAGGGGCGAGCATGGGACCATCTGTGAC	853		
781	ACCAAGGGAATGCGACCGCGGGCTGTGCTGTGCTTCAGAGAGGCTCTGTTCCTCG	840		
854	ACCAAGGGAATGCGACCGCGGGCTGTGCTGTGCTTCAGAGAGGCTCTGTTCCTCG	913		
841	TGTGACACCCCTGCGCGCGAGGCGAGCTTTGCAATACCCCGCACCGCGCTTCTGG	900		
914	TGTGACACCCCTGCGCGCGAGGCGAGCTTTGCAATACCCCGCACCGCGCTTCTGG	973		
901	ACCTCATCACTGGAGGATGAGCTTGTAGAGCCTTGGACCGATGCCCTGTGTGCAATG	960		

Db 974 ACCCTATCAGCTGGAGCTAGAGCTGTATGGAGCTTGGACCGATGCGCTTGTGCCAGTG 1033  
 Qy 961 GCTCTCTCTGACAGCCCAACAGCCAGCTGTGTATGTGTGCAAGCCAGCTTGTGG 1020  
 Db 1034 GCTCTCTCTGACAGCCCAACAGCCAGCTGTGTATGTGTGCAAGCCAGCTTGTGG 1093  
 Qy 1021 GGAGCCCGGACCAAGATGGGAGATCCGTGCTGCCAGAGAGGTGCCGATGAGATGAG 1080  
 Db 1094 GGAAGCCCGACCAAGATGGGAGATCCGTGCTGCCAGAGAGGTGCCGATGAGATGAG 1153  
 Qy 1081 TTGGACGCTTATGAGAGAGGTGTGCGCCAGAGCTGAGAGAGCTGGAGAGAGAGAGAG 1140  
 Db 1154 TTGGACGCTTATGAGAGAGGTGTGCGCGCCAGAGCTGAGAGAGCTGGAGAGAGAGAG 1213  
 Qy 1141 AAGAGATGGCGCTGGGAGAGCTGTGCGCGCCAGAGCTGAGAGAGAGAGAGAGAGAG 1200  
 Db 1214 AAGAGATGGCGCTGGGAGAGCTGTGCGCGCCAGAGCTGAGAGAGAGAGAGAGAGAG 1273  
 Qy 1201 TTATGATCTGAGACAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCA 1260  
 Db 1274 TTATGATCTGAGACAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCA 1333  
 Qy 1261 GGTGTGTCTTATGAGCGGTGGAGCTGACCCAGAGCTTCTTCTTCAATCTTCTTCCAGTAGT 1320  
 Db 1334 GGTGTGTCTTATGAGCGGTGGAGCTGACCCAGAGCTTCTTCTTCAATCTTCTTCCAGTAGT 1393  
 Qy 1321 TCCCTCTGAGCTTACAGCATGAGGTGTGTGCAATTTGTTCAGCTTCCCGAGAGCTGTCT 1380  
 Db 1394 TCCCTCTGAGCTTACAGCATGAGGTGTGTGCAATTTGTTCAGCTTCCCGAGAGCTGTCT 1453  
 Qy 1381 CAGGCTTCAAGCTGTGTGTCTTGGAGAGTCAAGCAGAGGTTAAACTGTGCAAGAGAGCTTT 1440  
 Db 1454 CAGGCTTCAAGCTGTGTGTCTTGGAGAGTCAAGCAGAGGTTAAACTGTGCAAGAGAGCTTT 1513  
 Qy 1441 GCAACCCCTGTCAGATTTATGAGCTGTGCTTGCCTTCAAGCTGAGAGAGAGAGAGCTTTGT 1500  
 Db 1514 GCAACCCCTGTCAGATTTATGAGCTGTGCTTGCCTTCAAGCTGAGAGAGAGAGAGCTTTGT 1573  
 Qy 1501 TCTACATGCTTTGTAATTTGTTAGAGGAGAGAGATGGAATGATGAGTCTCCTC 1560  
 Db 1574 TCTACATGCTTTGTAATTTGTTAGAGGAGAGAGATGGAATGATGAGTCTCCTC 1633  
 Qy 1561 TGATTTGTTTGGGAAATGTGAGAGAGAGTCCCTGTTTGGCAAACTCAAGCTGGCAA 1620  
 Db 1634 TGATTTGTTTGGGAAATGTGAGAGAGAGTCCCTGTTTGGCAAACTCAAGCTGGCAA 1693  
 Qy 1621 AAATGCAACAATGAAATTTTCCAGCAGTCTTTCATGAGGCATAGTAAGCTGTGCTT 1680  
 Db 1694 AAATGCAACAATGAAATTTTCCAGCAGTCTTTCATGAGGCATAGTAAGCTGTGCTT 1753  
 Qy 1681 CAGCTGTGGAGAGAAATGTTCTGTGTCAACCTGATTAACATGTGTTATTAATCCAGCA 1740  
 Db 1754 CAGCTGTGGAGAGAAATGTTCTGTGTCAACCTGATTAACATGTGTTATTAATCCAGCA 1813  
 Qy 1741 GTGTGCTCAGCTCCTACCTCTGTGTCAGAGGAGAGATTTTCAATCCAAAGTCAATCCC 1800  
 Db 1814 GTGTGCTCAGCTCCTACCTCTGTGTCAGAGGAGAGATTTTCAATCCAAAGTCAATCCC 1873  
 Qy 1801 TCTCTCAGACAGCTGGGAGAGGGGTCAATGTTCTCTGCTCCATCAGGATCTCAGAG 1860  
 Db 1874 TCTCTCAGACAGCTGGGAGAGGGGTCAATGTTCTCTGCTCCATCAGGATCTCAGAG 1933  
 Qy 1861 GCTCAGAGACTGCAAGCTGCTTGGCCCAAGTCAACAGCTAATGAAACCAAGAGAGTTTC 1920  
 Db 1934 GCTCAGAGACTGCAAGCTGCTTGGCCCAAGTCAACAGCTAATGAAACCAAGAGAGTTTC 1993  
 Qy 1921 ATCTGTTGTGACTTAAAGCTGAGTCTCTCCACTAATCCCAACACAGAGCTTGTGCCA 1980  
 Db 1994 ATCTGTTGTGACTTAAAGCTGAGTCTCTCCACTAATCCCAACACAGAGCTTGTGCCA 2053  
 Qy 1981 CCAAAAGTCTCCCAAAAGAGAGAGATGAGATTTTTC--TTGAGGATGACATCTG 2038

Db 2054 CCAAAAGTCTCCCAAAAGAGAGAGATGAGATTTTCTTTGAGGATGACATCTG 2113  
 Qy 2039 GAATTAAGTCAAACTAATTTCTCAATCCCTTAAAGTAACTCTTTAGAGACAGA 2098  
 Db 2114 GAATTAAGTCAAACTAATTTCTCAATCCCTTAAAGTAACTCTTTAGAGACAGA 2173  
 Qy 2099 GTGTTCTCAGTGTGGGAGAGCCGCTCTCTAATGAAGACATGATATGACACTGTC 2158  
 Db 2174 GTGTTCTCAGTGTGGGAGAGCCGCTCTCTAATGAAGACATGATATGACACTGTC 2233  
 Qy 2159 CTCTTTGGAGTGTGATTAATGATCTTTGAAAGTATAGTCTGAGAGGATTAAGATT 2218  
 Db 2234 CTCTTTGGAGTGTGATTAATGATCTTTGAAAGTATAGTCTGAGAGGATTAAGATT 2293  
 Qy 2219 AACCTGCAAGAACATGATCTTAAGTATGTTAGGAGAGAGATTAATGAATTTGCAA 2278  
 Db 2294 AACCTGCAAGAACATGATCTTAAGTATGTTAGGAGAGAGATTAATGAATTTGCAA 2353  
 Qy 2279 ATCACTTACAGCAAGTGAAGCAATTTATCAACAGTGGAGAAATCAACCGAGCAG 2338  
 Db 2354 ATCACTTACAGCAAGTGAAGCAATTTATCAACAGTGGAGAAATCAACCGAGCAG 2413  
 Qy 2339 GCTGTGTGAAGAGTGTGATATATGCGAGCTGCAACCTGAACCTTACGCCACTCCA 2398  
 Db 2414 GCTGTGTGAAGAGTGTGATATATGCGAGCTGCAACCTGAACCTTACGCCACTCCA 2473  
 Qy 2399 AATGATGTTTTCAGGTGTGATGAGTGTGTCACCATGATTAATCAAGAGTCTTAAAG 2458  
 Db 2474 AATGATGTTTTCAGGTGTGATGAGTGTGTCACCATGATTAATCAAGAGTCTTAAAG 2533  
 Qy 2459 TTAAAGTGCACAGATGTTGTTAAGCATGCTTCTTGAAGTTTAAATTAATGATTAAC 2518  
 Db 2534 TTAAAGTGCACAGATGTTGTTAAGCATGCTTCTTGAAGTTTAAATTAATGATTAAC 2593  
 Qy 2519 ATGAGTGCATTTAGAAATCAAGCATTAATCACTTCAACTGC 2560  
 Db 2594 ATGAGTGCATTTAGAAATCAAGCATTAATCACTTCAACTGC 2635

RESULT 17  
 AB281805  
 ID AB281805 standard; DNA; 2450 BP.  
 XX  
 AC AB281805;  
 XX  
 DT 11-JUN-2003 (first entry)  
 XX  
 DE Human dickkopf2 nucleic acid sequence.  
 XX  
 KW Human; dickkopf2; stem cell; stem-loop RNA; anti-naemic;  
 KW cerebroprotective; neuroprotective; nootropic; antiparkinsonian;  
 KW cardiant; hepatotropic; antidiabetic; vulnerary; gene therapy;  
 KW gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO2003012082-A2.  
 XX  
 PD 13-FEB-2003.  
 XX  
 PF 25-JUL-2002; 2002MO-GB03409.  
 XX  
 PR 26-JUL-2001; 2001GB-0018223.  
 XX  
 PA (AXOR-) AXORDIA LTD.  
 PI Andrews P, Walsh J, Gokhale P;  
 XX  
 DR WPI; 2003-278398/27.  
 XX  
 PT Modulating the differentiation state of a stem cell, useful for  
 PT treating e.g. pernicious anemia, stroke, cirrhosis, diabetes or a  
 PT neurodegenerative disease, comprises contacting a stem cell with a stem

PT loop RNA -  
XX  
PS Claim 7; Fig 15; 85bp; English.  
XX  
CC The present sequence is the nucleic acid sequence of human  
CC dikekopf2. The invention relates to a method of modulating the  
CC differentiation state of a stem cell, such as an embryonic stem  
CC cell, embryonic germ cell, embryonal carcinoma cell, hematopoietic  
CC stem cell, muscle stem cell, nerve stem cell, skin dermal sheath  
CC stem cell, liver stem cell or teratocarcinoma cell. The method  
CC involves contacting the stem cell with a stem-loop RNA molecule or  
CC a nucleic acid molecule or vector encoding the stem-loop RNA, where  
CC the nucleic acid is preferably derived from one of the nucleic acid  
CC sequences in AB281794-844, including the present sequence, and may  
CC encode a cell surface receptor expressed by a stem cell, or a ligand.  
CC The RNA molecule, the nucleic acid molecule or the vector is useful  
CC for promoting the differentiation of stem cells and for providing  
CC differentiated cells/tissues for the treatment of diseases in which  
CC cell/tissues are destroyed by the disease. These diseases include  
CC pernicious anaemia, stroke, neurodegenerative diseases such as  
CC Parkinson's disease and Alzheimer's disease, coronary heart disease,  
CC cirrhosis, diabetes, or nerve damage as a consequence of trauma  
CC (e.g. replacement of spinal cord tissue) (claimed).  
XX

Sequence 2450 BP; 595 A; 622 C; 664 G; 569 T; 0 other;

Query Match 87.28; Score 2255; DB 25; Length 2450;  
Best Local Similarity 99.98; Pred. No. 0;  
Matches 2435; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 126 GGGCGCGCTGCGCGCGCGAGCGAGATGCGCGCTTGCGGCGACCTGCTGCTG 185  
Db 8 GCGCGCGCGCTGCGCGCGCGAGCGAGATGCGCGCTTGCGGCGACCTGCTGCTG 67  
QY 186 CTGCTGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 245  
Db 68 CTGCTGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 127  
QY 246 GTCAAGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 305  
Db 128 GTCAAGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 187  
QY 306 CGCGAGGTGAGAACTGATGAGAGAGACCGAGACAAATTGCGAGCGCGGTGAGAG 365  
Db 188 CGCGAGGTGAGAACTGATGAGAGAGACCGAGACAAATTGCGAGCGCGGTGAGAG 247  
QY 366 ATGAGAGCGAGAGAGCGCTGCTAAGCATCAAGAGTGAACCTGCGAACTTAACCT 425  
Db 248 ATGAGAGCGAGAGAGCGCTGCTAAGCATCAAGAGTGAACCTGCGAACTTAACCT 307  
QY 426 CCCAGCTATCAATGAGACCAAGACAGACAGAAAGTTGAAATATATACCATCATGTG 485  
Db 308 CCCAGCTATCAATGAGACCAAGACAGACAGAAAGTTGAAATATATACCATCATGTG 367  
QY 486 CACCGAATAATTCACAGATTAACCAACACAGACTGGAATGCTTTTANAGACA 545  
Db 368 CACCGAATAATTCACAGATTAACCAACACAGACTGGAATGCTTTTANAGACA 427  
QY 546 GTTATCATCTGTGGAG 605  
Db 428 GTTATCATCTGTGGAG 487  
QY 606 GACTGTGGCGCCAGCATGTACTGCGAGTTGGCCAGCTTCCAGTACACTCCGACGCCATGC 665  
Db 488 GACTGTGGCGCCAGCATGTACTGCGAGTTGGCCAGCTTCCAGTACACTCCGACGCCATGC 547  
QY 666 CGGGAGCCAGAGAGTCTGTGACCGCGGAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 725  
Db 548 CGGGAGCCAGAGAGTCTGTGACCGCGGAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 607  
QY 726 TGGGATCTGCAACCAAAATGCGACAGGGGCGAGCATGGGACCATCTGTGACCAACGAG 785  
Db 608 TGGGATCTGCAACCAAAATGCGACAGGGGCGAGCATGGGACCATCTGTGACCAACGAG 667

QY 786 AGGAGCTGCAAGCCCGGCGCTGCTGCTGCTTCCAGAGAGGCGTGTGTGTGTGTGTGTGC 845  
Db 668 AGGAGCTGCAAGCCCGGCGCTGCTGCTGCTTCCAGAGAGGCGTGTGTGTGTGTGTGTGC 727  
QY 846 ACAACCTTGGCCCGTGGAGAGGCGAGAGTTTGGCATGACCCCGCAGCCGCTTCTGAGACTTC 905  
Db 728 ACAACCTTGGCCCGTGGAGAGGCGAGAGTTTGGCATGACCCCGCAGCCGCTTCTGAGACTTC 787  
QY 906 ATCACTTGGAGAGCTGATGAGAGCTTGGACCGAGTCCCTTGGCCAGTGGACTTC 965  
Db 788 ATCACTTGGAGAGCTGATGAGAGCTTGGACCGAGTCCCTTGGCCAGTGGACTTC 847  
QY 966 CTCTGCGAGCCCGCAGCGACAGCCCTGTGTATGTGTGCAACCGACCTTGTGGGAGAC 1025  
Db 848 CTCTGCGAGCCCGCAGCGACAGCCCTGTGTATGTGTGCAACCGACCTTGTGGGAGAC 907  
QY 1026 CGTGAACCAAGATGGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1085  
Db 908 CGTGAACCAAGATGGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 967  
QY 1086 AGCTTCATGAGAGAGTGTGCGCAGAGAGCTGAGAGACCTGAGAGAGAGCTGAGAGAG 1145  
Db 968 AGCTTCATGAGAGAGTGTGCGCAGAGAGCTGAGAGACCTGAGAGAGAGCTGAGAGAGAG 1027  
QY 1146 ATGCGCTGCGGGGAGACCTGCGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1205  
Db 1028 ATGCGCTGCGGGGAGACCTGCGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1087  
QY 1206 ATCTGGAACAGGCTGTGGGTATGTGTGATGTGCAATAGAAATAGTAATTTATTTCCAGAGTGT 1265  
Db 1088 ATCTGGAACAGGCTGTGGGTATGTGTGATGTGCAATAGAAATAGTAATTTATTTCCAGAGTGT 1147  
QY 1266 GTGCTTTAGGCGTGGGCTGACCAAGCTTCTTCTCATCTTCTTCTCCAGTAAATTTCCCC 1325  
Db 1148 GTGCTTTAGGCGTGGGCTGACCAAGCTTCTTCTCATCTTCTTCTCCAGTAAATTTCCCC 1207  
QY 1326 TCTGCTTGAACAGATGAGTGTGTGTGATTTGTTAGCTCCCGCAGGCTGTTCTCCAGG 1385  
Db 1208 TCTGCTTGAACAGATGAGTGTGTGTGATTTGTTAGCTCCCGCAGGCTGTTCTCCAGG 1267  
QY 1386 CTTCAAGCTGTGTGCTTGGAGAGTGAAGAGGAGGTTAACTGCAAGAGCAGTTTGCAC 1445  
Db 1268 CTTCAAGCTGTGTGCTTGGAGAGTGAAGAGGAGGTTAACTGCAAGAGCAGTTTGCAC 1327  
QY 1446 CCTGTGCAAGATTAATGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 1505  
Db 1328 CCTGTGCAAGATTAATGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 1387  
QY 1506 ATGCTTTGATTAATTTGTTGAGGAGAGAGATGAGAAATATGTGAGTCTTCTGTGATT 1565  
Db 1388 ATGCTTTGATTAATTTGTTGAGGAGAGAGATGAGAAATATGTGAGTCTTCTGTGATT 1447  
QY 1566 GGTTTTGGGAGAAATGTGAGAGAGTGTGCTGCTTGGCAATCAACCTGCGAAAAATG 1625  
Db 1448 GGTTTTGGGAGAAATGTGAGAGAGTGTGCTGCTTGGCAATCAACCTGCGAAAAATG 1507  
QY 1626 CAACCAATGAATTTTCCAGAGATTTTCCATGAGGCAATGATGATGATGATGATGATGATGAT 1685  
Db 1508 CAACCAATGAATTTTCCAGAGATTTTCCATGAGGCAATGATGATGATGATGATGATGATGAT 1567  
QY 1686 GTTGAAGATGAATTTTCTGTTCAACCTTGCATTAAGTGTGTTATTCATCCAGAGAGTGT 1745  
Db 1568 GTTGAAGATGAATTTTCTGTTCAACCTTGCATTAAGTGTGTTATTCATCCAGAGAGTGT 1627  
QY 1746 GCTGAGCTTCACTCTGTGCGAGGCGAGATTTTCAATATCAAGATCAATATTCCTCTCTCT 1805  
Db 1628 GCTGAGCTTCACTCTGTGCGAGGCGAGATTTTCAATATCAAGATCAATATTCCTCTCTCT 1687  
QY 1806 CAGCAACCTTGGGAGAGGAGGATGTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1865  
Db 1688 CAGCAACCTTGGGAGAGGAGGATGTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1747



QY 1866 GAGAGTCAAGCTGTTGCCAAGTCAACAGCTAGTGAAGACAGAGAGTTTCATCTG 1925  
 DB 1748 GAGAGTCAAGCTGTTGCCAAGTCAACAGCTAGTGAAGACAGAGAGTTTCATCTG 1807  
 QY 1926 GTTGTGACTTAAAGCTGAGTCTCTCTCCACTACCCCAACAGCCTTGTGTCCACCAA 1985  
 DB 1808 GTTGTGACTTAAAGCTGAGTCTCTCTCCACTACCCCAACAGCCTTGTGTCCACCAA 1867  
 QY 1986 AGTGTCTCCCAAGAGAGAGATGGGATTTTC--TTGAGGACATGACATCTGGAAT 2043  
 DB 1868 AGTGTCTCCCAAGAGAGAGATGGGATTTTC--TTGAGGACATGACATCTGGAAT 1927  
 QY 2044 AAGTCAAACTAATTTCTACATCCCTCTAAAGTAACTACTGTAGGAAACAGAGTGT 2103  
 DB 1928 AAGTCAAACTAATTTCTACATCCCTCTAAAGTAACTACTGTAGGAAACAGAGTGT 1987  
 QY 2104 CTGCAAGTGGGGGACCCGCTCTCTTAAGAGACAAATATTTGACCTGCTCCCTT 2163  
 DB 1988 CTGCAAGTGGGGGACCCGCTCTCTTAAGAGACAAATATTTGACCTGCTCCCTT 2047  
 QY 2164 TGGCAGTTGATTAAGTCTTGAAGATATGACTGAGCGTATACAGGTTAACT 2223  
 DB 2048 TGGCAGTTGATTAAGTCTTGAAGATATGACTGAGCGTATACAGGTTAACT 2107  
 QY 2224 GCAGAAACAGTACTAGTAAATTTAGGGGAGAGATTAATAAGTAAATTTGCAAAATCAC 2283  
 DB 2108 GCAGAAACAGTACTAGTAAATTTAGGGGAGAGATTAATAAGTAAATTTGCAAAATCAC 2167  
 QY 2284 TTACAGCAACTGAGAACAAATTAATCAACACAGTGAAGAAATCAACCGAGAGGCTGT 2343  
 DB 2168 TTACAGCAACTGAGAACAAATTAATCAACACAGTGAAGAAATCAACCGAGAGGCTGT 2227  
 QY 2344 GTGAAACATGTTTAATATGCGACTGCGAACACTGAATCTTACGCCACTCCCAAAATGA 2403  
 DB 2228 GTGAAACATGTTTAATATGCGACTGCGAACACTGAATCTTACGCCACTCCCAAAATGA 2287  
 QY 2404 TGTTCAGGTCATGAGACTGTTGCCACCATGATTCATCCAGTCTTAAGTTAA 2463  
 DB 2288 TGTTCAGGTCATGAGACTGTTGCCACCATGATTCATCCAGTCTTAAGTTAA 2347  
 QY 2464 AGTTCACATGATTTGATTAAGCATGCTTTCTTTGAGTTTAAATTAATTAATTAAG 2523  
 DB 2348 AGTTCACATGATTTGATTAAGCATGCTTTCTTTGAGTTTAAATTAATTAATTAAG 2407  
 QY 2524 TTGCAATTAGAAATCAAGCATTAATCACTCAACTGC 2560  
 DB 2408 TTGCAATTAGAAATCAAGCATTAATCACTCAACTGC 2444  
 RESULT 18  
 AAD52535  
 ID AAD52535 standard; DNA; 2450 BP.  
 AC AAD52535;  
 XX 02-MAY-2003 (first entry)  
 DT Human dickopf3 DNA.  
 DE Human dickopf3; de.  
 XX Human; drug screening; toxicology assay; signalling pathway; gene;  
 KM dickopf3; de.  
 XX Homo sapiens.  
 OS WO200209992-A2.  
 PN 14-NOV-2002.  
 PD 29-APR-2002; 2002WO-GB01946.  
 PF 04-MAY-2001; 2001GB-0011004.  
 XX (AXOR-) AXORDIA LTD.  
 PA

XX Andrews P, Draper J, Walsh J;  
 PI WPI; 2003-120579/11.  
 DR  
 XX  
 PT Identifying biologically active agents comprises cloning transfected  
 PT cells into a cell array, exposing the array to an agent to be tested,  
 PT and detecting signals generated by a reporter molecule as a result of  
 PT exposure to the agent  
 PR  
 XX  
 PS Claim 19; Fig 22; 90pp; English.

CC The present invention relates to a novel screening method which enables  
 CC the identification of biologically active agents which mediate their  
 CC effect through the activation of genes. The method involves providing a  
 CC population of cells stably transfected with a nucleic acid encoding a  
 CC reporter molecule, cloning the transfected cells into a cell array,  
 CC exposing the array to at least one agent to be tested and detecting a  
 CC signal generated by the reporter molecule as a result of exposure to  
 CC the agent. The method is useful in identifying biologically active agents  
 CC and the genes through which the agents act, in screening potential drugs  
 CC for their ability to activate certain drug targets in a high-throughput  
 CC assay, in identifying relationships between signalling pathways and  
 CC specific signals that could be useful in eventually directing the  
 CC differentiation of embryonic stem cells and in toxicology assays by  
 CC testing for unwanted activation or inhibition of specific signalling  
 CC pathways. The present sequence is human dickopf3 DNA used to illustrate  
 CC the method of the invention.  
 CC  
 XX  
 SQ Sequence 2450 BP; 595 A; 622 C; 664 G; 569 T; 0 other;

Query Match 87.2%; Score 2255; DB 25; Length 2450;  
 Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 2; Gaps 1;  
 Matches 2435; Conservative 0;

QY 126 GAGCGCGGCTGCGGCGGAGAGCGGAGTGAAGCGGCTTGAGGCGCCACCTGTGCTG 185  
 DB 8 GAGCGCGGCTGCGGCGGAGAGCGGAGTGAAGCGGCTTGAGGCGCCACCTGTGCTG 67  
 QY 186 CTGCTGGGGGGGGGGTCCCAAGCGGCGCGCGCTCCGAGGGGAGCCCGGCTCA 245  
 DB 68 CTGCTGGGGGGGGGGTCCCAAGCGGCGCGCTCCGAGGGGAGCCCGGCTCA 127  
 QY 246 GTCAAGCCCGGCGCGCTCTCAGTACCAGAGAGAGCGCACCTCAATGATGATTC 305  
 DB 128 GTCAAGCCCGGCGCGCTCTCAGTACCAGAGAGAGCGCACCTCAATGATGATTC 187  
 QY 306 CCGGAGCTTGAAGAACTGATGAGAGACAGCGACCAATTCGAGGCGGTGGAAG 365  
 DB 188 CCGGAGCTTGAAGAACTGATGAGAGACAGCGACCAATTCGAGGCGGTGGAAG 247  
 QY 366 ATGAGAGCGAAGAGCTGCTCTAAACATCATGAGAGTGAACCTGGCAACTTACT 425  
 DB 248 ATGAGAGCGAAGAGCTGCTCTAAACATCATGAGAGTGAACCTGGCAACTTACT 307  
 QY 426 CCGAGCTATCAATGAGACCAACAGACAGAGAGTTGAGAAATTAATTCATCATG 485  
 DB 308 CCGAGCTATCAATGAGACCAACAGACAGAGAGTTGAGAAATTAATTCATCATG 367  
 QY 486 CACCGAATATCAAGATTAACAACAACAGACTGGAACAATGGTCTTTCAAGAGA 545  
 DB 368 CACCGAATATCAAGATTAACAACAACAGACTGGAACAATGGTCTTTCAAGAGA 427  
 QY 546 GTTATCAATCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 605  
 DB 428 GTTATCAATCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487  
 QY 606 GACTGTGGGCCAGAGATGACTGACAGTTTGGCAGCTTCAATACCTGCCAGCATGC 665  
 DB 488 GACTGTGGGCCAGAGATGACTGACAGTTTGGCAGCTTCAATACCTGCCAGCATGC 547  
 QY 666 CCGGCGCAGAGAGATGCTGACCCGGGACAGTGAAGTGTGTGAGAGACAGTGTGTGC 725

Db 548 CGGGGCGAGAGATGCTGTGCAACCCGGGACAGTGAAGTGTGTGAGACCAAGCTGTGTGTC 607  
 Qy 726 TGGGCTACTGTCACCAAAATGCGCACTAGGGGGCAGCAATGGAGCACTGTGTGAACCAAG 785  
 Db 608 TGGGCTACTGTCACCAAAATGCGCACTAGGGGGCAGCAATGGAGCACTGTGTGAACCAAG 667  
 Qy 786 AGGAGCTGCCAGCGGGGCTGTGTGTGCTTCCAGAGAGGCTGTGTGTGCTGTGTGTGTC 845  
 Db 668 AGGAGCTGCCAGCGGGGCTGTGTGTGCTTCCAGAGAGGCTGTGTGTGCTGTGTGTGTC 727  
 Qy 846 ACACCCCTGCTGCTGTGAGGGGAGCTTGCATGATACCCCGCAGCGGCTTCTGAGCTTC 905  
 Db 728 ACACCCCTGCTGCTGTGAGGGGAGCTTGCATGATACCCCGCAGCGGCTTCTGAGCTTC 787  
 Qy 906 ATCACTGTGGAGCTAGAGGCTGTGATGAGAGCTTGGACCGATGCTGTGTGCTGTGTGCTTC 965  
 Db 788 ATCACTGTGGAGCTAGAGGCTGTGATGAGAGCTTGGACCGATGCTGTGTGCTGTGTGCTTC 847  
 Qy 966 CTCTGCCAGGCCCAACAGCCACAGCTGTGTGTATGTGTGCAAGCCGACCTTCTGTGGGAGC 1025  
 Db 848 CTCTGCCAGGCCCAACAGCCACAGCTGTGTGTATGTGTGCAAGCCGACCTTCTGTGGGAGC 907  
 Qy 1026 CGTGAACCAAGATGGGGAGATCCGTGTGCTGCCAGAGAGGTCGCCGATGATATGAAGTTGGC 1085  
 Db 908 CGTGAACCAAGATGGGGAGATCCGTGTGCTGCCAGAGAGGTCGCCGATGATATGAAGTTGGC 967  
 Qy 1086 AGCTTCAATGAGAGAGTGTGCGCCAGAGAGCTGAGAGAGCTGTGAGAGAGAGCTGTGAAGAG 1145  
 Db 968 AGCTTCAATGAGAGAGTGTGCGCCAGAGAGCTGAGAGAGCTGTGAAGAGAGCTGTGAAGAG 1027  
 Qy 1146 ATGGCCCTGTGGGGGAGGCTGTGCGGCTGTGCGGCTGTGCACTGTGTGAGAGAGAGAGATTAG 1205  
 Db 1028 ATGGCCCTGTGGGGGAGGCTGTGCGGCTGTGCGGCTGTGCACTGTGTGAGAGAGAGATTAG 1087  
 Qy 1206 ATCTGACCAAGAGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTTCCCAAGGTGT 1265  
 Db 1088 ATCTGACCAAGAGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTTCCCAAGGTGT 1147  
 Qy 1266 GTGCTTTTAGGGGTGGGCTGTGACCAAGGCTTCTTCTCACTTCTTCCAGATAGTTTCCC 1325  
 Db 1148 GTGCTTTTAGGGGTGGGCTGTGACCAAGGCTTCTTCTCACTTCTTCCAGATAGTTTCCC 1207  
 Qy 1326 TCTGAGCTTGAAGAGATGAGTGTGTGTGCAATTTTCACTTCTTCCAGAGGCTTCTCCAGG 1385  
 Db 1208 TCTGAGCTTGAAGAGATGAGTGTGTGTGCAATTTTCACTTCTTCCAGAGGCTTCTCCAGG 1267  
 Qy 1386 CTTCACAGCTGTGTGTGTGAGAGTCAAGGAGGTTAACTGTGAGAGAGAGATTGTCCAC 1445  
 Db 1268 CTTCACAGCTGTGTGTGTGAGAGTCAAGGAGGTTAACTGTGAGAGAGAGATTGTCCAC 1327  
 Qy 1446 CCTGTCCAGATTTATGTGCTGCTTGTGCTTACCAAGTTGGCAGACCGGTTGTGTAC 1505  
 Db 1328 CCTGTCCAGATTTATGTGCTGCTTGTGCTTCTTACCAAGTTGGCAGACCGGTTGTGTAC 1387  
 Qy 1506 ATGCTTTGATTAATTTTGTGAGGGGAGAGATGAAAAATGTGAGTCTTCCCTGTGATT 1565  
 Db 1388 ATGCTTTGATTAATTTTGTGAGGGGAGAGATGAAAAATGTGAGTCTTCCCTGTGATT 1447  
 Qy 1566 GCTTTTGGGGGAAATGTGAGAAAGTGTGCTTGTGCAAAATCAACTGTGGCAAAAATG 1625  
 Db 1448 GCTTTTGGGGGAAATGTGAGAAAGTGTGCTTGTGCAAAATCAACTGTGGCAAAAATG 1507  
 Qy 1626 CAACAAATGAATTTTCAACGCAAGTTCTTTCATGGGCAATAGTAAAGTGTGCTTCACT 1685  
 Db 1508 CAACAAATGAATTTTCAACGCAAGTTCTTTCATGGGCAATAGTAAAGTGTGCTTCACT 1567  
 Qy 1686 GTTGAGATGAATTTCTGTTCACCCGTCACTCAATGTGTGTTTATCATCAGAGAGTGT 1745  
 Db 1568 GTTGAGATGAATTTCTGTTCACCCGTCACTCAATGTGTGTTTATCATCAGAGAGTGT 1627  
 Qy 1746 GCTCAGCTCTTACCTGTGTGCGCAGGCGAGCAATTTCAATCAAGATCAATTTCCCTCTCT 1805  
 Db 1628 GCTCAGCTCTTACCTGTGTGCGCAGGCGAGCAATTTCAATCAAGATCAATTTCCCTCTCT 1687

Qy 1806 CAGCAGACCTTGGGAGAGGGGTCAATGTTCTTCCCTGCTCATCAGAGATCTCAGAGGCTCA 1865  
 Db 1688 CAGCAGACCTTGGGAGAGGGGTCAATGTTCTTCCCTGCTCATCAGAGATCTCAGAGGCTCA 1747  
 Qy 1866 GAGACTGCAAGCTGCTTGGCCCAAGTCAACAGCTAGTGAAGACCAAGAGCAATTCATCTG 1925  
 Db 1748 GAGACTGCAAGCTGCTTGGCCCAAGTCAACAGCTAGTGAAGACCAAGAGCAATTCATCTG 1807  
 Qy 1926 GTTGAGATCTTAAGTCAAGTGTCTCTTCCACTATCCCAACACACCTTGTGGCCACAAA 1985  
 Db 1808 GTTGAGATCTTAAGTCAAGTGTCTCTTCCACTATCCCAACACACCTTGTGGCCACAAA 1867  
 Qy 1986 AGTGTCTCCCAAAAGGAAGGAATGGGATTTTTC--TTGAGGAGATGACATCTGAATT 2043  
 Db 1868 AGTGTCTCCCAAAAGGAAGGAATGGGATTTTTC--TTGAGGAGATGACATCTGAATT 1927  
 Qy 2044 AAGGTCAAACTAATTTCTCACTCCCTCTTAAAGTAACTACTGTATGAGAACAGAGAGTGT 2103  
 Db 1928 AAGGTCAAACTAATTTCTCACTCCCTCTTAAAGTAACTACTGTATGAGAACAGAGAGTGT 1987  
 Qy 2104 CTCAAGTGTGGGCGAGCGGTCTCTTATGAGAACATGATATTTGACACTGTCCCTCT 2163  
 Db 1988 CTCAAGTGTGGGCGAGCGGTCTCTTATGAGAACATGATATTTGACACTGTCCCTCT 2047  
 Qy 2164 TGGCACTTGCAATTAATCTTTGAAAGGTATATGACTGAGGCTATGACATGAGTTAACT 2223  
 Db 2048 TGGCACTTGCAATTAATCTTTGAAAGGTATATGACTGAGGCTATGACATGAGTTAACT 2107  
 Qy 2224 GCAGAAACAGTACTTAGGTAAATTTAGGGGAGAGATTAATGAAATTTGCCAAATGAC 2283  
 Db 2108 GCAGAAACAGTACTTAGGTAAATTTAGGGGAGAGATTAATGAAATTTGCCAAATGAC 2167  
 Qy 2284 TTAGCAGCACTGGAACCAATTAATCAACAGCTGAGAAATCAAACCGAGAGGGCTGT 2343  
 Db 2168 TTAGCAGCACTGGAACCAATTAATCAACAGCTGAGAAATCAAACCGAGAGGGCTGT 2227  
 Qy 2344 GTGAACAATGTTTAAATATGAGCACTGCGAACAAGTCACTGAGCACTGAGCAAAATGA 2403  
 Db 2228 GTGAACAATGTTTAAATATGAGCACTGCGAACAAGTCACTGAGCACTGAGCAAAATGA 2287  
 Qy 2404 TGTTCAGAGTGTCAATGAGACTGTGTCACCAATGTATTCATCCAGAGTTCTTAAAGTTTAA 2463  
 Db 2288 TGTTCAGAGTGTCAATGAGACTGTGTCACCAATGTATTCATCCAGAGTTCTTAAAGTTTAA 2347  
 Qy 2464 AGTTGCAATGATTTGTATTAAGATGCTTCTTGTAGTTTAAATATGATTAACATAG 2523  
 Db 2348 AGTTGCAATGATTTGTATTAAGATGCTTCTTGTAGTTTAAATATGATTAACATAG 2407  
 Qy 2524 TTGCATTTAGAAATCAAGATTAATCACTTCAACTGC 2560  
 Db 2408 TTGCATTTAGAAATCAAGATTAATCACTTCAACTGC 2444

RESULT 19  
 ABX75308  
 ID ABX75308 standard; cDNA; 2450 BP.  
 XX  
 AC ABX75308;  
 XX  
 DT 25-MAR-2003 (first entry)  
 XX  
 DE Human cDNA for dickkopf3.  
 XX  
 XX Gene; Notch; Wnt; embryonic stem cell; embryogenesis; sv;  
 KM differentiation; ligand; parkinson's disease; Huntington's disease;  
 KM motor neuron disease; heart disease; diabetes; liver disease; human;  
 KM cirrhosis; renal disease; AIDS; acquired immunodeficiency syndrome.  
 OS Homo sapiens.  
 OS  
 XX  
 PN W0200277204-A2.  
 XX

03-OCT-2002.  
PF 25-MAR-2002; 2002NO-GBO1195.  
XX 23-MAR-2001; 2001GB-0007296.  
PR 23-MAR-2001; 2001GB-0007299.  
PR 17-APR-2001; 2001GB-0009346.  
XX  
XX (AXOR-) AXORDIA LTD.  
PA  
XX  
XX Andrews P, Walsh J, Gokhaile P;  
PI WPI; 2003-092852/08.  
XX  
XX  
XX Modulating the differentiation of embryonic stem cells by providing ligands which bind receptors in the Notch and Wnt pathways, useful for treating diseases such as Parkinson's, Huntington's, heart disease, diabetes and AIDS -  
PT disclosure; Fig 28; 121pp; English.  
PS  
XX The invention relates to modulating the differentiation of an embryonic stem cell, comprising: (a) providing a culture of embryonic stem cells; (b) providing at least one ligand or its active binding fragment, capable of binding its cognate receptor polypeptide expressed by the embryonic stem cell; (c) forming a culture comprising embryonic stem cells and the ligand; and (d) growing the cell culture. Also included are: (1) Modulating the differentiation of embryonic stem cells, comprising: (a) providing a cell transfected with a nucleic acid molecule selected from: (i) any of 9 fully defined Wnt nucleic acid sequences; (ii) a nucleic acid molecule that hybridises to the nucleic acid in (i); and which encodes a ligand capable of modulating embryonic stem cell differentiation, or capable of binding a Wnt receptor; or (iii) nucleic acid molecules which are degenerate as a result of the genetic code to the sequences of (i) or (ii); (b) forming a culture comprising the cell identified in (a) with an embryonic stem cell; and (c) growing the culture for the maintenance of embryonic stem cells in an undifferentiated state; or (3) Inhibiting the differentiation of embryonic stem cells, comprising: (a) providing a cell transfected with a nucleic acid molecule selected from: (i) a molecule encoding a Wnt inhibitory polypeptide; (ii) a molecule which hybridises to the molecule of (i) and encodes a polypeptide capable of inhibiting Wnt signaling; and (iii) nucleic acid molecules which are degenerate as a result of the genetic code to the sequences of (i) or (ii); (b) forming a culture comprising the cell identified in (a) with an embryonic stem cell; and (c) growing the culture for the maintenance of embryonic stem cells in an undifferentiated state; and (4) A cell, therapeutic cell or cell culture obtainable by any of the methods cited above.  
CC The therapeutic cell of the present invention is useful in the treatment of an animal, preferably a human, comprising administering a cell composition comprising embryonic stem cells which have been induced to differentiate into at least one cell-type. The cell is also useful for the manufacture of a composition for use in treatment of diseases such as Parkinson's disease, Huntington's disease, motor neuron disease, heart disease, diabetes, liver disease (e.g. cirrhosis), renal disease and AIDS (acquired immunodeficiency syndrome).  
CC The present sequence encodes a Wnt or Notch pathway protein (i.e. a ligand for the method of the invention).  
XX  
XX Sequence 2450 BP; 595 A; 622 C; 664 G; 569 T; 0 other;  
SQ  
Query Match 87.2%; Score 2255; DB 25; Length 2450;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2433; Conservative 0; Mismatches 0; Indels 2; Gaps 1

126 GGCGGCGGGCTGGCGGAGCGGAGATGCACGGCTTGGGGGCCACCTGTGTCCTGG 185  
db 8 GGCGGCGGGCTGGCGGAGCGGAGATGCACGGCTTGGGGGCCACCTGTGTCCTGG 67

OY	186	TGCTGGCGGGGGGGGGTCCCAAGGCCCCCGCGCGCGCTCCGAAGGGAAGCTCGGCTCCA	245
Db	68	CTGCTGGCGGGGGGGTCCCAAGGCCCCCGCGCGCGCTCCGAAGGGAAGCTCGGCTCCA	127
OY	246	GTCAAGCCCGGCGCGCTCTCAAGCTACCCGAGAGAGGAGCCACCTCAATGAGATGTTCC	305
Db	128	GTCAAGCCCGGCGCGCTCTCAAGCTACCCGAGAGAGGAGCCACCTCAATGAGATGTTCC	187
OY	306	CGCAGAGTTGAGGAACTGATGAGAGAACCCGAGCAAAATTGCGCAGCGCGTGGAGAG	365
Db	188	CGCAGAGTTGAGGAACTGATGAGAGAACCCGAGCAAAATTGCGCAGCGCGTGGAGAG	247
OY	366	ATGAGGCGAGAGAGGCTGCTGCTTAAGCATCATAGAGTGAACCTGGCAACTTACCT	425
Db	248	ATGAGGCGAGAGAGGCTGCTGCTTAAGCATCATAGAGTGAACCTGGCAACTTACCT	307
OY	426	CCGAGCTATCAAAATGAGCAACAACAGACAGAGGTTGAAATTAATACATCATGTG	485
Db	308	CCGAGCTATCAAAATGAGCAACAACAAGAGTTGAAATTAATACATCATGTG	367
OY	486	CACCGAATAATTCAGAGATPACCAACAACAGACTGGAATAATGTTCTTTACAGACA	545
Db	368	CACCGAATAATTCAGAGATPACCAACAACAAGACTGGAATAATGTTCTTTACAGACA	427
OY	546	GTATTCACATCTGTGGGAGACGAAGAGGCGAAGAGGACAGAGTGCATCATGAGAG	605
Db	428	GTATTCACATCTGTGGGAGACGAAGAGGCGAAGAGGACAGAGTGCATCATGAGAG	487
OY	606	GACTGTGGGCCAGACATGTACTGCAGTTTGCCAGCTTCCAGTACACTGCGACCATGC	665
Db	488	GACTGTGGGCCAGACATGTACTGCAGTTTGCCAGTACACTGCGACCATGC	547
OY	666	CGGGGCGAGAGATGCTCTGCACCCGGGACAGTAGTGTCTGTGGAGCCAGCTGTGTGC	725
Db	548	CGGGGCGAGAGATGCTCTGCACCCGGGACAGTAGTGTGTGTGGAGCCAGCTGTGTGC	607
OY	726	TGGGTCATCTGCACAAATAATGGCCAACAAGGAGCGACATGGACATCTGTGAACAACG	785
Db	608	TGGGTCATCTGCACAAATAATGGCCAACAAGGAGCGACATGGACATCTGTGAACAACG	667
OY	786	AGGAGACTGCCAGCGGGGCTGTGTGTGACCTTCAGAGAGGCGTGTCCCTGTGTGC	845
Db	668	AGGAGACTGCCAGCGGGGCTGTGTGTGACCTTCAGAGAGGCGTGTCCCTGTGTGC	727
OY	846	ACACCCCTGCTGAGAGGGGAGCTTTGCCATGACCCCGCAGCGCGCTTCTGACCTC	905
Db	728	ACACCCCTGCTGAGAGGGGAGCTTTGCCATGACCCCGCAGCGCGCTTCTGACCTC	787
OY	906	ATCACCTGGGAGCTAGAGCTGTGATGAGAGCTTGGACCGATGCTTGTGCAATGGGCTC	965
Db	788	ATCACCTGGGAGCTAGAGCTGTGATGAGAGCTTGGACCGATGCTTGTGCAATGGGCTC	847
OY	966	CTCTTGCAGCCCGCCACAGCCACAGCTGTGTGTATGTGTGCAAGCCGACCTTGTGTGGAGC	1025
Db	848	CTCTTGCAGCCCGCCACAGCCACAGCTGTGTGTATGTGTGCAAGCCGACCTTGTGTGGAGC	907
OY	1026	CGTACCAAGATGGAGAGATCTGCTGCGCCAGAGAGGTCGCCGATGAGTATGAGATTGAC	1085
Db	908	CGTACCAAGATGGAGAGATCTGCTGCGCCAGAGAGGTCGCCGATGAGTATGAGATTGAC	967
OY	1086	AGCTTCATGAGAGAGGTGCGCCAGAGGCTGGAGACTCTGAGAGAGACCTGTACCTGAAGAG	1145
Db	968	AGCTTCATGAGAGAGGTGCGCCAGAGGCTGGAGACTCTGAGAGAGACCTGTACCTGAAGAG	1027
OY	1146	ATGGCGCTGGGAGAGCTGCGCGCTGTGCGCGCTCACAATGCTGTGGAGGGGAGAGATTAG	1205
Db	1028	ATGGCGCTGGGAGAGCTGCGCGCTGTGCGCGCTCACAATGCTGTGGAGGGGAGAGATTAG	1087
OY	1206	ATCTGAGACCAAGCTGTGTGTATGATGTCAATGAAATAATGCTAATTTATTTCCCAAGGCT	1265
Db	1088	ATCTGAGACCAAGCTGTGTGTATGATGTCAATGAAATAATGCTAATTTATTTCCCAAGGCT	1147

QY 1266 GTGCTTAAAGGGGTGGGCTGACAGGCTTCTCTACATCTTCTTCCAGTAAGTTTCCC 1325  
 DB 1148 GTGCTTAAAGGGGTGGGCTGACAGGCTTCTCTACATCTTCTTCCAGTAAGTTTCCC 1207  
 QY 1326 TCTGGCTTGAAGAGATGAGTGTGTGCAATTTGTTACAGTCTCCCGAGGCTGTCTCCAGG 1385  
 DB 1208 TCTGGCTTGAAGAGATGAGTGTGTGCAATTTGTTACAGTCTCCCGAGGCTGTCTCCAGG 1267  
 QY 1386 CTTCACATCTGTGTGCTTGGAGAGTCAAGGAGGTTAACTGACAGAGCATTTGGCCAC 1445  
 DB 1268 CTTCACATCTGTGTGCTTGGAGAGTCAAGGAGGTTAACTGACAGAGCATTTGGCCAC 1327  
 QY 1446 CCTGTCCAGATTAATTGGCTCTTGGCTCTACACAGTTGGACAGACCGCTTGTCTAC 1505  
 DB 1328 CCTGTCCAGATTAATTGGCTCTTGGCTCTACACAGTTGGACAGACCGCTTGTCTAC 1387  
 QY 1506 ATGCTTTGATTAATTGTTTGAAGGAGAGATGGAACAAATGTGAGTCTCCCTGATT 1565  
 DB 1388 ATGCTTTGATTAATTGTTTGAAGGAGAGATGGAACAAATGTGAGTCTCCCTGATT 1447  
 QY 1566 GGTTTTGGGAAATGTGAGAGAGTGCCTGCTTTCACAAACATCACTGGCAAAAATG 1625  
 DB 1448 GGTTTTGGGAAATGTGAGAGAGTGCCTGCTTTCACAAACATCACTGGCAAAAATG 1507  
 QY 1626 CAACAAATGAATTTTCCACGCAAGTCTTTCATGCGCATAGTAAAGCTGTGCTTGAAGT 1685  
 DB 1508 CAACAAATGAATTTTCCACGCAAGTCTTTCATGCGCATAGTAAAGCTGTGCTTGAAGT 1567  
 QY 1686 GTTGCAGATGAATTTGTTCTGTTCACCTGCAATTCATGTTTATTTATTCAGAGTGT 1745  
 DB 1568 GTTGCAGATGAATTTGTTCTGTTCACCTGCAATTCATGTTTATTTATTCAGAGTGT 1627  
 QY 1746 GCTCAGCTCTTACCTCTGTGCGCAGGAGAGATTTTCATATCCAAAGATCAATTCCTCTCT 1805  
 DB 1628 GCTCAGCTCTTACCTCTGTGCGCAGGAGAGATTTTCATATCCAAAGATCAATTCCTCTCT 1687  
 QY 1806 CAGACAGAGCTGGGAGAGGGGTCTATTTCTCTCTGTCATCAGGATCTCAGAGGCTCA 1865  
 DB 1688 CAGACAGAGCTGGGAGAGGGGTCTATTTCTCTCTGTCATCAGGATCTCAGAGGCTCA 1747  
 QY 1866 GAGACTGAGAGCTGTGCGCAGGAGAGATTTTCATATCCAAAGATCAATTCCTCTCT 1925  
 DB 1748 GAGACTGAGAGCTGTGCGCAGGAGAGATTTTCATATCCAAAGATCAATTCCTCTCT 1807  
 QY 1926 GTTGTGACTTGAAGCTCAGTGTCTCTCTCACTACCCACACAGCCTTGTGTCACCAAA 1985  
 DB 1808 GTTGTGACTTGAAGCTCAGTGTCTCTCTCACTACCCACACAGCCTTGTGTCACCAAA 1867  
 QY 1986 AGTGTCTCCCAAGAGAGAGAGATGGGATTTTTC -TTGAGGCAATGCAATCTGGAATT 2043  
 DB 1868 AGTGTCTCCCAAGAGAGAGAGATGGGATTTTTC -TTGAGGCAATGCAATCTGGAATT 1927  
 QY 2044 AAGGTCAAACTAATTTCTCACTATCCCTCTAAAGAACTACTGTTAGAAACAGCAGTGT 2103  
 DB 1928 AAGGTCAAACTAATTTCTCACTATCCCTCTAAAGAACTACTGTTAGAAACAGCAGTGT 1987  
 QY 2104 CTCACTGTGTGGGACACCGTCTTCTTAATGAAGACATATATTTGACACTGTCTCTT 2163  
 DB 1988 CTCACTGTGTGGGACACCGTCTTCTTAATGAAGACATATATTTGACACTGTCTCTT 2047  
 QY 2164 TGGCAGTTGCAATTTGTAAGTATTTGAAGTATGACAGTGAAGTAAAGTAAAGT 2223  
 DB 2048 TGGCAGTTGCAATTTGTAAGTATTTGAAGTATGACAGTGAAGTAAAGTAAAGT 2107  
 QY 2224 GCAGAAACAGTACTTGAAGTATTTGAGGCGAGGATTAATGAATTTGCAAAATCAC 2283  
 DB 2108 GCAGAAACAGTACTTGAAGTATTTGAGGCGAGGATTAATGAATTTGCAAAATCAC 2167  
 QY 2284 TTAGCAGCACTGAAGCAATTTATCAACGAGTGAAGAAATCAAAACCGAGCGAGCTGT 2343  
 DB 2168 TTAGCAGCACTGAAGCAATTTATCAACGAGTGAAGAAATCAAAACCGAGCGAGCTGT 2227  
 QY 2344 GTGAACAATGAGTTGTAATATGCACTGCGAAACACTGAATCTTACGCCATCCCAAAATGA 2403

DB 2228 GTGAACAATGTTGTAATATGAGTGCAGAACACTGAACCTACCCACTCCACAAATGA 2287  
 QY 2404 TGTTTTCAAGGTGTGAGGACCTGTGCGACCATGTATTCACAGAGTCTTAAAGTTAA 2463  
 DB 2288 TGTTTTCAAGGTGTGAGGACCTGTGCGACCATGTATTCACAGAGTCTTAAAGTTAA 2347  
 QY 2464 AGTTGCAATGATTTGTAATGAGTCTTCTTGAAGTTTAAATTAATGATTAACATAAG 2523  
 DB 2348 AGTTGCAATGATTTGTAATGAGTCTTCTTGAAGTTTAAATTAATGATTAACATAAG 2407  
 QY 2524 TTGCATTTAGAAATCAAGCATTAATCACTTCACTGC 2560  
 DB 2408 TTGCATTTAGAAATCAAGCATTAATCACTTCACTGC 2444

RESULT 20  
 AAH45491  
 ID AAH45491 standard; DNA; 2632 BP.  
 AC AAH45491;  
 DT 10-SEP-2001 (first entry)  
 DE Human reduced expression in immortalised cells DNA sequence SEQ ID 4.  
 XX  
 XX REIC; reduced expression in immortalised cells; cancer; tumour;  
 KM proliferation inhibitor; viral infection; human; ds.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 198..1250  
 FT /tag=a  
 FT /product="REIC"  
 FT /note="Reduced expression in immortalised cells protein"  
 XX  
 PN WO200138528-A1.  
 PD 31-MAY-2001.  
 PP 30-AUG-2000; 2000MO-JP05879.  
 XX  
 PR 19-NOV-1999; 99JP-0330604.  
 PA (HISM ) HISAM-TSU PHARM CO LTD.  
 PI Namba M, Tsuji T;  
 XX  
 XX WPI; 2001-367688/38.  
 DR P-PSDB; AAG62468.  
 XX  
 PT Cell proliferation inhibiting protein REIC and polynucleotide encoding  
 PT it for diagnosis and therapy of cancer and as an antiviral agent -  
 XX  
 PS Claim 2; Page 59-60; 66pp; Japanese.  
 CC This invention relates to a protein designated REIC (reduced expression  
 CC in immortalised cells) which inhibits proliferation. REIC shows reduced  
 CC or suppressed expression in immortalised cells such as cancer cells. The  
 CC invention includes DNA and protein sequences for REIC. The protein is  
 CC useful for the treatment and diagnosis of a wide range of benign and  
 CC malignant tumours and of viral infections (including HIV, influenza,  
 CC hepatitis and Epstein-Barr virus). The present sequence represents DNA  
 CC encoding REIC.  
 CC  
 SQ Sequence 2632 BP; 646 A; 647 C; 740 G; 599 T; 0 other;

Query Match 87.2%; Score 2255; DB 22; Length 2632;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 2435; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 126 GCGCGCGGCTGCGGCGCGAGAGCGAGATGCGAGCGGCTTGGGCGCACCCCTGCTGCTG 185

Db 171 GGGCGGCGCTGCGGCGAGAGCGAGATGCGCGCTGGGCGCCACCTGCTGTGCTG 230  
Qy 186 CTGCTGGGCGGCGGCTCCCAAGGCCCCCGGCGGCTCCGAGGGGACCTGGCTCCA 245  
Db 231 CTGCTGGGCGGCGGCTCCCAAGGCCCCCGGCGGCTCCGAGGGGACCTGGCTCCA 290  
Qy 246 GTCAGCCCGCGCGCTCTCAGCTACCCGAGAGAGGCGCACCTCAATGAGATGTC 305  
Db 291 GTCAGCCCGCGCGCTCTCAGCTACCCGAGAGAGGCGCACCTCAATGAGATGTC 350  
Qy 306 CGCGAGGTTGAGGAACTGATGAGAGACAGAGACCAATTTGCCAGCGGCTGAGAGAG 365  
Db 351 CGCGAGGTTGAGGAACTGATGAGAGACAGAGACCAATTTGCCAGCGGCTGAGAGAG 410  
Qy 366 ATGAGAGGAGAAAGCTGCTGCTAAAGCATCATGAGAGTGAAGCTGGCAAACTTACT 425  
Db 411 ATGAGAGGAGAAAGCTGCTGCTAAAGCATCATGAGAGTGAAGCTGGCAAACTTACT 470  
Qy 426 CCCAGCTATCAAAATGAGACCAACAGACGAGAGGTTGAAATTAATACATCATGTG 485  
Db 471 CCCAGCTATCAAAATGAGACCAACAGACGAGAGGTTGAAATTAATACATCATGTG 530  
Qy 486 CACGAGAAATTCACAGATTAACCAACAGACGAGCTGGAACAAATGCTTTTCAGAGCA 545  
Db 531 CACGAGAAATTCACAGATTAACCAACAGACGAGCTGGAACAAATGCTTTTCAGAGCA 590  
Qy 546 GTTATCATCTGTGGAG 605  
Db 591 GTTATCATCTGTGGAG 650  
Qy 606 GACTGTGGGCGGCGAGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 665  
Db 651 GACTGTGGGCGGCGAGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 710  
Qy 666 CGGAGCGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 725  
Db 711 CGGAGCGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 770  
Qy 726 TGGGCTCACTGCAACCAAAATGGCCACAGAGGCGAGCAATGGGACCAATCTGTGACACAG 785  
Db 771 TGGGCTCACTGCAACCAAAATGGCCACAGAGGCGAGCAATGGGACCAATCTGTGACACAG 830  
Qy 786 AGGAGCTGCAAGCGGCGGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 845  
Db 831 AGGAGCTGCAAGCGGCGGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 890  
Qy 846 ACACCCCTGCTGTGAGAGGCGAGCTTTGCCATGACCCCGGCGAGCTGCTGAGACTC 905  
Db 891 ACACCCCTGCTGTGAGAGGCGAGCTTTGCCATGACCCCGGCGAGCTGCTGAGACTC 950  
Qy 906 ATCACTGGGAGCTGAGAGCTGATGAGAGCTTGGACGATGAGAGCTTGGAGAGGCTG 965  
Db 951 ATCACTGGGAGCTGAGAGCTGATGAGAGCTTGGAGAGCTTGGAGAGGCTGAGAGGCTG 1010  
Qy 966 CTGTGCGAGCCCAAGCCAGAGCTGTGTATGTGTGCAAGCCGACCTTGTGTGGAGAG 1025  
Db 1011 CTGTGCGAGCCCAAGCCAGAGCTGTGTATGTGTGCAAGCCGACCTTGTGTGGAGAG 1070  
Qy 1026 CGTGAACCAAGTGGGAGATCTGTGCTGCCAGAGAGTCCCGCATGATGATGAGATTGGC 1085  
Db 1071 CGTGAACCAAGTGGGAGATCTGTGCTGCCAGAGAGTCCCGCATGATGATGAGATTGGC 1130  
Qy 1086 AGCTTCAATGAGAGGTTGCGCAGAGAGCTGAGAGAGCTGAGAGAGAGCTGAGAGAG 1145  
Db 1131 AGCTTCAATGAGAGGTTGCGCAGAGAGCTGAGAGAGAGCTGAGAGAGAGCTGAGAGAG 1190  
Qy 1146 ATGGCGCTGGGAGAGCTGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1205  
Db 1191 ATGGCGCTGGGAGAGCTGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1250  
Qy 1206 ATCTGAGCAAGGCTGTGGGTGATGTGCAATAGCAATATGCTAATTTATTTCCAGAGTGT 1265

Db 1251 ATCTGAGCAAGGCTGTGGGTGATGTGCAATAGCAATATGCTAATTTATTTCCAGAGTGT 1310  
Qy 1266 GTGCTTTTGGCGGTGGCTGACACAGGCTTCTCTCACTCACTTCTTCCAGTAGTTCCCC 1325  
Db 1311 GTGCTTTTGGCGGTGGCTGACACAGGCTTCTCTCACTCACTTCTTCCAGTAGTTCCCC 1370  
Qy 1326 TCTGGCTTACAGCATGAGGTTGTGCAATTTGTTCACTCCCGAGGCTGTTCTCAGG 1385  
Db 1371 TCTGGCTTACAGCATGAGGTTGTGCAATTTGTTCACTCCCGAGGCTGTTCTCAGG 1430  
Qy 1386 CTTCACGCTGTGCTTGGGAGAGTCAAGCGAGGTTAACTGCGAGAGCACTTGGCCAC 1445  
Db 1431 CTTCACGCTGTGCTTGGGAGAGTCAAGCGAGGTTAACTGCGAGAGCACTTGGCCAC 1490  
Qy 1446 CCTGTCCAGATTATTTGGCTGCTTGCCTTACAGTGTGGCAGAGCGGTTGTTCTAC 1505  
Db 1491 CCTGTCCAGATTATTTGGCTGCTTGCCTTACAGTGTGGCAGAGCGGTTGTTCTAC 1550  
Qy 1506 ATGGCTTTGATTAATGTTTGAAGGAGAGATGAAACAATGAGATCTCCCTGAT 1565  
Db 1551 ATGGCTTTGATTAATGTTTGAAGGAGAGATGAAACAATGAGATCTCCCTGAT 1610  
Qy 1566 GGTTTTGGGAAATGTGAGAGAGAGTGGCCCTGCTTGCACATCAACCTGGCAAAATG 1625  
Db 1611 GGTTTTGGGAAATGTGAGAGAGAGTGGCCCTGCTTGCACATCAACCTGGCAAAATG 1670  
Qy 1626 CAACAAATGAATTTTCCAGAGAGTCTTTCATGGGCAATGGAGCTGTGCTTCACT 1685  
Db 1671 CAACAAATGAATTTTCCAGAGAGTCTTTCATGGGCAATGGAGCTGTGCTTCACT 1730  
Qy 1686 GTTGAGAGAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1745  
Db 1731 GTTGAGAGAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1790  
Qy 1746 GCTAGCTCTTACTCTGTGCGAGGAGCATTTTCATATCCAGATCAATCCCTCTCT 1805  
Db 1791 GCTAGCTCTTACTCTGTGCGAGGAGCATTTTCATATCCAGATCAATCCCTCTCT 1850  
Qy 1806 CAGCAAGCTTGGGAGAGGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1865  
Db 1851 CAGCAAGCTTGGGAGAGGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1910  
Qy 1866 GAGACTGCAAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1925  
Db 1911 GAGACTGCAAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1970  
Qy 1926 GTTGTGACTTAAGCTCAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1985  
Db 1971 GTTGTGACTTAAGCTCAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2030  
Qy 1986 AGTGCTCCCAAAAGAGAGAGATGGGATTTTCTTTTGAAGCATGCACTGTGGAT 2043  
Db 2031 AGTGCTCCCAAAAGAGAGAGATGGGATTTTCTTTTGAAGCATGCACTGTGGAT 2090  
Qy 2044 AAGTTCAAATTAATCTCACTCCCTTAAAGTAACTACTGTGATGAGAGAGAGT 2103  
Db 2091 AAGTTCAAATTAATCTCACTCCCTTAAAGTAACTACTGTGATGAGAGAGAGT 2150  
Qy 2104 CTCAAGTGTGGGAGAGCGCTCTCTAATGAGACATGATATTGACAGCTGCTCCCTCT 2163  
Db 2151 CTCAAGTGTGGGAGAGCGCTCTCTAATGAGACATGATATTGACAGCTGCTCCCTCT 2210  
Qy 2164 TGGAGTTGCAATTAATCTTGAAGGATTAAGTAGAGCTAGCATPACAGTTAACT 2223  
Db 2211 TGGAGTTGCAATTAATCTTGAAGGATTAAGTAGAGCTAGCATPACAGTTAACT 2270  
Qy 2224 GAGAGAAACATCTTAATGATTAATGAGGAGAGATTAATGAAATTTGCAAAATCAC 2283  
Db 2271 GAGAGAAACATCTTAATGATTAATGAGGAGAGATTAATGAAATTTGCAAAATCAC 2330  
Qy 2284 TTAGCAGCAACTGAAGACATTAATCAACAGTGGAGAAATCAAAACGAGAGGAGCTGT 2343  
Db 2331 TTAGCAGCAACTGAAGACATTAATCAACAGTGGAGAAATCAAAACGAGAGGAGCTGT 2390

QY	2344	GTGAACAATGGTTGTAATATGCACTGGAAACACTGAACCTTAAGCGCACTCCAAATGA	2403
Db	2391	GTGAACAATGGTTGTAATATGCACTGGAAACACTGAACCTTAAGCGCACTCCAAATGA	2450
QY	2404	TGTTTTCAGGTGTCATGAGCACTGGTCCACCACTGATTCATCCAGATTCCTTAAAGTTAA	2463
Db	2451	TGTTTTCAGGTGTCATGAGCACTGGTCCACCACTGATTCATCCAGATTCCTTAAAGTTAA	2510
QY	2464	AGTGCACATGATGTTGATATAGCATGCTTCTTGAGCTTTAAATTAATGATATTAACATAG	2523
Db	2511	AGTGCACATGATGTTGATATAGCATGCTTCTTGAGCTTTAAATTAATGATATTAACATAG	2570
QY	2524	TTGCATTTAGAAATCAAGCATTAATCACTTCAACTGC	2560
Db	2571	TTGCATTTAGAAATCAAGCATTAATCACTTCAACTGC	2607

RESULT 21

ABL92089	ABL92089	standard; cDNA; 2608 BP.
XX	XX	ABL92089;
XX	XX	30-MAY-2002 (first entry)
DE	XX	Human Tumour Endothelial Marker polynucleotide SEQ ID NO 201.
XX	XX	Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW	XX	normal endothelial marker; pan-endothelial marker; immunostimulant;
KW	XX	antiangiogenic; tumour; neovascularization; vascularised tumour;
KW	XX	polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
XX	XX	psoriasis; gene; ss.
OS	XX	Homo sapiens.
PN	XX	WO200210217-A2.
PD	XX	07-FEB-2002.
PF	XX	01-AUG-2001; 2001WO-US24031.
XX	XX	02-AUG-2000; 2000US-222599P.
PR	XX	11-AUG-2000; 2000US-224360P.
PR	XX	11-APR-2001; 2001US-282850P.
XX	XX	(UYJO ) UNIV JOHNS HOPKINS.
XX	XX	St Croix B, Kinzler KM, Vogelstein B;
XX	XX	WPI; 2002-291856/33.
DR	XX	P-PSDB; ABB90735.
XX	XX	An isolated molecule comprising an antibody variable region which
PT	XX	specifically binds to an extracellular domain of a tumor endothelial
PT	XX	marker (TEM) protein, useful for inhibiting tumor growth -
XX	XX	Claim 58; Page 155-156; 331p; English.
PS	XX	The invention relates to an isolated molecule comprising an antibody
XX	XX	variable region which specifically binds to an extracellular domain of a
CC	XX	tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC	XX	ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC	XX	proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC	XX	They are useful for inhibiting tumour growth, neovascularization in
CC	XX	subjects bearing a vascularised tumour, polycystic kidney disease,
CC	XX	diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
CC	XX	and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
CC	XX	ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
CC	XX	sequences: tumour endothelial markers (TEM) ABL91986-ABL92041 and
CC	XX	ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
CC	XX	and pan-endothelial markers (PEM) ABL91903-ABL91995.

Seq	Sequence	2608 BP	623 A	647 C	739 G	599 T	0 other
Query	Match	86.2%	Score 2228	DB 24	Length 2608		
	Best Local Similarity	99.9%	Pred. No. 0				
	Matches 2408	Conservative	0	Mismatches	0	Indels	2
						Gaps	14
QY	153	ATGCAGCGGCTTGGAGGCACCCCTCTGTCCTGCTGTCGCGGCGCGGTCCTCCACAGCC	212				
DB	198	ATGCAGCGGCTTGGAGGCACCCCTCTGTCCTGTCGCTGTCGCGGCGGTCCTCCACAGCC	257				
QY	213	CCCGCGCCCGCTCCGAGCGGCACCTCGGCTCGACTCAAGCCCCGCGCTCTCAGCTAC	272				
DB	258	CCCGCGCCCGCTCCGAGCGGCACCTCGGCTCGACTCAAGCCCCGCGCTCTCAGCTAC	317				
QY	273	CCGCGAGGAGGAGCCACCTCATAGATGTTCCGCGAGGTTGAGGAACTATGAGAGAC	332				
DB	318	CCGCGAGGAGGAGCCACCTCATAGATGTTCCGCGAGGTTGAGGAACTATGAGAGAC	377				
QY	333	ACGCGAGCAAAATTGGCCGAGCGCGCTGGAGAGATGAGAGGAGAGAGAAAGCTGCTCTAA	392				
DB	378	ACGCGAGCAAAATTGGCCGAGCGCGCTGGAGAGATGAGAGGAGAGAAAGCTGCTCTAA	437				
QY	393	GCATCATCAGAAAGTGAACCTGGCAAATCTACCTCCAGCTATCAAAATGAGACCAACACA	452				
DB	438	GCATCATCAGAAAGTGAACCTGGCAAATCTACCTCCAGCTATCAAAATGAGACCAACACA	497				
QY	453	GACACGAAAGTTGGAAATTAATACCATCATGTGACCCGAGAAATTCACAAATTAACAAAC	512				
DB	498	GACACGAAAGTTGGAAATTAATACCATCATGTGACCCGAGAAATTCACAAATTAACAAAC	557				
QY	513	AACCAAGCTGAGCAAAATGCTTTTTCAGAGACAGTTATCACTCTGTGGAGACGAGAA	572				
DB	558	AACCAAGCTGAGCAAAATGCTTTTTCAGAGACAGTTATCACTCTGTGGAGACGAGAA	617				
QY	573	GCGCAGAGGAGCCACGAGTGCATATGACGAGGACATGTGGGCCACAGATGTACTGCCAG	632				
DB	618	GCGCAGAGGAGCCACGAGTGCATATGACGAGGACATGTGGGCCACAGATGTACTGCCAG	677				
QY	633	TTTTCGACCTTCCAGTACACCTGCGACCATCCGCGGCGCCAGAGATGCTTGCACCCGG	692				
DB	678	TTTTCGACCTTCCAGTACACCTGCGACCATCCGCGGCGCCAGAGATGCTTGCACCCGG	737				
QY	693	GACAGTGAAGTCTGTGAGACGAGCTGTGTGCTGGGGGTCACTGCAACCAAAATGGCCAC	752				
DB	738	GACAGTGAAGTCTGTGAGACGAGCTGTGTGCTGGGGGTCACTGCAACCAAAATGGCCAC	797				
QY	753	AGGGGAGCAATGGGACCATCTGTGACAAACCAAGGGGATGTCCAGCCGGGCTGTGCTGT	812				
DB	798	AGGGGAGCAATGGGACCATCTGTGACAAACCAAGGGGATGTCCAGCCGGGCTGTGCTGT	857				
QY	813	GCCCTTCAGAGAGGCGCTGCTGTTCCCTGTGTGACACCCCTGCGCCGTTGAGAGGGGAGCTT	872				
DB	858	GCCCTTCAGAGAGGCGCTGCTGTTCCCTGTGTGACACCCCTGCGCCGTTGAGAGGGGAGCTT	917				
QY	873	TGCCATAGACCCCGCAGCCGACTTCTGTGACCTCATCACTTGGAGCTTGAAGCTTGATGGA	932				
DB	918	TGCCATAGACCCCGCAGCCGACTTCTGTGACCTCATCACTTGGAGCTTGAAGCTTGATGGA	977				
QY	933	GCCCTTCAGAGAGGCGCTGCTGTTCCCTGTGTGACACCCCTGCGCCGTTGAGAGGGGAGCTT	992				
DB	978	GCCCTTCAGAGAGGCGCTGCTGTTCCCTGTGTGACACCCCTGCGCCGTTGAGAGGGGAGCTT	1037				
QY	993	GTTGTAATGTGTGCAAGCCGACCTTGTGTGGGAGCCGTGACCAAGTGGGAGATCTTGCTG	1052				
DB	1038	GTTGTAATGTGTGCAAGCCGACCTTGTGTGGGAGCCGTGACCAAGTGGGAGATCTTGCTG	1097				
QY	1053	CCGAGAGAGGCTCCCGCATGAGTATGAGTTGCGAGCTTACATGAGAGAGTGTGCGCAGAG	1112				
DB	1098	CCGAGAGAGGCTCCCGCATGAGTATGAGTTGCGAGCTTACATGAGAGAGTGTGCGCAGAG	1157				
QY	1113	CTGAGAGGACTTGGAGAGGAGGACTTGACTGAAGAAGTGGCGCTGGGGGAGCTTGCCTGCTC	1172				
DB	1158	CTGAGAGGACTTGGAGAGGAGGACTTGACTGAAGAAGTGGCGCTGGGGGAGCTTGCCTGCTC	1217				



QY 1173 GCCGCTGACCTGCGGAGGAGAAAGATTAGATCTGGAACGAGGCTGTGGGTAGATGTG 1232  
 Db 1218 GCCGCTGACCTGCGGAGGAGAAAGATTAGATCTGGAACGAGGCTGTGGGTAGATGTG 1277  
 QY 1233 CAATGAAATAGCTTAATTTATTTCCCGAGGTGTGCTTTAGGCGTGGCTGACGAGGCT 1292  
 Db 1278 CAATGAAATAGCTTAATTTATTTCCCGAGGTGTGCTTTAGGCGTGGCTGACGAGGCT 1337  
 QY 1293 TCTTCTCATCTTTCTTCCGAGTAAGTTCCCTGTGGCTTGAAGAGATGAGGTGTG 1352  
 Db 1338 TCTTCTCATCTTTCTTCCGAGTAAGTTCCCTGTGGCTTGAAGAGATGAGGTGTG 1397  
 QY 1353 CATTTGTTCACTTCCCGAGGCTGTTCTCAAGGCTTCAAGTGTGTGTGGAGAGTC 1412  
 Db 1398 CATTTGTTCACTTCCCGAGGCTGTTCTCAAGGCTTCAAGTGTGTGTGGAGAGTC 1457  
 QY 1413 AGGAGAGGTTAACTGACGAGAGCAGTTGGCAACCCGCTGCAAGATTAATTTGGCTTTGC 1472  
 Db 1458 AGGAGAGGTTAACTGACGAGAGCAGTTGGCAACCCGCTGCAAGATTAATTTGGCTTTGC 1517  
 QY 1473 CTCTACAGTTGGAGAGACAGCCGTTGTCTACATGCTTTGATTAATTTGTTGAGGGAG 1532  
 Db 1518 CTCTACAGTTGGAGAGACAGCCGTTGTCTACATGCTTTGATTAATTTGTTGAGGGAG 1577  
 QY 1533 GAGATGGAAGAAATGTGAGTCTCCCTCTGATTTGTTGGGAAATGTGAGAGAGTG 1592  
 Db 1578 GAGATGGAAGAAATGTGAGTCTCCCTCTGATTTGTTGGGAAATGTGAGAGAGTG 1637  
 QY 1593 CCTGCTTTGGCAACATCAACCTGGCAAAATGCAAAATGATTTTCCAGCGAGTCT 1652  
 Db 1638 CCTGCTTTGGCAACATCAACCTGGCAAAATGCAAAATGATTTTCCAGCGAGTCT 1697  
 QY 1653 TTCCATGGGCAATGTAAGCTGTGCTTCAAGCTTTGCAAGATTAATTTCTGTCAACC 1712  
 Db 1698 TTCCATGGGCAATGTAAGCTGTGCTTCAAGCTTTGCAAGATTAATTTCTGTCAACC 1757  
 QY 1713 TGCATTACATGTGTTTATTCATCCAGAGGTGTGCTCAAGCTTCTGTGCAAGGCT 1772  
 Db 1758 TGCATTACATGTGTTTATTCATCCAGAGGTGTGCTCAAGCTTCTGTGCAAGGCT 1817  
 QY 1773 AGCATTTTCATATCCAAATCAATTCCTCTCTCAGACAGCTGTGGGAGGGGCTATTG 1832  
 Db 1818 AGCATTTTCATATCCAAATCAATTCCTCTCTCAGACAGCTGTGGGAGGGGCTATTG 1877  
 QY 1833 TTCTCCTGTCATCAGGAGATCTCAGAGGCTCAGAGCTCAGAGCTGCTGCCAAGTCA 1892  
 Db 1878 TTCTCCTGTCATCAGGAGATCTCAGAGGCTCAGAGCTGCTGCCAAGTCA 1937  
 QY 1893 CACAGCTAGTGAAGACAGAGCAGTTTCACTGTGTGTGACTTAAGCTCAGTCTCTCT 1952  
 Db 1938 CACAGCTAGTGAAGACAGAGCAGTTTCACTGTGTGTGACTTAAGCTCAGTCTCTCT 1997  
 QY 1953 CCACTACCCCAACAGCAGCTGTGTGCAACCAAAAGTCTCCCAAAAGAGAGAGATG 2012  
 Db 1998 CCACTACCCCAACAGCAGCTGTGTGCAACCAAAAGTCTCCCAAAAGAGAGATG 2057  
 QY 2013 GATTTTTC--TTGAGGATGACATCTGGAATTAAGTCAAACTAATTTCCATCCCTC 2070  
 Db 2058 GATTTTTC--TTGAGGATGACATCTGGAATTAAGTCAAACTAATTTCCATCCCTC 2117  
 QY 2071 TAAAGTAACTACTGTTAGGAAGAGAGGTGTTCACAGTGTGGGAGCCCTCTCTCT 2130  
 Db 2118 TAAAGTAACTACTGTTAGGAAGAGAGGTGTTCACAGTGTGGGAGCCCTCTCTCT 2177  
 QY 2131 AATGAGACATGATTAATGACATGCTCCCTTTTGGAGTGTGATTAGTAATTTGAAG 2190  
 Db 2178 AATGAGACATGATTAATGACATGCTCCCTTTTGGAGTGTGATTAGTAATTTGAAG 2237  
 QY 2191 GTATATGACTGAGGCTGACATACAGGTTAACTGCAAGAAACAGTACTTAAAGTATG 2250  
 Db 2238 GTATATGACTGAGGCTGACATACAGGTTAACTGCAAGAAACAGTACTTAAAGTATG 2297

QY 2251 GCGAGATTTATTAATGAATTTGGAAAATCACTTAGCAGCACTGAAGCAATTATCA 2310  
 Db 2298 GCGAGATTTATTAATGAATTTGGAAAATCACTTAGCAGCACTGAAGCAATTATCA 2357  
 QY 2311 CCACTGAGAAAATCAAAACGAGAGGCTGTGTGAACATGTTGTAATATGCACTG 2370  
 Db 2358 CCACTGAGAAAATCAAAACGAGAGGCTGTGTGAACATGTTGTAATATGCACTG 2417  
 QY 2371 CGAACACTGAACCTTAAGGCACTCCACAAATGATGTTTCAAGTGTGCACTGTG 2430  
 Db 2418 CGAACACTGAACCTTAAGGCACTCCACAAATGATGTTTCAAGTGTGCACTGTG 2477  
 QY 2431 ACCATGATTCATCCAGAGTCTTAAAGTTAAAGTTGACATGATTAAGATGCT 2490  
 Db 2478 ACCATGATTCATCCAGAGTCTTAAAGTTAAAGTTGACATGATTAAGATGCT 2537  
 QY 2491 TTTCTTGAATTTAAATTAATTAATTAACCTAAGTTCATTTGAATCAAGATTAATCA 2550  
 Db 2538 TTTCTTGAATTTAAATTAATTAATTAACCTAAGTTCATTTGAATCAAGATTAATCA 2597  
 QY 2551 CTTCAACTGC 2560  
 Db 2598 CTTCAACTGC 2607

RESULT 22  
 ABX72014  
 ID ABX72014 standard; DNA; 2608 BP.  
 XX  
 AC ABX72014;  
 XX  
 DT 12-NOV-2003 (first entry)  
 XX  
 DE DNA encoding human tumour endothelial marker TEM 4.  
 XX  
 KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
 KW Tumour endothelial marker; normal endothelial marker; PEM;  
 KW pan-endothelial marker; polycystic kidney disease; psoriasis;  
 KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
 KW neovascularization; immune response; cytostatic; antidiabetic; gene;  
 KW ophthalmological; antirheumatic; antiarthritic; antiproliferative; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200283874-A2.  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002MO-US08253.  
 PR 11-APR-2001; 2001US-282850P.  
 PR 06-FEB-2002; 2002US-354262P.  
 XX  
 PA (UICD) UNIT JOHNS HOPKINS.  
 PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;  
 XX  
 DR MPI; 2003-093016/08.  
 DR P-PSDB; ABUS4442.  
 XX  
 PT New purified human transmembrane protein, designated as tumour  
 PT endothelial marker (TEM) 3, useful for detecting, diagnosing or  
 PT treating tumours, polycystic kidney disease, diabetic retinopathy,  
 PT rheumatoid arthritis or psoriasis -  
 XX  
 PS Disclosure; Page 158-160; 374pp; English.  
 XX  
 CC The present invention relates to a novel method for the isolation of  
 CC endothelial cells (ECs), and the identification of genes expressed in  
 CC normal and tumour ECs. Tumour endothelial marker (TEM), normal  
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are  
 CC identified in human ECs. The human EC marker proteins and the  
 CC polynucleotide sequences encoding them are useful for detecting,





Dh 706 AGGAGTCCAGCGCGGCTGTGTCTGCTTCCAGAGAGGCTGTGTTCCCTGTGTGC 765  
Qy 846 AACCCCTGCGCCGTGGAGGGCGAGCTTTGCAAGACCCCGCCAGCCGGCTTGGACCTC 905  
Db 766 ACACCCCTGCGCCGTGGAGGGCGAGCTTTGCAAGACCCCGCCAGCCGGCTTGGACCTC 825  
Qy 906 ATCACTGGAGAGTGAAGCTGTATGAGACCTTGGACCGATGCCCTTGTGCAAGTGGCTC 965  
Db 826 ATCACTGGAGAGTGAAGCTGTATGAGACCTTGGACCGATGCCCTTGTGCAAGTGGCTC 885  
Qy 966 CTCTGCCAGCCCAAGCCAGACAGCTGTATGTGTGCAAGCCGACCTTGTGAGGAGC 1025  
Db 886 CTCTGCCAGCCCAAGCCAGACAGCTGTATGTGTGCAAGCCGACCTTGTGAGGAGC 945  
Qy 1026 CGTAGCAAGATGGAGAGATCTGTGCTGCCAGAGAGGCTCCCGATGAGTGAAGTTGAC 1085  
Db 946 CGTAGCAAGATGGAGAGATCTGTGCTGCCAGAGAGGCTCCCGATGAGTGAAGTTGAC 1005  
Qy 1086 AGCTTCATGAGAGAGTGTGCGCCAGAGCTGAGAGACCTTGGAGAGAGCTGAGTGAAG 1145  
Db 1006 AGCTTCATGAGAGAGTGTGCGCCAGAGCTGAGAGACCTTGGAGAGAGCTGAGTGAAG 1065  
Qy 1146 ATGGCGCTGGGGGAGCCCTGGCGGCTGCCGCGCTGACATGCTGGAGGAGGAGATTTAG 1205  
Db 1066 ATGGCGCTGGGGGAGCCCTGGCGGCTGCCGCGCTGACATGCTGGAGGAGGAGATTTAG 1125  
Qy 1206 ATCTGACACAGGCTGTGGGTGATGTGCAATGAAATAGCTAATTTATTTTCCCGAGGTG 1265  
Db 1126 ATCTGACACAGGCTGTGGGTGATGTGCAATGAAATAGCTAATTTATTTTCCCGAGGTG 1185  
Qy 1266 GTGCTTAAAGGCGTGGCTGACCAAGCTTCTTCCATCACTCTTCCAGTAAGTTTCC 1325  
Db 1186 GTGCTTAAAGGCGTGGCTGACCAAGCTTCTTCCATCACTCTTCCAGTAAGTTTCC 1245  
Qy 1326 TCTGGCTTGAAGAGATGAGTGTGTGCAATTTGTCAGCTCCCGAGGCTGTCTCCAG 1385  
Db 1246 TCTGGCTTGAAGAGATGAGTGTGTGCAATTTGTCAGCTCCCGAGGCTGTCTCCAG 1305  
Qy 1386 CTTTCAAGTCTGTGCTTGGAGAGATCAGGAGGTTTAACTGAGAGAGAGCTTTGGCAC 1445  
Db 1306 CTTTCAAGTCTGTGCTTGGAGAGATCAGGAGGTTTAACTGAGAGAGAGCTTTGGCAC 1365  
Qy 1446 CCTGTCCAGATTAATGTGCTCTTGTGCTTACAGATGGGAGAGAGCCGTTGTCTAC 1505  
Db 1366 CCTGTCCAGATTAATGTGCTCTTGTGCTTACAGATGGGAGAGAGCCGTTGTCTAC 1425  
Qy 1506 ATGCTTTGATTAATGTTTGAAGGAGAGATGAAACAAATGTGAGTCTTCCCTGAT 1565  
Db 1426 ATGCTTTGATTAATGTTTGAAGGAGAGATGAAACAAATGTGAGTCTTCCCTGAT 1485  
Qy 1566 GGTTTTGGGAAATGTGAGAAAGATGCCCTTGTGCAACATCAACTGGCAAAATG 1625  
Db 1486 GGTTTTGGGAAATGTGAGAAAGATGCCCTTGTGCAACATCAACTGGCAAAATG 1545  
Qy 1626 CAACAAATGAATTTTCAAGAGATTTCTTCAATGGGCAATAGTAACTGTGCTTCACT 1685  
Db 1546 CAACAAATGAATTTTCAAGAGATTTCTTCAATGGGCAATAGTAACTGTGCTTCACT 1605  
Qy 1686 GTTGCAGATGAAATGTTCTGTTCACCTGCAATACATGTGTTTATTCACAGAGAGTT 1745  
Db 1606 GTTGCAGATGAAATGTTCTGTTCACCTGCAATACATGTGTTTATTCACAGAGAGTT 1665  
Qy 1746 GCTCAGCTCTACCTGTGTGCGAGGAGAGATTTCAATCAACAGATCAATTCCTCTCT 1805  
Db 1666 GCTCAGCTCTACCTGTGTGCGAGGAGAGATTTCAATCAACAGATCAATTCCTCTCT 1725  
Qy 1806 CAGCAGAGCTGGGAGAGGAGGATGATGTTCTCTGTGCATCAGGAGATCTCAGAGCTCA 1865  
Db 1726 CAGCAGAGCTGGGAGAGGAGGATGATGTTCTCTGTGCATCAGGAGATCTCAGAGCTCA 1785  
Qy 1866 GAGACTGCAAGCTGTGGCCAAAGTCAACAGAGCTAGTGAAGACAGACAGATTCATCTG 1925  
Db 1786 GAGACTGCAAGCTGTGGCCAAAGTCAACAGAGCTAGTGAAGACAGACAGATTCATCTG 1845

Qy 1926 GTTGTGACTTAAGCTAGTCTCTCTTCACTACACCCACAGACCTTGTGACCAAAA 1985  
Db 1846 GTTGTGACTTAAGCTAGTCTCTCTTCACTACACCCACAGACCTTGTGACCAAAA 1905  
Qy 1986 AGTGTCTCCCAAAAGAGAGAAATGGAGATTTTTC--TTGAGGCAATGCAATCTGAAAT 2043  
Db 1906 AGTGTCTCCCAAAAGAGAGAAATGGAGATTTTTC--TTGAGGCAATGCAATCTGAAAT 1965  
Qy 2044 AAGGTCAAACTAATCTGACATCCCTCAAAAGTAATCACTGTAGGAGAGAGTGT 2103  
Db 1966 AAGGTCAAACTAATCTGACATCCCTCAAAAGTAATCACTGTAGGAGAGAGTGT 2025  
Qy 2104 CTACAGTGTGGGAGAGCCGTCCTTCTTAATGAAGCAATGATATTGACATGTCCTCTT 2163  
Db 2026 CTACAGTGTGGGAGAGCCGTCCTTCTTAATGAAGCAATGATATTGACATGTCCTCTT 2085  
Qy 2164 TGGCAGTGTGATTAATCTTGAAGGATTAATGATGAGGATGATGATGATGATGATGAT 2223  
Db 2086 TGGCAGTGTGATTAATCTTGAAGGATTAATGATGAGGATGATGATGATGATGATGAT 2145  
Qy 2224 GCAGAAACAGTACTTAAAGTAAATGAGGCGAGATTAATAATGAATTTGCAAAATCAC 2283  
Db 2146 GCAGAAACAGTACTTAAAGTAAATGAGGCGAGATTAATAATGAATTTGCAAAATCAC 2205  
Qy 2284 TTAGCAGCACTGAGAGCAATTAATCAACAGTGGAGAAATCAAACGAGAGGCTGT 2343  
Db 2206 TTAGCAGCACTGAGAGCAATTAATCAACAGTGGAGAAATCAAACGAGAGGCTGT 2265  
Qy 2344 GTGAAACATGATGATTAATGAGGAGCTGGCAACATGAACTTCAACGCACTCCAAATGA 2403  
Db 2266 GTGAAACATGATGATTAATGAGGAGCTGGCAACATGAACTTCAACGCACTCCAAATGA 2325  
Qy 2404 TGTGTTCAAGTGTCAATGAGCTGTGCAACATGATTAATCAAGGTTCTTAAATTTAA 2463  
Db 2326 TGTGTTCAAGTGTCAATGAGCTGTGCAACATGATTAATCAAGGTTCTTAAATTTAA 2385  
Qy 2464 AGTGCACATGATTAATGATGAGATGTTCTTGAAGTTTAAATTAATTAATTAATTAAG 2523  
Db 2386 AGTGCACATGATTAATGATGAGATGTTCTTGAAGTTTAAATTAATTAATTAATTAAG 2445  
Qy 2524 TTGCATTGAAATCAAGATTAATCACTTCAACTGC 2560  
Db 2446 TTGCATTGAAATCAAGATTAATCACTTCAACTGC 2482

RESULT 24  
AA169309  
ID AA169309 standard; DNA; 2479 BP.  
XX AA169309;  
AC  
DT 11-FEB-2002 (first entry)  
XX  
DE Human DKK-3 DNA.  
XX  
XX DKK-3; detection; schizophrenia; neuroleptic; vaccine; gene therapy;  
KM neuralgic defect; neuropsychiatric disorder; human; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 38..1090  
FT FT /tag= a  
FT FT /product= "DKK-3"  
XX  
XX MO200163295-A2.  
XX  
XX PD 30-AUG-2001.  
XX  
XX 26-FEB-2001; 2001MO-IB00259.  
XX  
XX 24-FEB-2000; 2000GB-0004412.  
PR

PR 24-FEB-2000; 2000GB-0004415.  
 PR 15-MAR-2000; 2000GB-0006285.  
 PR 24-NOV-2000; 2000GB-0028734.  
 PR 28-NOV-2000; 2000US-0724391.  
 PR 08-DEC-2000; 2000GB-0030050.  
 PR 12-DEC-2000; 2000US-0254830.  
 PR 28-DEC-2000; 2000US-0750395.  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX  
 XX Herath HMAc, Parekh RB, Rohlf C, Patel TP;  
 DR WPI; 2001-570652/64.  
 DR P-PSDB; AAG80271.  
 PT Diagnosing and monitoring Schizophrenia by detecting the presence of  
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein  
 PT Isoforms in samples of cerebrospinal fluid -  
 XX  
 XX Claim 5a; Fig 2; 91pp; English.  
 CC This invention describes a novel method for detecting the presence of  
 CC Schizophrenia associated features (SFS) and schizophrenia associated  
 CC protein isoforms (SPIs) in samples, e.g. by electrophoresis, immunoassay  
 CC or hybridisation assay, for diagnosing and monitoring schizophrenia,  
 CC studying the effectiveness of treatments and for identifying potential  
 CC therapeutic agents. The products of the invention have neuroleptic  
 CC activity and can be used in vaccines or for gene therapy. The method (I)  
 CC is used: (1) for screening or diagnosis of schizophrenia and the relative  
 CC abundance of at least 1 chosen feature correlates with the presence or  
 CC absence of schizophrenia and for monitoring the effect of therapy  
 CC administered to a subject with schizophrenia and the relative abundance  
 CC of at least 1 chosen feature which correlates with the severity of  
 CC schizophrenia. The expression and activity of the SFS, SPIs and related  
 CC molecules (e.g. secondary messengers) are studied to diagnose  
 CC schizophrenia, monitor the progress of the disorder and the effectiveness  
 CC of treatment and as targets to identify and produce potential therapeutic  
 CC agents for the treatment of schizophrenia. The paucity of detectable  
 CC neuroleptic defects distinguishes neuropsychiatric disorders such as  
 CC schizophrenia from neurological disorders, where manifestations of  
 CC anatomical and biochemical changes have been identified in many cases.  
 CC Consequently the identification and characterisation of cellular and/or  
 CC molecular causative defects and neuropathies are necessary for improved  
 CC treatment of neuropsychiatric disorders. This sequence encodes the human  
 CC DKX-3 protein described in the method of the invention.  
 CC  
 XX  
 SQ Sequence 2479 BP; 625 A; 618 C; 668 G; 567 T; 1 other;  
 Query Match 81.4%; Score 2104; DB 22; Length 2479;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 2434; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Db 309 CTCACAGCTATCATATGAGACCAACACAGACACGAAGTTGAAATATATACATCCATG 368  
 QY 484 TGCACCGAGAAATTTCAAGATTAACCAACACAGACTGACAAATGGTCTTTAGAGA 543  
 Db 369 TGCACCGAGAAATTTCAAGATTAACCAACACAGACTGACAAATGGTCTTTAGAGA 428  
 QY 544 CAGTTATCATCTGTGGGAGACGAAGAGGCAAGAGGACGACGATGATCATGACG 603  
 Db 429 CAGTTATCATCTGTGGGAGACGAAGAGGCAAGAGGACGACGATGATCATGACG 488  
 QY 604 AGGACTGTGGGACCAAGATGATCTGACAGTTTGGCAAGTTCCAGTACCTGCGACCAT 663  
 Db 489 AGGACTGTGGGACCAAGATGATCTGACAGTTTGGCAAGTTCCAGTACCTGCGACCAT 548  
 QY 664 GCGGGGGCCAGAGAGATGCTCTGACACCGGGGACAGTAGAGTGTGGAAGACAGCTGTGTG 723  
 Db 549 GCGGGGGCCAGAGAGATGCTCTGACACCGGGGACAGTAGAGTGTGGAAGACAGCTGTGTG 608  
 QY 724 TCTGGGTCATCTGCACCAAAATGACCAACGAGGAGGACCAATGGACCATCTGTGACAAAC 783  
 Db 609 TCTGGGTCATCTGCACCAAAATGACCAACGAGGAGGACCAATGGACCATCTGTGACAAAC 668  
 QY 784 AAGAGGATCCGACAGCGGGGCTGTGCTGTGCTTCAGAGAGGCTGTGCTGTGCTGTGCTGTG 843  
 Db 669 AAGAGGATCCGACAGCGGGGCTGTGCTGTGCTTCAGAGAGGCTGTGCTGTGCTGTGCTGTG 728  
 QY 844 GCACACCTCTGCGCGTGGAGGAGGAGGAGCTTGGCATGACCCGACAGCGGCTTGTGAGCC 903  
 Db 729 GCACACCTCTGCGCGTGGAGGAGGAGGAGCTTGGCATGACCCGACAGCGGCTTGTGAGCC 788  
 QY 904 TCATACCTGGAGAGCTAGAGCTGATGAGCCTTGGACCGGATGCTGTGACAGTGGCC 963  
 Db 789 TCATACCTGGAGAGCTAGAGCTGATGAGCCTTGGACCGGATGCTGTGACAGTGGCC 848  
 QY 964 TCTTGGCAGGCGCCACAGCCACAGCCTGTGATGTGCAAGCCGACTTGTGAGGGA 1023  
 Db 849 TCTTGGCAGGCGCCACAGCCACAGCCTGTGATGTGCAAGCCGACTTGTGAGGGA 908  
 QY 1024 GCGGTACCAAGATGGGAGATCTCTCTCCAGAGAGGTCCCGATGATGAAAGTTG 1083  
 Db 909 GCGGTACCAAGATGGGAGATCTCTCTCCAGAGAGGTCCCGATGATGAAAGTTG 968  
 QY 1084 GCAGCTTCAATGAGAGAGTGGCCACAGAGAGTGTGAGAGCTGTGAGAGAGCCTGACTGAAG 1143  
 Db 969 GCAGCTTCAATGAGAGAGTGGCCACAGAGAGTGTGAGAGCTGTGAGAGAGCCTGACTGAAG 1028  
 QY 1144 AGATGGCGCTGGGGAGGCTTGGCGCTGCGCGCTGCACTGCTGGAGGGGAAAGATTT 1203  
 Db 1029 AGATGGCGCTGGGGAGGCTTGGCGCTGCGCGCTGCACTGCTGGAGGGGAAAGATTT 1088  
 QY 1204 AGATTCGACACAGGCTGTGGGTGATGTGCAATAGCTAATTTATTTCCCAAGGT 1263  
 Db 1089 AGATTCGACACAGGCTGTGGGTGATGTGCAATAGCTAATTTATTTCCCAAGGT 1148  
 QY 1264 GTGTGCTTTAAGGGTGGCTGACCAAGCTTTCTTCAATCTTTCCCAAGTTTCC 1323  
 Db 1149 GTGTGCTTTAAGGGTGGCTGACCAAGCTTTCTTCAATCTTTCCCAAGTTTCC 1208  
 QY 1324 CCTTGGCTTGAAGAGATGAGGTGTGATTTGTTCAGCTCCCGCAGGCTTTCTCA 1383  
 Db 1209 CCTTGGCTTGAAGAGATGAGGTGTGATTTGTTCAGCTCCCGCAGGCTTTCTCA 1268  
 QY 1384 GGCCTTCAAGCTGTGTGCTTGGAGAGTCAAGGAGGTTAACTGACAGAGAGCTTGGC 1443  
 Db 1269 GGCCTTCAAGCTGTGTGCTTGGAGAGTCAAGGAGGTTAACTGACAGAGAGCTTGGC 1328  
 QY 1444 ACCCTGTCCAGATTAATGGCTCTTGTGCTTCAACAGTTGGAGACAGCGTTGTCT 1503  
 Db 1329 ACCCTGTCCAGATTAATGGCTCTTGTGCTTCAACAGTTGGAGACAGCGTTGTCT 1388  
 QY 1504 ACATGCTTGTATTAATTTTGAAGGAGAGAGATGAAACATGTGAGTCTCCCTCTGA 1563

Db 1389 ACATGCTTTGATTAATTTGTTAGAGGAGAGATGAAACAATGTGAGTCTCCCTCTGA 1448  
 QY 1564 TTGTTTTGGGGAAATGTGAGAAAGAGTGCCTGCTTTGCAAAACATCACTGGCAAAA 1623  
 Db 1449 TTGTTTTGGGGAAATGTGAGAAAGAGTGCCTGCTTTGCAAAACATCACTGGCAAAA 1508  
 QY 1624 TGCAACAAGAAATTTTCCACGAGTCTTTCCATGGGCAATAGCTAGTGTCTTCAG 1683  
 Db 1509 TGCAACAAGAAATTTTCCACGAGTCTTTCCATGGGCAATAGCTAGTGTCTTCAG 1568  
 QY 1684 CTGTTGAGATGAATGTTCTGTTCACTGATTCATCATGTTTATTCACGACAGTG 1743  
 Db 1569 CTGTTGAGATGAATGTTCTGTTCACTGATTCATCATGTTTATTCACGACAGTG 1628  
 QY 1744 TTGCTCAGCTCTACCTCTGTCGACGAGGAGCATTTTCATTCACAGATCAATTCCTCT 1803  
 Db 1629 TTGCTCAGCTCTACCTCTGTCGACGAGGAGCATTTTCATTCACAGATCAATTCCTCT 1688  
 QY 1804 CTCAGCAGCTCTGAGGAGGAGGATCATGTTCTCTGTCATTCAGGATCTCAGAGCT 1863  
 Db 1689 CTCAGCAGCTCTGAGGAGGAGGATCATGTTCTCTGTCATTCAGGATCTCAGAGCT 1748  
 QY 1864 CAGAGACTGCAAGCTGCTTGCCCAATGACACAGCTAGTGAAGACCGAGAGCTTTCATC 1923  
 Db 1749 CAGAGACTGCAAGCTGCTTGCCCAATGACACAGCTAGTGAAGACCGAGAGCTTTCATC 1808  
 QY 1924 TGTTGTTGACTCTTAAGCTCAGTGTCTCTCCTACATCCACACAGGCTTGTCACCA 1983  
 Db 1809 TGTTGTTGACTCTTAAGCTCAGTGTCTCTCCTACATCCACACAGGCTTGTCACCA 1868  
 QY 1984 AAAGTGTCTCCCAAAAGAGAGAGAAATGGGATTTTTC--TTAGGAGTGCACATCTGGAA 2041  
 Db 1869 AAAGTGTCTCCCAAAAGAGAGAGAAATGGGATTTTTC--TTAGGAGTGCACATCTGGAA 1928  
 QY 2042 TTAAAGTCAAACTAATTTCTCATCCCTCTAAAGTAACTAGTGAAGACAGCAGTG 2101  
 Db 1929 TTAAAGTCAAACTAATTTCTCATCCCTCTAAAGTAACTAGTGAAGACAGCAGTG 1988  
 QY 2102 TTCTCAGTGTGGGAGGAGCCGCTCTTAATGAAGACATGATTTGAACCTGTCCTC 2161  
 Db 1989 TTCTCAGTGTGGGAGGAGCCGCTCTTAATGAAGACATGATTTGAACCTGTCCTC 2048  
 QY 2162 TTGGGAGTGTGATTAAGTACTTTGAAAGGATATGACTGAGCTAGCATACAGTTTAC 2221  
 Db 2049 TTGGGAGTGTGATTAAGTACTTTGAAAGGATATGACTGAGCTAGCATACAGTTTAC 2108  
 QY 2222 CTGCAGAAACAGTACTTAAGTAAATGTAAGGCGAGATTAATGAATTTGCAAAATC 2281  
 Db 2109 CTGCAGAAACAGTACTTAAGTAAATGTAAGGCGAGATTAATGAATTTGCAAAATC 2168  
 QY 2282 ACTTAGCAGCAACCTGAAGCAATTAATCAACAGTGAAGAAATCAAAACGAGCAGGCT 2341  
 Db 2169 ACTTAGCAGCAACCTGAAGCAATTAATCAACAGTGAAGAAATCAAAACGAGCAGGCT 2228  
 QY 2342 GTGTGAACATGTTGTAATATGCGACTGCAACACTGAACTCTACGCACTCCCAAAAT 2401  
 Db 2229 GTGTGAACATGTTGTAATATGCGACTGCAACACTGAACTCTACGCACTCCCAAAAT 2288  
 QY 2402 GATGTTTTCAGGTGTCATGAGCTGTGGCACCAGTATTCATCCAGGTTCTTAAAGTT 2461  
 Db 2289 GATGTTTTCAGGTGTCATGAGCTGTGGCACCAGTATTCATCCAGGTTCTTAAAGTT 2348  
 QY 2462 AAAGTTCAGCATGATTTGTAAGCAATGCTTTCTTGAATTTTAAATTAATGTAATCA 2521  
 Db 2349 AAAGTTCAGCATGATTTGTAAGCAATGCTTTCTTGAATTTTAAATTAATGTAATCA 2408  
 QY 2522 AGTTGCAATTTAAGAAATCAAGCTAAATCACTTCAACTGC 2560  
 Db 2409 AGTTGCAATTTAAGAAATCAAGCTAAATCACTTCAACTGC 2447

RESULT 25  
 AAV07906

ID AAV07906 standard; cDNA; 2479 BP.  
 AC AAV07906;  
 XX 18-JAN-1999 (first entry)  
 DT 18-JAN-1999 (first entry)  
 XX Human cysteine-rich secreted protein CRSP-1 cDNA.  
 DE  
 XX CRSP-1; cysteine-rich secreted protein 1; tumour; cancer; leukaemia;  
 KW tissue repair; wound healing; infection; Parkinson's disease;  
 KW Alzheimer's disease; Huntington's chorea; multiple sclerosis;  
 KW amyotrophic lateral sclerosis; pontine myelinolysis;  
 KW human immunodeficiency associated myelopathy; bulbar palsy;  
 KW spinal muscular atrophy; primary lateral sclerosis; poliomyelitis;  
 KW Fazio-Londe syndrome; Charcot-Marie-Tooth disease; therapy;  
 KW diagnosis; drug screening; human; CRSP-1; TANGO 59;  
 KW signal transduction; cell differentiation; cell proliferation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 FH CDS 38..1090  
 FT /tag= a  
 FT /note= "claimed fragment"  
 FT sig\_peptide 38..106  
 FT /tag= b  
 FT /note= "putative signal peptide sequence may span nucleotides 38-94, 38-100 or 38-106"  
 FT mat\_peptide 107..1087  
 FT /tag= b  
 FT /note= "putative mature protein sequence may span nucleotides 95-1087, 101-1087 or 107-1087"  
 PN W08846755-A1.  
 XX  
 PD 22-OCT-1998.  
 XX  
 PF 16-APR-1998; 98WO-US07894.  
 XX  
 PR 20-JAN-1998; 98US-0008802.  
 PR 16-APR-1997; 97US-0843704.  
 PR 17-APR-1997; 97US-0842898.  
 PR 15-JAN-1998; 98US-0071589.  
 XX  
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 XX  
 XX McCarthy SA;  
 PI  
 PT WPI; 1998-568730/48.  
 DR P-PSDB; AAW73016.  
 XX  
 PT New isolated cysteine-rich secreted proteins - used to develop  
 PT products for treating, e.g. hyperproliferative disorders, cancers,  
 PT wounds, infectious lesions, degenerative lesions or demyelating  
 PT diseases  
 XX  
 PS Claim 1; Page 89-91; 142pp; English.  
 XX  
 CC This full-length cDNA clone, the coding region for which is also  
 CC claimed and is deposited as ATCC 98634, codes for novel human  
 CC cysteine-rich secreted protein 1 (CRSP-1, see AAW73016), also  
 CC referred to as CRSP-1 and TANGO 59. A partial cDNA was isolated  
 CC using a signal sequence trap method from human foetal brain tissue  
 CC cDNA. This partial clone was then used to isolate the full-length  
 CC cDNA. CRSP-1 is expressed in a tissue-specific manner, with  
 CC highest expression in brain, heart and spinal cord. CRSP-1 was  
 CC used to identify human CRSP-2, CRSP-3, CRSP-4 and CRSP-like-1  
 CC cDNAs (see AAV07906-10). The CRSPs have at least 1 of the following  
 CC activities: (i) modulation of cellular signal transduction, either  
 CC in vitro or in vivo (e.g. antagonism of the activity of members of  
 CC the wnt family of secreted proteins or suppression of wnt-dependent  
 CC signal transduction); (ii) regulation of communication between cells





```

QY 1744 TTGCTCAGTCTCTACCTCTGTGTCAGGAGGAGCAATTTTCATATCCAAAGATCAATTCCTCT 1803
DB 1629 TTGCTCAGTCTCTACCTCTGTGTCAGGAGGAGCAATTTTCATATCCAAAGATCAATTCCTCT 1688
QY 1804 CTCAGACAGCTGGGGAGGGGGTCAATGTTCTCCGTCGTCACAGGATTCAGAGGCT 1863
DB 1689 CTCAGACAGCTGGGGAGGGGGTCAATGTTCTCCGTCGTCACAGGATTCAGAGGCT 1748
QY 1864 CAGAGACTGCAAGCTGCTTCCCAAGTCACAGCTAGTAGAGACCAAGAGCTTCATC 1923
DB 1749 CAGAGACTGCAAGCTGCTTCCCAAGTCACAGCTAGTAGAGACCAAGAGCTTCATC 1808
QY 1924 TGGTTGTAATCTTAAGTCAAGTCTCTCTCACTACCCACACACACCTTGGGCCACA 1983
DB 1809 TGGTTGTAATCTTAAGTCAAGTCTCTCTCACTACCCACACACACCTTGGGCCACA 1868
QY 1984 AAAGTGTCTCCCAAAAGAGAGAAATGGGATTTTTC--TTGAGGATGACATCTGAA 2041
DB 1869 AAAGTGTCTCCCAAAAGAGAGAAATGGGATTTTTC--TTGAGGATGACATCTGAA 1928
QY 2042 TTAAGGTCAACTAATTTCTCACTCCCTCTAAAGATTAATCTGTTAGAGACAGAGT 2101
DB 1929 TTAAGGTCAACTAATTTCTCACTCCCTCTAAAGATTAATCTGTTAGAGACAGAGT 1988
QY 2102 TTCTCAGAGTGGGGAGCGCTCTCTAATGAGACATATGACACTGTCCTC 2161
DB 1989 TTCTCAGAGTGGGGAGCGCTCTCTAATGAGACATATGACACTGTCCTC 2048
QY 2162 TTTGGCAGTTGCAATTAATCTTGAAGGATATGACAGCGTAGCATACAGGTTAAC 2221
DB 2049 TTTGGCAGTTGCAATTAATCTTGAAGGATATGACAGCGTAGCATACAGGTTAAC 2108
QY 2222 CTGAGAAACAGTACTAGGTAATTTGAGGCGAGGATTAATGAAATTTGCAAAATC 2281
DB 2109 CTGAGAAACAGTACTAGGTAATTTGAGGCGAGGATTAATGAAATTTGCAAAATC 2168
QY 2282 ACTTAGCAGCACTGAAGACAAATTAATACACAGTGGAGAAATCAACCCAGCAGGCT 2341
DB 2169 ACTTAGCAGCACTGAAGACAAATTAATACACAGTGGAGAAATCAACCCAGCAGGCT 2228
QY 2342 GTGTAACAACTGGTGTAAATATGAGATGGAACACTGAACTTAGGCCACTCCAAAT 2401
DB 2229 GTGTAACAACTGGTGTAAATATGAGATGGAACACTGAACTTAGGCCACTCCAAAT 2288
QY 2402 GATGTTTTCAGGTGTCATGACTGTGTCACCAATGATTCATCCAGATTCCTAAAGTT 2461
DB 2289 GATGTTTTCAGGTGTCATGACTGTGTCACCAATGATTCATCCAGATTCCTAAAGTT 2348
QY 2462 AAAGTTCACATGATTTGTAATGAGATGCTCTTCTTTGAGTTTAAATATGTAATACATA 2521
DB 2349 AAAGTTCACATGATTTGTAATGAGATGCTCTTCTTTGAGTTTAAATATGTAATACATA 2408
QY 2522 AGTGCATTTTGAATCAAGCATTAATCACTTCAACTGC 2560
DB 2409 AGTGCATTTTGAATCAAGCATTAATCACTTCAACTGC 2447

```

RESULT 26  
 AA75128  
 ID AA75128 standard; cDNA; 2479 BP.

XX AAA75128;

XX 15-JAN-2001 (first entry)

DE cDNA encoding a human Dickkopf (Dkk)-3 protein.

KW Human; Dickkopf-3 protein; Dkk-3 protein; Soggy protein; optic disorder;  
 KW cysteine-rich secreted protein; glaucoma; conjunctivitis; brain disorder;  
 KW Alzheimer's disease; epilepsy; amnesia; inflammation; pulmonary disorder;  
 KW skeletal muscle disorder; Goodpasture's syndrome;  
 KW cardiovascular disorder; hyperproliferative disorder; cancer; ss.

```

OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 38..1090
FT /*tag= a
FT /*product= "Dickkopf (Dkk)-3 protein"
FT sig_peptide 38..109
FT /*tag= b
PN WO20052047-A2.
PN 08-SEP-2000.
PD 03-MAR-2000; 2000MO-US05452.
PR 05-MAR-1999; 99US-0263022.
PA (MILL-) MILLENNIUM PHARM INC.
PI McCarthy S;
PI WPI; 2000-579276/54.
DR P-PSDB; AAB08874.
XX Human Dickkopf (Dkk) and Soggy nucleic acids and proteins, useful as
XX modulating agents in regulating cellular processes and particularly for
XX treating disorders characterized by aberrant expression or activity of
XX Dkk, e.g. Alzheimer's, -
XX Claim 2; Fig 1A-B; 208bp; English.
XX
XX The present sequence encodes a human Dickkopf (Dkk)-3 protein. The
XX specification also describes Soggy (Dkk-related) sequences. Dkk is a
XX cysteine-rich secreted protein. The Dkk nucleic acids and proteins are
XX useful as modulating agents in regulating cellular processes. They are
XX particularly useful in treating subjects having a disorder characterized
XX by aberrant expression or activity of Dkk such as optic disorders
XX (glaucoma, conjunctivitis), brain disorders (Alzheimer's disease,
XX epilepsy, amnesia), inflammation, skeletal muscle disorders, pulmonary
XX disorders (Goodpasture's syndrome), cardiovascular disorders, and
XX hyperproliferative disorders (cancer). The Dkk proteins and nucleic
XX acids may also be used for research purposes, such as for chromosome
XX mapping, tissue typing and in screening assays to identify modulators.
XX
XX Sequence 2479 BP; 627 A; 619 C; 665 G; 567 T; 1 other;

```

Query Match 75.4%; Score 1951; DB 21; Length 2479;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 2431; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

```

QY 124 GGGGCGGCGGCTGCGGGCGCAGAGCGGATGCAAGCGGCTTGGGGCCACCTGCTGTGCC 183
DB 9 GGGGCGGCGGCTGCGGGCGCAGAGCGGATGCAAGCGGCTTGGGGCCACCTGCTGTGCC 68
QY 184 TGCCTGCGGCGGCGGCTGCGGGCGCAGAGCGGATGCAAGCGGCTTGGGGCCACCTGCTGTGCC 243
DB 69 TGCCTGCGGCGGCGGCTGCGGGCGCAGAGCGGATGCAAGCGGCTTGGGGCCACCTGCTGTGCC 128
QY 244 CAGTCAAGCCCGCGGCGGCTGCTCAAGCTTCCGAGAGAGAGGCCACCTCATATAGATGT 303
DB 129 CAGTCAAGCCCGCGGCGGCTGCTCAAGCTTCCGAGAGAGAGGCCACCTCATATAGATGT 188
QY 304 TCCGCGAGGTTGAGGAATGTAATGAGAGCAGCGACCAATTTGGCGAGCGCGGTGGAAG 363
DB 189 TCCGCGAGGTTGAGGAATGTAATGAGAGCAGCGACCAATTTGGCGAGCGCGGTGGAAG 248
QY 364 AGATGAGGCGAAGAGAGCTGCTTAAGCATATCAAGAGTAAGTAACTGGCAAACTTAC 423
DB 249 AGATGAGGCGAAGAGAGCTGCTGTAAGCATATCAAGAGTAAGTAACTGGCAAACTTAC 308
QY 424 CTCCTCAGTATCACAGTATGAGCAACACAGACAGAGAGTGAATTAATCATTCATG 483
DB 309 CTCCTCAGTATCACAGTATGAGCAACACAGACAGAGAGTGAATTAATCATTCATG 368

```

QY 484 TGACCCGGAATTCACAGATAACCAACACAGACTGACCAATGGTCTTTACAGA 543  
DB 369 TGCAACCGAATTCACAGATTAACCAACACAGACTGACCAATGGTCTTTACAGA 428  
QY 544 CAGTTATCACTCTGTGGAGACGAGAGAGGACAGAGAGGACAGAGTGCATCATCAG 603  
DB 429 CAGTTATCACTCTGTGGAGACGAGAGAGGACAGAGAGGACAGAGTGCATCATCAG 488  
QY 604 AGGACTGGGGCCAGAGATGATGACGCTTGGCAGCTTCAGTACACCGGACGACAT 663  
DB 489 AGGACTGGGGCCAGAGATGATGACGCTTGGCAGCTTCAGTACACCGGACGACAT 548  
QY 664 GCCGGGACAGAGATGCTGTGACCCCGGACAGTGAATGCTGTGAGACCAAGCTGTGTG 723  
DB 549 GCCGGGACAGAGATGCTGTGACCCCGGACAGTGAATGCTGTGAGACCAAGCTGTGTG 608  
QY 724 TCTGGGCTCACTGACCAAAATGGCCACAGGGGACAGATGGGACATCTGTGACCAAC 783  
DB 609 TCTGGGCTCACTGACCAAAATGGCCACAGGGGACAGATGGGACATCTGTGACCAAC 668  
QY 784 AGAGGACTGCGCAGCCGGGCTGTGTGCTGTGCTTCCAGAGAGGCTGTGTCTGTGT 843  
DB 669 AGAGGACTGCGCAGCCGGGCTGTGTGCTGTGCTTCCAGAGAGGCTGTGTCTGTGT 728  
QY 844 GCACACCCCTGCGCTGTGAGGGGACGCTTGTGCATGACCCCGCAGCCGCTTGTGAGAC 903  
DB 729 GCACACCCCTGCGCTGTGAGGGGACGCTTGTGCATGACCCCGCAGCCGCTTGTGAGAC 788  
QY 904 TCATCACTGGGAGGTAGAGCTGTGATGAGAGCTTGGACCGATGCTTGTGCTGTGCTGT 963  
DB 789 TCATCACTGGGAGGTAGAGCTGTGATGAGAGCTTGGACCGATGCTTGTGCTGTGCTGT 848  
QY 964 TCTCTGTGACCCGACAGCAAGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1023  
DB 849 TCTCTGTGACCCGACAGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 908  
QY 1024 GCCCGTACCAAGATGGGAGATCTGTGCTGCCAGAGAGGTCCCGATGAGATGAGTTG 1083  
DB 909 GCCCGTACCAAGATGGGAGATCTGTGCTGCCAGAGAGGTCCCGATGAGATGAGTTG 968  
QY 1084 GCAGCTTATGAGAGAGGTGCGCCAGAGAGTGTGAGAGACCTGTGAGAGAGGCTGTGAG 1143  
DB 969 GCAGCTTATGAGAGAGGTGCGCCAGAGAGTGTGAGAGACCTGTGAGAGAGGCTGTGAG 1028  
QY 1144 AGATGGGCTGTGGGGAGGCTGTGCGCTGTGCGCGCTGTGCACTGTGGAGGGGAAAGATT 1203  
DB 1029 AGATGGGCTGTGGGGAGGCTGTGCGCTGTGCGCGCTGTGCACTGTGGAGGGGAAAGATT 1088  
QY 1204 AGATCTGACCAAGGCTGTGGGTAGATGTGCAATGAAATAGCTAATTTATTTCCCAAGT 1263  
DB 1089 AGATCTGACCAAGGCTGTGGGTAGATGTGCAATGAAATAGCTAATTTATTTCCCAAGT 1148  
QY 1264 GTGTCTTTAGGCGGTGGGCTGACCAAGGCTTCTTCTCAATCTTCTTCCCAAGTGTTC 1323  
DB 1149 GTGTCTTTAGGCGGTGGGCTGACCAAGGCTTCTTCTCAATCTTCTTCCCAAGTGTTC 1208  
QY 1324 CCTCTGCTTGAACAGATGAGGTGTGTGCAATTTGTCAAGCTGCCCAAGGCTGTTCCTCA 1383  
DB 1209 CCTCTGCTTGAACAGATGAGGTGTGTGCAATTTGTCAAGCTGCCCAAGGCTGTTCCTCA 1268  
QY 1384 GGCTTCAACAGTCTGT 1443  
DB 1269 GGCTTCAACAGTCTGT 1328  
QY 1444 ACCCTGTGCAAGATTTAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1503  
DB 1329 ACCCTGTGCAAGATTTAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1388  
QY 1504 ACATGGCTTTGATTAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1563  
DB 1389 ACATGGCTTTGATTAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1448

QY 1564 TTGGTTTGGGGAAATGTGAGAGAGTGCCTGTGTTGCCAAACATCAACTGGCAAAA 1623  
DB 1449 TTGGTTTGGGGAAATGTGAGAGAGTGCCTGTGTTGCCAAACATCAACTGGCAAAA 1508  
QY 1624 TGCAACAAATGAATTTTCCAGCAGGCTTCTTTCATGTGGGACATGTAAGTGTGCTTCA 1683  
DB 1509 TGCAACAAATGAATTTTCCAGCAGGCTTCTTTCATGTGGGACATGTAAGTGTGCTTCA 1568  
QY 1684 CTGTTCAGATGAATGTTCTGTGACCTGTGACCTGTGACCTGTGACCTGTGACCTGTG 1743  
DB 1569 CTGTTCAGATGAATGTTCTGTGACCTGTGACCTGTGACCTGTGACCTGTGACCTGTG 1628  
QY 1744 TTGCTCAGCTCTTACTCTGTGTGCGCAGGGGACGATTTTCATATCCAAATTCCTCT 1803  
DB 1629 TTGCTCAGCTCTTACTCTGTGTGCGCAGGGGACGATTTTCATATCCAAATTCCTCT 1688  
QY 1804 CTCAGACAGCCCTGGGGAGAGGGGGGTATGTTTCCTCCGTCATCCAGGGATCTCAGAGGT 1863  
DB 1689 CTCAGACAGCCCTGGGGAGAGGGGGGTATGTTTCCTCCGTCATCCAGGGATCTCAGAGGT 1748  
QY 1864 CAGAGACTGCAAGCTGCTTGTGCCAAGTCAACAGCTAGTGAAGACCAAGAGTTTCATC 1923  
DB 1749 CAGAGACTGCAAGCTGCTTGTGCCAAGTCAACAGCTAGTGAAGACCAAGAGTTTCATC 1808  
QY 1924 TGGTGTGACTCTAAGCTCAGTGTCTCTCTCACTACCCCAACAGCCTGTGGTGCACCA 1983  
DB 1809 TGGTGTGACTCTAAGCTCAGTGTCTCTCTCACTACCCCAACAGCCTGTGGTGCACCA 1868  
QY 1984 AAAGTCTCCCCAAAAGAGAGAGATGGATTTTTC - TTGAGGATGACATCTGGA 2041  
DB 1869 AAAGTCTCCCCAAAAGAGAGAGATGGATTTTTC - TTGAGGATGACATCTGGA 1928  
QY 2042 TTAAAGTCAACTAATTTCTCAATCCTTTAAAGTAACTCTGTAGGAACAGAGTG 2101  
DB 1929 TTAAAGTCAACTAATTTCTCAATCCTTTAAAGTAACTCTGTAGGAACAGAGTG 1988  
QY 2102 TTCTCAGTGTGGGGCAGCCGCTCTTCTAATGAAGACATATATTGACCTGTCCCTC 2161  
DB 1989 TTCTCAGTGTGGGGCAGCCGCTCTTCTAATGAAGACATATATTGACCTGTCCCTC 2048  
QY 2162 TTGTGCAATTTGCTAATGTAATCTTTGAAAGTATATGACTGAGCTGTACATCAAGTTAAC 2221  
DB 2049 TTGTGCAATTTGCTAATGTAATCTTTGAAAGTATATGACTGAGCTGTACATCAAGTTAAC 2108  
QY 2222 CTGCAGAAACAGACTTAGTATTTGTAGGGGAGAGATTATATGAAATTTGCAAAATC 2281  
DB 2109 CTGCAGAAACAGACTTAGTATTTGTAGGGGAGAGATTATATGAAATTTGCAAAATC 2168  
QY 2282 ACTTAGACCAACTGAGACAAATTAATCAACAGCTGAGAGAAATCAACCGAGCAGGCT 2341  
DB 2169 ACTTAGACCAACTGAGACAAATTAATCAACAGCTGAGAGAAATCAACCGAGCAGGCT 2228  
QY 2342 GTGTGAAGATGTTGTAATATGCGACTGCGAACTGAACTCTAGCCACTCCCAAT 2401  
DB 2229 GTGTGAAGATGTTGTAATATGCGACTGCGAACTGAACTCTAGCCACTCCCAAT 2288  
QY 2402 GATGTTTCAAGTGTCAAGAGCTGTGCAACATGATTCATCCAGAGTCTTAAAGTT 2461  
DB 2289 GATGTTTCAAGTGTCAAGAGCTGTGCAACATGATTCATCCAGAGTCTTAAAGTT 2348  
QY 2462 AAAGTGCACATGATGTAAGCAATGCTTCTTGAAGTTAAATTAATGTAATTAACATA 2521  
DB 2349 AAAGTGCACATGATGTAAGCAATGCTTCTTGAAGTTAAATTAATGTAATTAACATA 2408  
QY 2522 AGTTGATTTAGAAATCAAGACATAATCACTTCAACTGC 2560  
DB 2409 AGTTGATTTAGAAATCAAGACATAATCACTTCAACTGC 2447

RESULT 27  
AB281839  
ID AB281839 standard; DNA; 2124 BP.  
XX



QY 1751 GCTCTACTCTGTGCGGAGGAGCATTTTTCATATCCAAATGCAATTCCTCTCTGCA 1810  
 DB 1321 GCTCTACTCTGTGCGGAGGAGCATTTTTCATATCCAAATGCAATTCCTCTCTGCA 1380  
 QY 1811 CAGCTGGGAGGAGGAGGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1869  
 DB 1381 CAGCTGGGAGGAGGAGGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1440  
 QY 1870 CTGCAAGCTGCTGCGGAGGAGGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1329  
 DB 1441 CTGCAAGCTGCTGCGGAGGAGGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1500  
 QY 1930 TGACTCTAGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1989  
 DB 1501 TGACTCTAGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1560  
 QY 1990 CTCCCAAAAGGAGGAGGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2047  
 DB 1561 CTCCCAAAAGGAGGAGGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1620  
 QY 2048 TCAACTATTTCTGACATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2107  
 DB 1621 TCAACTATTTCTGACATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1680  
 QY 2108 CAGTGTGGGAGGAGGAGGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2167  
 DB 1681 CAGTGTGGGAGGAGGAGGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740  
 QY 2168 AGTTCATTTAGTATCTTGAAGGATTTGAGGATTTGAGGATTTGAGGATTTGAGG 2227  
 DB 1741 AGTTCATTTAGTATCTTGAAGGATTTGAGGATTTGAGGATTTGAGGATTTGAGG 1800  
 QY 2228 AAACAGTATTAGTATTTGAGGAGGATTTGAGGATTTGAGGATTTGAGGATTT 2287  
 DB 1801 AAACAGTATTAGTATTTGAGGAGGATTTGAGGATTTGAGGATTTGAGGATTT 1860  
 QY 2288 CAGCACTGAGGAGGATTTGAGGAGGATTTGAGGATTTGAGGATTTGAGGATTT 2347  
 DB 1861 CAGCACTGAGGAGGATTTGAGGAGGATTTGAGGATTTGAGGATTTGAGGATTT 1920  
 QY 2348 AACATGTTGATTTGAGGAGGATTTGAGGATTTGAGGATTTGAGGATTTGAGG 2407  
 DB 1921 AACATGTTGATTTGAGGAGGATTTGAGGATTTGAGGATTTGAGGATTTGAGG 1980  
 QY 2408 TTGAGGTGATGAGGATTTGAGGAGGATTTGAGGATTTGAGGATTTGAGGATTT 2467  
 DB 1981 TTGAGGTGATGAGGATTTGAGGAGGATTTGAGGATTTGAGGATTTGAGGATTT 2040  
 QY 2468 GCACATGATTTGATTTGAGGAGGATTTGAGGATTTGAGGATTTGAGGATTTG 2527  
 DB 2041 GCACATGATTTGATTTGAGGAGGATTTGAGGATTTGAGGATTTGAGGATTTG 2100  
 QY 2528 ATTGAGAAATCAAGCATTAATAC 2551  
 DB 2101 ATTGAGAAATCAAGCATTAATAC 2124  
 RESULT 28  
 ID AAD52567 standard; DNA; 2124.BP.  
 AC AAD52567;  
 XX  
 DT 02-MAY-2003 (first entry)  
 XX  
 DE DK 3 DNA.  
 XX  
 KW Drug screening; toxicology assay; signalling pathway; DK 3; gene; ds.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers

FT CDS 2..775  
 FT /\*tag= a  
 FT /product= "DK 3 protein"  
 FT /transl\_except= (pos:2..4, aa:aa)  
 FT /note= "Xaa corresponds to amino acids 1-94 of DK 3  
 FT protein (AAE34069); CDS does not include start codon"  
 FT /partial  
 PN MO20029092-A2.  
 PD 14-NOV-2002.  
 XX  
 XX 29-APR-2002; 2002WO-GB01946.  
 PF  
 PR 04-MAY-2001; 2001GB-0011004.  
 XX  
 PA (AXOR-) AXORDIA LTD.  
 FT Andrews P, Draper J, Walsh J;  
 XX  
 XX WPI; 2003-120579/11.  
 DR P-PSDB; AAE34069.  
 XX  
 PT Identifying biologically active agents comprises cloning transfected  
 PT cells into a cell array, exposing the array to an agent to be tested,  
 PT and detecting signals generated by a reporter molecule as a result of  
 PT exposure to the agent  
 PT  
 PS Claim 19; Fig 89; 90p; English.  
 XX  
 CC The present invention relates to a novel screening method which enables  
 CC the identification of biologically active agents which mediate their  
 CC effect through the activation of genes. The method involves providing a  
 CC population of cells stably transfected with a nucleic acid encoding a  
 CC reporter molecule, cloning the transfected cells into a cell array,  
 CC exposing the array to at least one agent to be tested and detecting a  
 CC signal generated by the reporter molecule as a result of exposure to  
 CC the agent. The method is useful in identifying biologically active agents  
 CC and the genes through which the agents act, in screening potential drugs  
 CC for their ability to activate certain drug targets in a high-throughput  
 CC assay. In identifying relationships between signalling pathways and  
 CC specific signals that could be useful in eventually directing the  
 CC differentiation of embryonic stem cells and in toxicology assays by  
 CC testing for unwanted activation or inhibition of specific signalling  
 CC pathways. The present sequence is DK 3 DNA used to illustrate the  
 CC method of the invention.  
 CC  
 XX  
 SQ Sequence 2124 BP; 528 A; 516 C; 558 G; 521 T; 1 other;  
 Query Match 70.4%; Score 1821; DB 25; Length 2124;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 2121; Conservative 0; Mismatches 0; Indels 3; Gaps 2;  
 QY 431 CTATCAATGAGACCAACCAACGAGGATTTGAGGATTTGAGGATTTGAGGATTT 490  
 DB 1 CTATCAATGAGACCAACCAACGAGGATTTGAGGATTTGAGGATTTGAGGATTTGAGG 60  
 QY 491 AGAATTCACAAGATTAACAACAACGAGGATTTGAGGATTTGAGGATTTGAGGATTT 550  
 DB 61 AGAATTCACAAGATTAACAACAACGAGGATTTGAGGATTTGAGGATTTGAGGATTT 120  
 QY 551 CACATCTGTGGAGAGCAAAAGGAGGAGGATTTGAGGATTTGAGGATTTGAGGATTT 610  
 DB 121 CACATCTGTGGAGAGCAAAAGGAGGAGGATTTGAGGATTTGAGGATTTGAGGATTT 180  
 QY 611 TGGGCCAGAGTATGTCAGGATTTGAGGATTTGAGGATTTGAGGATTTGAGGATTT 670  
 DB 181 TGGGCCAGAGTATGTCAGGATTTGAGGATTTGAGGATTTGAGGATTTGAGGATTT 240  
 QY 671 CCAGAGGATGCTGCAACCCGAGGAGGATTTGAGGATTTGAGGATTTGAGGATTTG 730  
 DB 241 CCAGAGGATGCTGCAACCCGAGGAGGATTTGAGGATTTGAGGATTTGAGGATTTG 300

QY 731 TCACGACCAAAATGCGCCACCAAGGGGAGCAATGGGACCATCTGTGACCAACCAAGGGA 790  
 DB 301 TCACGACCAAAATGCGCCACCAAGGGGAGCAATGGGACCATCTGTGACCAACCAAGGGA 360  
 QY 791 CTGCGCAGCGGGGCTGTGTGTGCTTCCAGAGAGGCTGTGTGTGCTGTGTGCAACC 850  
 DB 361 CTGCGCAGCGGGGCTGTGTGTGCTTCCAGAGAGGCTGTGTGTGCTGTGTGCAACC 420  
 QY 851 CCGGCCCGTGGAGGGGAGCTTGGCATGACCCCGCAGCGGCTTCTGGAACCTATCAG 910  
 DB 421 CCGGCCCGTGGAGGGGAGCTTGGCATGACCCCGCAGCGGCTTCTGGAACCTATCAG 480  
 QY 911 CTGGAGAGCTGAGCCTGATGAGACCTTGAACCGATGCTGTGTGCAAGTGTGCTGTG 970  
 DB 481 CTGGAGAGCTGAGCCTGATGAGACCTTGAACCGATGCTGTGTGCAAGTGTGCTGTG 540  
 QY 971 CCAAGCCCAACGACCAAGCCTGTGTGATGTGTGCAAGCGGACCTTGTGTGGAGCCGTGA 1030  
 DB 541 CCAAGCCCAACGACCAAGCCTGTGTGATGTGTGCAAGCGGACCTTGTGTGGAGCCGTGA 600  
 QY 1031 CCAAGATGGGAGAGATCTGTGTGCTCCAGAGAGGTCCCGATGATGATGAAGTTGGCAGCTT 1090  
 DB 601 CCAAGATGGGAGAGATCTGTGTGCTCCAGAGAGGTCCCGATGATGATGAAGTTGGCAGCTT 660  
 QY 1091 CATGAGAGAGGTGCGCAGAGAGCTGTGAGAGACCTGTGATGAGAGAGATGAG 1150  
 DB 661 CATGAGAGAGGTGCGCAGAGAGCTGTGAGAGACCTGTGATGAGAGAGATGAG 720  
 QY 1151 GCTGGGGAGAGCCTGCGGCTGCGCCGCTGCACTGTGTGGAGGGAGAGATTTAGATCTG 1210  
 DB 721 GCTGGGGAGAGCCTGCGGCTGCGCCGCTGCACTGTGTGGAGGGAGAGATTTAGATCTG 780  
 QY 1211 GACCAAGCTGTGTGATGATGATGCAATGAAATAGCTAATTTATTTCCCGAGGTGTGCT 1270  
 DB 781 GACCAAGCTGTGTGATGATGATGCAATGAAATAGCTAATTTATTTCCCGAGGTGTGCT 840  
 QY 1271 TTAGGCGTGGGCTGACAGAGCTTCTTCTCATCTTCTTCCAGTAGATTCCCTCTG 1330  
 DB 841 TTAGGCGTGGGCTGACAGAGCTTCTTCTCATCTTCTTCCAGTAGATTCCCTCTG 900  
 QY 1331 CTGACAGCATGAGGTGTGTGCAATTTGTCAGTCTCCCGAGGCTGTGTCTCCAGGCTTCA 1390  
 DB 901 CTGACAGCATGAGGTGTGTGCAATTTGTCAGTCTCCCGAGGCTGTGTCTCCAGGCTTCA 960  
 QY 1391 CAGCTGTGTGTGGAGAGCTCAGGAGGGTTAACTGACAGAGCACTTTGCCACCCCTG 1450  
 DB 961 CAGCTGTGTGTGGAGAGCTCAGGAGGGTTAACTGACAGAGCACTTTGCCACCCCTG 1020  
 QY 1451 TCCAGATTATGCGTGTGCTTCTCTACCAAGTTGGCAGAGCGGTTGTCTTACATGTC 1510  
 DB 1021 TCCAGATTATGCGTGTGCTTCTCTCTACCAAGTTGGCAGAGCGGTTGTCTTACATGTC 1080  
 QY 1511 TTTGATTAATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCCTGATGTGTT 1570  
 DB 1081 TTTGATTAATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCCTGATGTGTT 1140  
 QY 1571 TGGGGAATGTGAGAGAGTGCCTGCTTTCACAAACATCACTGTGCAAAATGACACA 1630  
 DB 1141 TGGGGAATGTGAGAGAGTGCCTGCTTTCACAAACATCACTGTGCAAAATGACACA 1200  
 QY 1631 AATGAAATTTTCCAGCAGTCTTCTTCATGAGGCAATGTAACCTGTGCTGAGTGTG 1690  
 DB 1201 AATGAAATTTTCCAGCAGTCTTCTTCATGAGGCAATGTAACCTGTGCTGAGTGTG 1260  
 QY 1691 AGATGAATGTCTGTTCACCTGATACATGATGTTTATTCATCCAGCAGTGTGTGCTCA 1750  
 DB 1261 AGATGAATGTCTGTTCACCTGATACATGATGTTTATTCATCCAGCAGTGTGTGCTCA 1320  
 QY 1751 GCTCTTACCTGTGTGCGCAGGGGAGCATTTTCAATCCAAAGTCAATTTCCCTCTTCAGCA 1810  
 DB 1321 GCTCTTACCTGTGTGCGCAGGGGAGCATTTTCAATCCAAAGTCAATTTCCCTCTTCAGCA 1380  
 QY 1811 CAGCTGGGAGGGGGTCAATTGTCTCTCTGTCATCAAGGATCTCAGAGG-CTCAGAGA 1869

DB 1381 CAGCTGGGAGGGGGTCAATTGTCTCTCTGTCATCAGGAGATCTCAGAGNCTCAGAGA 1440  
 QY 1870 CTGCAAGCTCTTGGCCCAAGTTCACAGCTAGTGAAGACAGAGCAGATTTCATCTGTTG 1529  
 DB 1441 CTGCAAGCTCTTGGCCCAAGTTCACAGCTAGTGAAGACAGAGCAGATTTCATCTGTTG 1500  
 QY 1930 TGACTCTAAGCTCAGTCTCTCTCTACCTACCCCAACAGCCTTGTGTGCAACCAAGTG 1589  
 DB 1501 TGACTCTAAGCTCAGTCTCTCTCTACCTACCCCAACAGCCTTGTGTGCAACCAAGTG 1560  
 QY 1990 CTCCCAAAAGAGAGAGATGGAGATTTTC--TTGAGGATGACACTGTGAATTAGG 2047  
 DB 1561 CTCCCAAAAGAGAGAGATGGAGATTTTC--TTGAGGATGACACTGTGAATTAGG 1620  
 QY 2048 TCAAACTAATCTCAGATCCCTCTTAAAGTAACTACTGTGAGACAGCAGTGTCTCA 2107  
 DB 1621 TCAAACTAATCTCAGATCCCTCTTAAAGTAACTACTGTGAGACAGCAGTGTCTCA 1680  
 QY 2108 CAGTGTGGGAGAGCCGCTCTCTTAAGTGAACATGATTAATGACATGTCCTCTTGGC 2167  
 DB 1681 CAGTGTGGGAGAGCCGCTCTCTTAAGTGAACATGATTAATGACATGTCCTCTTGGC 1740  
 QY 2168 AGTGCATTAGTAATCTTGAAGGTATATGACTGAGGTCATACAGTTAACTCAG 2227  
 DB 1741 AGTGCATTAGTAATCTTGAAGGTATATGACTGAGGTCATACAGTTAACTCAG 1800  
 QY 2228 AAACAGTACTTAAGTAATTTGAGGCGAGATTTAAATGAATTTGCAAAATCAGTTAG 2287  
 DB 1801 AAACAGTACTTAAGTAATTTGAGGCGAGATTTAAATGAATTTGCAAAATCAGTTAG 1860  
 QY 2288 CAGCACTGAAGACATTAATCAACAGTGAAGAAATCAAAACGAGAGGCTGTGTGA 2347  
 DB 1861 CAGCACTGAAGACATTAATCAACAGTGAAGAAATCAAAACGAGAGGCTGTGTGA 1920  
 QY 2348 AACATGTTGTATATGAGACTGCGAATCTGAATCTAACCCACTCCAAAGATGT 2407  
 DB 1921 AACATGTTGTATATGAGACTGCGAATCTGAATCTAACCCACTCCAAAGATGT 1980  
 QY 2408 TTCAGGTGTCATGAGCTGTGCCACATGATATTCAGAGTCTTAAAGTTAAAGTT 2467  
 DB 1981 TTCAGGTGTCATGAGCTGTGCCACATGATATTCAGAGTCTTAAAGTTAAAGTT 2040  
 QY 2468 GCACATGATTTGATTAAGATGCTTTCTTGAATTTAAATATGATTAACATAGTTC 2527  
 DB 2041 GCACATGATTTGATTAAGATGCTTTCTTGAATTTAAATATGATTAACATAGTTC 2100  
 QY 2528 ATTGAAATCAAGCATTAATCAG 2551  
 DB 2101 ATTGAAATCAAGCATTAATCAG 2124

RESULT 29  
 ABX75346  
 ID ABX75346 standard; cDNA; 2124 BP.  
 AC ABX75346;  
 DT 25-MAR-2003 (first entry)  
 DE Human cDNA encoding secreted frizzled related protein 4.  
 XX  
 XX Gene; Notch; Wnt; embryonic stem cell; embryogenesis; ss;  
 XX differentiation; ligand; Parkinson's disease; Huntington's disease;  
 XX motor neuron disease; heart disease; diabetes; liver disease; human;  
 XX cleftosis; renal disease; AIDS; acquired immunodeficiency syndrome.  
 OS Homo sapiens.  
 XX  
 XX W0200277204-A2.  
 XX  
 XX 03-OCT-2002.  
 XX





Db	1141	TGGGGAAATGTGGAGAGAGTGCCCTTGCTTTGGCAACATCAACCTGGGCAAAAATGCAACA	1200
Qy	1631	AATGAATTTTCCAGGCACTTCTTTCCATGGGCAATAGTAAGCTGTGCGCTTCAAGCTGTGCG	1690
Db	1201	AATGAATTTTCCAGGCACTTCTTTCCATGGGCAATAGTAAGCTGTGCGCTTCAAGCTGTGCG	1260
Qy	1691	AGATGAATTTGTCTGTGTCACCCCTGATTTACATGATGTGTTATTCACTCCAGAGATGTGCTCA	1750
Db	1261	AGATGAATTTGTCTGTGTCACCCCTGATTTACATGATGTGTTATTCACTCCAGAGATGTGCTCA	1320
Qy	1751	GCTGCTACTCTGTGCGCCAGGGCAGACATTTTCAATGCCAGATCAATTCCTCTCTCAGCA	1810
Db	1321	GCTGCTACTCTGTGCGCCAGGGCAGACATTTTCAATGCCAGATCAATTCCTCTCTCAGCA	1380
Qy	1811	CAGCCTGGGGAAGGGGGTCAATGTGTTCTCCTGATCATCAGGATCTCAGAG - CTCAGAGA	1869
Db	1381	CAGCCTGGGGAAGGGGGTCAATGTGTTCTCCTGATCATCAGGATCTCAGAG - CTCAGAGA	1440
Qy	1870	CTGCAAGCTGCTGTGCCCAATGCAACAAGCATAGTAAGACCAAGAGAGTTTCACTGTGCTG	1929
Db	1441	CTGCAAGCTGCTGTGCCCAATGCAACAAGCATAGTAAGACCAAGAGAGTTTCACTGTGCTG	1500
Qy	1930	TGACTCTAAGCTCACTGCTCTCTCCACTACCCCAACACAGCCTTGCTGCGACCAAAAGTG	1989
Db	1501	TGACTCTAAGCTCACTGCTCTCTCCACTACCCCAACACAGCCTTGCTGCGACCAAAAGTG	1560
Qy	1990	CTCCCCAAAGGAAGGAATGGGATTTTTC - TTGAGGATGCAACATGTGGAATTAAG	2047
Db	1561	CTCCCCAAAGGAAGGAATGGGATTTTTC - TTGAGGATGCAACATGTGGAATTAAG	1620
Qy	2048	TCAAACTAATTCACATCCCTCTAAAAGTAACATGTTAGGAACAGCAGCTGTCTCA	2107
Db	1621	TCAAACTAATTCACATCCCTCTAAAAGTAACATGTTAGGAACAGCAGCTGTCTCA	1680
Qy	2108	CAGTGTGGGGGACCGGCTCTCTAATGAAGCAATGATATTAACAATGTCCTCTTTGAC	2167
Db	1681	CAGTGTGGGGGACCGGCTCTCTAATGAAGCAATGATATTAACAATGTCCTCTTTGAC	1740
Qy	2168	AGTTGATTAGTAACCTTTGAAAAGGTAATGAATGACGTGAGCATACAGGTTAACTGCAG	2227
Db	1741	AGTTGATTAGTAACCTTTGAAAAGGTAATGAATGACGTGAGCATACAGGTTAACTGCAG	1800
Qy	2228	AAACAGTACTTAAGTAATGTTAGGGCCAGGATTTAAATGAATTTGCAAAATCACTTAC	2287
Db	1801	AAACAGTACTTAAGTAATGTTAGGGCCAGGATTTAAATGAATTTGCAAAATCACTTAC	1860
Qy	2288	CAGCAACTGAAAGACATTAATACACAGGTGAGAAAATCAACCGAGCAAGGCTGTGTGA	2347
Db	1861	CAGCAACTGAAAGACATTAATACACAGGTGAGAAAATCAACCGAGCAAGGCTGTGTGA	1920
Qy	2348	AACATGTTGTAAATGAGACCTGGGACACTGAACCTTAAGCAGCTCCCAAAATGATGT	2407
Db	1921	AACATGTTGTAAATGAGACCTGGGACACTGAACCTTAAGCAGCTCCCAAAATGATGT	1980
Qy	2408	TTCAAGGTGTCATGACTGTGTGCAACATGATTTCAATCAAGTTCTTAAAGTTAAAGTT	2467
Db	1981	TTCAAGGTGTCATGACTGTGTGCAACATGATTTCAATCAAGTTCTTAAAGTTAAAGTT	2040
Qy	2468	GCACATGATTTGTATAGAGATGCTTCTTGTAGTTTAAATATATGTATTAACATAGTTC	2527
Db	2041	GCACATGATTTGTATAGAGATGCTTCTTGTAGTTTAAATATATGTATTAACATAGTTC	2100
Qy	2528	ATTAGAAATCAAGCATTAATCAC 2551	
Db	2101	ATTAGAAATCAAGCATTAATCAC 2124	

XX	14-FEB-2002	(first entry)	
XX	CDNA sequence #71 encoding novel human secreted protein.		
XX			
XX	Human secreted protein; hyperproliferative disorder; autoimmune disorder;		
KW	immune deficiency disorder; blood disorder; inflammatory disorder;		
KW	infectious disorder; gene therapy; antimicrobial; hepatotropic;		
KW	immunosuppressive; antirheumatic; ss.		
XX			
OS	Homo sapiens.		
FN	WO200177291-A2.		
XX			
PD	18-OCT-2001.		
XX			
PF	29-MAR-2001; 2001WO-US10485.		
XX			
PR	06-APR-2000; 2000US-195604P.		
XX			
PA	(GEMY ) GENETICS INST INC.		
PI	Wong GG, Clark HF, Recheil K, Agostino MJ, Howes SH, Resnick RJ;		
PI	Gulick K, Graham JR;		
DR	WPI, 2002-010900/01.		
PT			
PT	New polynucleotides encoding secreted proteins useful for treating e.g.		
XX	asthma, HIV and Crohn's disease -		
PS	Claim 1; Page 112-113; 391pp; English.		
CC			
CC	The present invention relates to the isolation of novel cDNA sequences		
CC	which encode human secreted proteins. The cDNA sequences have been		
CC	derived from a variety of human tissues. The invention also provides		
CC	a method for producing proteins from these polynucleotide sequences.		
CC	The proteins are useful for identifying compounds that modulate their		
CC	activity and production, and the cell is also useful for identifying		
CC	compounds that modulate expression of the polynucleotide sequences		
CC	encoding the secreted proteins. The sequences of the invention are		
CC	useful for treating diseases such as hyperproliferative disorders		
CC	(e.g. cancer), immune deficiency disorders (e.g. severe combined		
CC	immunodeficiency (SCID)), autoimmune disorders (e.g. multiple		
CC	sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory		
CC	disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis).		
CC	The polynucleotide sequences of the invention are also useful in gene		
CC	therapy. AAS62214-AAS62838 represent the cDNA sequences of the		
CC	invention that encode for novel human secreted proteins.		
SQ	Sequence 2102 BP; 517 A; 510 C; 554 G; 521 T; 0 other;		
Query Match	69.6%; Score 1799; DB 24; Length 2102;		
Best Local Similarity	99.9%; Pred. No. 0;		
Matches 2099; Conservative	0; Mismatches 0; Indels 3; Gaps 2;		
QY	462 GTTGGAAATTAATACCATTCATCTGTCGACCCGAGAAATTTCACAAAGATPACCAAGACAGCT	521	
DB	1 GTTGGAAATTAATACCATTCATCTGTCGACCCGAGAAATTTCACAAAGATPACCAAGACAGCT	60	
QY	522 GGACAAATGATGCTTTTCAGAGACAGTTATACATCTGTGGAGAGACGAAGAGACAGAGG	581	
DB	61 GGACAAATGATGCTTTTCAGAGACAGTTATACATCTGTGGAGAGACGAAGAGAGCAAGG	120	
QY	582 AGCAGCAGTGCATCATCGAGAGAGACGTGTGGGCCGACAGCATGTCTGCAATTTGGCCAGC	641	
DB	121 AGCAGCAGTGCATCATCGAGAGAGACGTGTGGGCCGACAGCATGTCTGCAATTTGGCCAGC	180	
QY	642 TTCCAGTACACCTGCGACAGCCATGCGCGGGCCAGAGATGCTCTGCAACCCGGGACAGTAG	701	
DB	181 TTCCAGTACACCTGCGACAGCCATGCGCGGGCCAGAGATGCTCTGCAACCCGGGACAGTAG	240	
QY	702 TGCTGTGAGACCAAGCTGTGTGTCTGGGGGTCACTGCAGCAAAATGTGGCCACAGGGGCGAGC	761	

[illegible]

OY		1841	GTCATCAGGGAACTCTGAGAGGCTCGAGA	CTGAAGTGCCTTGCCCAAGTCACAGACTA	1900
Db		1381	GTCCATTAGGGAACTCTGAGAGGCTCGAGA	CTGAAGTGCCTTGCCCAAGTCACAGACTA	1440
OY		1901	GTGAAGACCAGAGCAGTTTCACTGAGTGTG	AAGCTCTTAAGGCTCAGTGCCTCTCCACTAAC	1960
Db		1441	GTGAAGACCAGAGCAGTTTCACTGAGTGTG	AAGCTCTTAAGGCTCAGTGCCTCTCCACTAAC	1500
OY		1961	CCACAACCAAGCCTTGTGTGTGCCAACAAA	TGCTCCCCCAAAGAAGAGAAATGGCATTTTTTC	2020
Db		1501	CCACAACCAAGCCTTGTGTGTGCCAACAAA	TGCTCCCCCAAAGAAGAGAAATGGCATTTTTTC	1560
OY		2021	--TTGAGGCAATGACATCTGGAATAAGTCAA	ACTAATCTCACATCCCCTCTAAAAAGTA	2078
Db		1561	TTTTHGAGGCATGACATCTGGAATAAGTCAA	ACTAATCTCACATCCCCTCTAAAAAGTA	1620
OY		2079	AACCTACTGTTTAGGAACAGACAGTGTCTC	CACAGTGTGGGGCAGCCGCTCTTCTAATGAAGA	2138
Db		1621	AACCTACTGTTTAGGAACAGACAGTGTCTC	CACAGTGTGGGGCAGCCGCTCTTCTAATGAAGA	1680
OY		2139	CAATGATATTGACACACTGTCCCTCTTTGG	CAAGTTCGCACTTAAGTAACTTTGAAAGTATATGA	2198
Db		1681	CAATGATATTGACACACTGTCCCTCTTTGG	CAAGTTCGCACTTAAGTAACTTTGAAAGTATATGA	1740
OY		2199	CTGAGCGTAGCATACAGGTTAACCTGTG	CAAAAACAGTACTTAAGTAACTTTGTAAGGCGAGGA	2258
Db		1741	CTGAGCGTAGCATACAGGTTAACCTGTG	CAAAAACAGTACTTAAGTAACTTTGTAAGGCGAGGA	1800
OY		2259	TTATTAATGAAATTGTGCAAAATCACTTA	GACAGCAACTGAAGAACAATTATCAACCAAGTGG	2318
Db		1801	TTATTAATGAAATTGTGCAAAATCACTTA	GACAGCAACTGAAGAACAATTATCAACCAAGTGG	1860
OY		2319	AGAAAATCAAAACCGAGCAGGGCTGTGTGA	AAACATGTTGTATATATGCACTGCGAACACT	2378
Db		1861	AGAAAATCAAAACCGAGCAGGGCTGTGTGA	AAACATGTTGTATATATGCACTGCGAACACT	1920
OY		2379	GAACTCTACGCAACTGCACAAAATGATG	TTTTCAGGTGTCACTGAGCTGTGGCCAACATATGA	2438
Db		1921	GAACTCTACGCAACTGCACAAAATGATG	TTTTCAGGTGTCACTGAGCTGTGGCCAACATATGA	1980
OY		2439	TTCATCCAGAGTTCTTAAAGTTTAAAGTTC	CAATGATGTGTATATAGCATGTCTTCTTTTGA	2498
Db		1981	TTCATCCAGAGTTCTTAAAGTTTAAAGTTC	CAATGATGTGTATATAGCATGTCTTCTTTTGA	2040
OY		2499	GTTTTAATATATGATATAAACATATAGTTC	GAATTGGAATCAAGCATTAATCACTTCAACT	2558
Db		2041	GTTTTAATATATGATATAAACATATAGTTC	GAATTGGAATCAAGCATTAATCACTTCAACT	2100
OY		2559	GC 2560		
Db		2101	GC 2102		
 RESULT_31 AAAO8839 standard; DNA; 1053 BP.					
ID	AAO8839				
XX	AAO8839;				
XX	AC				
DT	01-AUG-2000	(first entry)			
XX					
DE	Human DKR-3 DNA.				
XX					
KW	DKR-3; human r1g-like 7-1 mRNA; chicken lens fiber protein; cIestc 4;				
KW	dkr-1; dickkopf-1; antagonist; wnt-8 signaling; morphogenesis;				
KW	growth factor; cytoskeletal; sonic hedgehog; tissue differentiation; ss.				
OS	Homo sapiens.				
XX					
RH	Key	Location/Qualifiers			
FT	sigs_peptide	1..60			
		/tag= a			





modulating agents in regulating cellular processes and particularly for treating disorders characterized by aberrant expression or activity of Dkk, e.g. Alzheimer's.

Claim 2; Page 72-73; 208bp; English.

The present sequence encodes a human Dickkopf (Dkk)-3 protein. The specification also describes Soggy (Dkk-related) sequences. Dkk is a cysteine-rich secreted protein. The Dkk nuclear acids and proteins are useful as modulating agents in regulating cellular processes. They are particularly useful in treating subjects having a disorder characterized by aberrant expression or activity of Dkk such as optic disorders (glaucoma, conjunctivitis), brain disorders (Alzheimer's disease, epilepsy, amnesia), inflammation, skeletal muscle disorders, pulmonary disorders (Goodpasture's syndrome), cardiovascular disorders, and hyperproliferative disorders (cancer). The Dkk proteins and nuclear acids may also be used for research purposes, such as for chromosome mapping, tissue typing and in screening assays to identify modulators.

Sequence 1050 BP; 235 A; 306 C; 332 G; 177 T; 0 other;

Query Match 36.8%; Score 951; DB 21; Length 1050;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1001; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

153 ATGCAGCGGCTTGGGCGCCACCTGCTGTGCTGCTGCGGCGGCTGCCACGCGC 212  
1 ATGCAGCGGCTTGGGCGCCACCTGCTGTGCTGCTGCGGCGGCTGCCACGCGC 60

213 CCGCGCGCGCTTCCGAGCGGCACTCGGCTCCATCAAGCCCGCGCTCAGCTAC 272  
61 CCGCGCGCGCTTCCGAGCGGCACTCGGCTCCATCAAGCCCGCGCTCAGCTAC 120

273 CCGCAGAGAGAGCGCCACCTCATGAGATGTTCCGCGAGGTTGAGAACTGATGAGAC 332  
121 CCGCAGAGAGAGCGCCACCTCATGAGATGTTCCGCGAGGTTGAGAACTGATGAGAC 180

333 AGCGAGCAAAATTGCGGAGCGCGGTGGAAGATGAGAGGAGAAAGCTGCTGCTAA 392  
181 AGCGAGCAAAATTGCGGAGCGCGGTGGAAGATGAGAGGAGAAAGCTGCTGCTAA 240

393 GCATCATGAGAGTGAACCTGCGAACTTACCTCCAGCTATCAAAATGAGACCAACA 452  
241 GCATCATGAGAGTGAACCTGCGAACTTACCTCCAGCTATCAAAATGAGACCAACA 300

453 GACAGCAAGGTTGGAATTAATTCATCATGTCGACCGAGAAATTCACAAATTAACA 512  
301 GACAGCAAGGTTGGAATTAATTCATCATGTCGACCGAGAAATTCACAAATTAACA 360

513 AACGAGACTGGGCAAAATGCTCTTTCAGAGACAGTTATCAATCTGTGAGAGCAAGAA 572  
361 AACGAGACTGGGCAAAATGCTCTTTCAGAGACAGTTATCAATCTGTGAGAGCAAGAA 420

573 GGCAGAGAGAGCGCAGAGTGCATGCAAGAGACTGTGAGGCCAGATGATGCTGACCG 632  
421 GGCAGAGAGAGCGCAGAGTGCATGCAAGAGACTGTGAGGCCAGATGATGCTGACCG 480

633 TTTCGCAAGTTCCAGTACACCTGCGAGCCATGCGGCGCAGAGGATGCTGACCGCG 692  
481 TTTCGCAAGTTCCAGTACACCTGCGAGCCATGCGGCGCAGAGGATGCTGACCGCG 540

693 GACAGTGAAGTGTGAGAGCAGCTGTGTGTCTGAGGCTCACTGACCAAAATGCGCAC 752  
541 GACAGTGAAGTGTGAGAGCAGCTGTGTGTCTGAGGCTCACTGACCAAAATGCGCAC 600

753 AAGGAGAGAGATGGGACATCTGTGACCAACAGAGGAGACTGSCAGCGGCTGTGCTGT 812  
601 AAGGAGAGAGATGGGACATCTGTGACCAACAGAGGAGACTGSCAGCGGCTGTGCTGT 660

813 GCCTTCAGAGAGGCGCTGTGTTCCCTGTGTGCAACCCCTGCTCCGTGAGGCGAGCTT 872  
661 GCCTTCAGAGAGGCGCTGTGTTCCCTGTGTGCAACCCCTGCTCCGTGAGGCGAGCTT 720

873 TGCCATGACCCCGCCAGCCGCGCTTGTGAGACTTCATGACCTGAGAGCTTAAATGA 932  
721 TGCCATGACCCCGCCAGCCGCGCTTGTGAGACTTCATGACCTGAGAGCTTAAATGA 780

933 GCCTTGAACCGATGCTTGTGTGCAAGTGGCTGCTGCGAGCCGCAAGCCAGACGCTG 992  
781 GCCTTGAACCGATGCTTGTGTGCAAGTGGCTGCTGCGAGCCGCAAGCCAGACGCTG 840

993 GTGTATGTGCAAGCCGACCTTGTGTGAGAGCGGCGTGAACCAAGTGGAGATCTGCTG 1052  
841 GTGTATGTGCAAGCCGACCTTGTGTGAGAGCGGCGTGAACCAAGTGGAGATCTGCTG 900

1053 CCGAGAGAGTCCCGCATGATGATGAAGTGTGCGAGCTTCAATGAGAGAGTGGCGCAGAG 1112  
901 CCGAGAGAGTCCCGCATGATGATGAAGTGTGCGAGCTTCAATGAGAGAGTGGCGCAGAG 960

1113 CTGAGAGAGCTTGAAGAGAGCTGACTGAAGAGATGGCGCTG 1154  
961 CTGAGAGAGCTTGAAGAGAGCTGACTGAAGAGATGGCGCTG 1002

RESULT 34

AAVS2115  
ID AAVS2115 standard; CDNA; 410 BP.

AAVS2115;

09-NOV-1998 (first entry)

Homo sapiens CESP gene related EST clone.

CESP; cerebellum and embryo specific protein; restenosis;

myocardial infarction; arrhythmia; heart disease;

atherosclerosis; expressed sequence tag; ds.

Homo sapiens.

W09827932-A2.

02-JUL-1998.

18-DEC-1997; 97WO-US23518.

20-DEC-1996; 96US-0033870.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Soppet DR;

WPI; 1998-377366/32.

New isolated cerebellum and embryo specific polypeptide - used to develop products for treating e.g. coronary restenosis, myocardial infarction, heart disease and artery or venous thrombosis

Disclosure; Page 56; 77p; English.

The sequence is that of an EST clone related to the cerebellum and

embryo specific protein (CESP) gene.

Sequence 410 BP; 72 A; 118 C; 141 G; 78 T; 1 other;

Query Match 14.0%; Score 361; DB 19; Length 410;  
Best Local Similarity 100.0%; Pred. No. 1e-130;  
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

765 GGGACATCTGTGACCAACAGAGGAGCTGCAACCGGGCTGTGCTGCTTCCAGAGA 824  
1 GGGACATCTGTGACCAACAGAGGAGCTGCAACCGGGCTGTGCTGCTTCCAGAGA 60

825 GGCTGTGTTTCCCTGTGTGCAACCCCTGCGCTGGAAGGCGAGCTTTGCATGACCC 884  
61 GGCTGTGTTTCCCTGTGTGCAACCCCTGCGCTGGAAGGCGAGCTTTGCATGACCC 120



QY 885 GCGACGCGGCTTGTGACCTCATCACTGGAGAGCTGATGAGCTTGGACCGA 944  
 DB 121 GCGACGCGGCTTGTGACCTCATCACTGGAGAGCTGATGAGCTTGGACCGA 180  
 QY 945 TGGCCTTGTGACGAGTGGCCCTCTCTGCGACGCCCCACAGCCACGCTGTGTATGTGTC 1004  
 DB 181 TGGCCTTGTGACGAGTGGCCCTCTCTGCGACGCCCCACAGCCACGCTGTGTATGTGTC 240  
 QY 1005 AAGCCGACCTTCTGTGGGAGACCGTGAACCAAGATGGGAGATCTCTGCTGCCACAGAGCTC 1064  
 DB 241 AAGCCGACCTTCTGTGGGAGACCGTGAACCAAGATGGGAGATCTCTGCTGCCACAGAGCTC 300  
 QY 1065 CCGCATGATGATGAAGTTGGCAGCTTCATGAGAGAGTGGCCAGAGAGCTGAGAGACCTG 1124  
 DB 301 CCGCATGATGATGAAGTTGGCAGCTTCATGAGAGAGTGGCCAGAGAGCTGAGAGACCTG 360  
 QY 1125 G 1125  
 DB 361 G 361

RESULT 35  
 AAS80820/C  
 ID AAS80820 standard; cDNA; 439 BP.  
 XX  
 AC AAS80820;  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE DNA encoding novel human diagnostic protein #16624.  
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KM food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX Homo sapiens.  
 OS WO200175067-A2.  
 PN 11-OCT-2001.  
 PD 30-MAR-2001; 2001WO-US08631.  
 PF 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Dmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI: 2001-639362/73.  
 XX P-PSDB; ABG16633.  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity  
 XX  
 PS Claim 1; SEQ ID No 16624; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (II) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS84197-AAS94564 represent novel human  
 CC diagnostic coding sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 439 BP; 69 A; 128 C; 124 G; 118 T; 0 other;  
 Query Match 11.7%; Score 303; DB 23; Length 439;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-108;  
 Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 274 GCGAGGAGAGAGCCACCCCTCAATGATGATGTCGCGAGGTGAGAGAACTGATGAGAGCA 333  
 DB 303 GCGAGGAGAGAGCCACCCCTCAATGATGATGTCGCGAGGTGAGAGAACTGATGAGAGCA 244  
 QY 334 GCGAGCACAATTTGGCGACGCGGCTGGAAGATGAGAGCGCAAGAAAGCTGCTAAAG 393  
 DB 243 GCGAGCACAATTTGGCGACGCGGCTGGAAGATGAGAGCGCAAGAAAGCTGCTAAAG 184  
 QY 394 CATCATCAAGAGTGAACCTGGCAAACTTAACCTCCAGCTATCACAATGAGCAACAAG 453  
 DB 183 CATCATCAAGAGTGAACCTGGCAAACTTAACCTCCAGCTATCACAATGAGCAACAAG 124  
 QY 454 ACACGAAAGTTGAAATATATACCATCCATGTGACACCGAAGAAATTCACAAGTAACCAACA 513  
 DB 123 ACACGAAAGTTGAAATATATACCATCCATGTGACACCGAAGAAATTCACAAGTAACCAACA 64  
 QY 514 ACCAGACTGGAACAATGGTCTTTTCAGAGACAGTTATACATCTCTGGAGAACGAAGAAG 573  
 DB 63 ACCAGACTGGAACAATGGTCTTTTCAGAGACAGTTATACATCTCTGGAGAACGAAGAAG 4  
 QY 574 GCA 576  
 DB 3 GCA 1

RESULT 36  
 ABEK84291/C  
 ID ABEK84291 standard; cDNA; 2569 BP.  
 XX  
 AC ABEK84291;  
 DT 14-AUG-2002 (first entry)  
 XX  
 DE Human cDNA differentially expressed in granulocytic cells #662.  
 XX  
 KM Human; ss; granulocytic cell; DNA chip; bacterial infection;  
 KM viral infection; parasitic infection; protozoal infection;  
 KM fungal infection; sterile inflammatory disease; psoriasis;  
 KM rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
 KM cardiac reperfusion injury; renal reperfusion injury; ARDS;  
 KM adult respiratory distress syndrome; inflammatory bowel disease;  
 KM Crohn's disease; ulcerative colitis; periodontal disease;  
 KM granulocyte activation; chronic inflammation; allergy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PF 03-OCT-2001; 2001WO-US30821.  
 PR 03-OCT-2000; 2000US-237189P.  
 PA (GENE-) GENE LOGIC INC.  
 XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

DR WPI; 2002-435328/46.  
 XX  
 PT Detecting granulocyte activation by detecting differential expression  
 PT of genes associated with granulocyte activation, which serves as  
 PT diagnostic markers that is useful for monitoring disease states and  
 PT drug toxicity  
 PS  
 PS Claim 1, SEQ ID No 862; 114pp; English.

CC The invention relates to detecting (M1) granulocyte (GC) activation  
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by  
 CC DNA chip analysis as given in the specification, and comparing  
 CC the expression level to an expression level in an unactivated  
 CC GC, where differential expression of Gs is indicative of GCA.  
 CC Also included are modulating (M2) Gs by contacting GC with an agent  
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)  
 CC for an agent capable of modulating GCA or an inflammation (especially  
 CC chronic) in a tissue, an allergic response in a subject, exposure of a  
 CC subject to a pathogen or sterile inflammatory disease using the  
 CC gene expression profile; (3) detecting (M4) an inflammation (especially  
 CC chronic) in a tissue, an allergic response in a subject, exposure of a  
 CC subject to a pathogen or sterile inflammatory disease, by detecting the  
 CC level of expression in a sample of the tissue of gene(s) from Gs, where  
 CC the level of expression of the gene is indicative of inflammation;  
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,  
 CC an allergic response in a subject, exposure of a subject to a pathogen  
 CC or sterile inflammatory disease, by contacting a tissue having  
 CC inflammation with an agent that modulates the expression of gene(s)  
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for  
 CC modulating Gs; M3 is useful for screening an agent capable of modulating  
 CC GCA preferably in an inflammation in a tissue; M4 is useful for  
 CC detecting an inflammation (especially chronic) in a tissue, an allergic  
 CC response in a subject, exposure of a subject to a pathogen or sterile  
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,  
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal  
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,  
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
 CC periodontal disease), also bacterial infection, viral infection, and  
 CC parasitic infection, protozoal infection, fungal infection, and M5 is  
 CC useful for treating one of the above conditions. The present  
 CC sequence represents a gene differentially expressed in granulocytes.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WPIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

CC Sequence 2569 BP; 685 A; 601 C; 537 G; 740 T; 6 other;

Query Match 11.4%; Score 294; DB 24; Length 2569;

Best Local Similarity 100.0%; Pred. No. 9.1e-105; Indels 0; Gaps 0;

Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2267 GAAATTTGCAAAATCACTTAGCAGCACTGAAGCAATTAATCAACGCTGAGAAAATC 2326  
 DB 2568 GAAATTTGCAAAATCACTTAGCAGCACTGAAGCAATTAATCAACGCTGAGAAAATC 2509  
 QY 2227 AAACCGAGCGGGCTGTGTGAACATGTTGTAATAGCAGCTGCAAGCACTGAACCTCA 2386  
 DB 2508 AAACCGAGCGGGCTGTGTGAACATGTTGTAATAGCAGCTGCAAGCACTGAACCTCA 2449  
 QY 2387 CGCCACTCCAAATGATGTTTCAGGTGTCATGAGCTGTGGCCACCATGATTCATCCA 2446  
 DB 2448 CGCCACTCCAAATGATGTTTCAGGTGTCATGAGCTGTGGCCACCATGATTCATCCA 2389  
 QY 2447 GAGTTCTTAAGTTTAAGTGCATGATTTGTAAGCAGTCTGTTGAGTTTAA 2505  
 DB 2388 GAGTTCTTAAGTTTAAGTGCATGATTTGTAAGCAGTCTGTTGAGTTTAA 2329  
 QY 2507 TTATGTATAACATAGTTGATTTAGAAATCAAGCAATAATCACTTCAACTGC 2560  
 DB 2328 TTATGTATAACATAGTTGATTTAGAAATCAAGCAATAATCACTTCAACTGC 2275

RESULT 37  
 ID AAV52114 standard; cDNA; 557 BP.

AC AAV52114;  
 XX  
 XX 09-NOV-1998 (first entry)

XX Homo sapiens CESP gene related EST clone.  
 DE  
 KW CESP; cerebellum and embryo specific protein; restenosis;  
 KW myocardial infarction; arrhythmia; heart disease;  
 KW atherosclerosis; expressed sequence tag; ds.

OS Homo sapiens.  
 XX  
 XX W09827932-A2.  
 PN  
 XX 02-JUL-1998.  
 PD

PF 18-DEC-1997; 97WO-US23518.  
 XX  
 XX 20-DEC-1996; 96US-0033870.  
 PR

PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Ruben SM, Soppet DR,  
 PI

DR WPI; 1998-377366/32.  
 XX  
 XX

PT New isolated cerebellum and embryo specific polypeptide - used to  
 PT develop products for treating e.g. coronary restenosis, myocardial  
 PT infarction, heart disease and artery or venous thrombosis  
 PS Disclosure; Page 55; 77pp; English.

CC The sequence is that of an EST clone related to the cerebellum and  
 CC embryo specific protein (CESP) gene.

CC Sequence 557 BP; 112 A; 160 C; 176 G; 106 T; 3 other;

Query Match 11.3%; Score 292; DB 19; Length 557;

Best Local Similarity 99.6%; Pred. No. 6.7e-104; Indels 1; Gaps 1;

Matches 462; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 583 GCCACGAGTCATCATGACAGAGACTGTGGGCCCAAGCATCTGCGCACTTGGCCAGCT 642  
 DB 1 GCCACGAGTCATCATGACAGAGACTGTGGGCCCAAGCATCTGCGCACTTGGCCAGCT 60  
 QY 643 TCACGTACACCTGCGCAGCATGCGGAGCAGAGATGCTTGACACCGGAGCAGTAGT 702  
 DB 61 TCACGTACACCTGCGCAGCATGCGGAGCAGAGATGCTTGACACCGGAGCAGTAGT 120  
 QY 703 GCTGTGAGACCAAGCTGTGTCTGTGGGCTCACTGACCAAAATGGCCACAGGGGACGA 762  
 DB 121 GCTGTGAGACCAAGCTGTGTCTGTGGGCTCACTGACCAAAATGGCCACAGGGGACGA 180  
 QY 763 ATGGACCATCTGTGACAAACAGAGGAGCTGCGCGGCTGTGCTGTGCTTCCAGA 822  
 DB 181 ATGGACCATCTGTGACAAACAGAGGAGCTGCGCGGCTGTGCTGTGCTTCCAGA 240  
 QY 823 GAGGCTGTGCTTCCGTGTGTGACACCCCTGCGGTGAGAGGCGAGCTTGGCATGAC 882  
 DB 241 GAGGCTGTGCTTCCGTGTGTGACACCCCTGCGGTGAGAGGCGAGCTTGGCATGAC 299  
 QY 883 CGGCGAGCGGCTTGTGACCTCATCACTGAGAGCTAGAGCTGATGAGACTTGGACC 942  
 DB 300 CGGCGAGCGGCTTGTGACCTCATCACTGAGAGCTAGAGCTGATGAGACTTGGACC 359  
 QY 943 GATGCCCTTGTGACAGTGGCTCTTGTGACAGCCCAAGCCCAAGCCCAAGCCCTGTGATGTGT 1002  
 DB 360 GATGCCCTTGTGACAGTGGCTCTTGTGACAGCCCAAGCCCAAGCCCAAGCCCTGTGATGTGT 419

QY 1003 GCACCCGACCTTCGTGGGAGCCGTGACCAAGATGGGAGATC 1046  
Db 420 GCAAGCCGACCTTCGTGGGAGCCGTGACCAAGATGGGAGATC 463

## RESULT 38

AAH45500  
ID AAH45500 standard; DNA; 266-BP.

AC AAH45500;

DT 10-SEP-2001 (first entry)

DE Human REIC related DNA sequence SEQ ID 5.

KW REIC; reduced expression in immortalised cells; cancer; tumour;  
KW proliferation inhibitor; viral infection; human; ds.

OS Homo sapiens.

PN WO200138528-A1.

PD 31-MAY-2001.

PF 30-AUG-2000; 2000WO-JP05879.

PR 19-NOV-1999; 99JP-0330604.

PA (HISM ) HISAMITSU PHARM CO LTD.

PI Namba M, Tsuji T;

PI WPI; 2001-367688/38.

PT Cell proliferation inhibiting protein REIC and polynucleotide encoding  
PT it for diagnosis and therapy of cancer and as an antiviral agent -

PS Disclosure; Page 61; 66pp; Japanese.

CC This invention relates to a protein designated REIC (reduced expression  
CC in immortalised cells) which inhibits proliferation. REIC shows reduced  
CC or suppressed expression in immortalised cells such as cancer cells. The  
CC invention includes DNA and protein sequences for REIC. The protein is  
CC useful for the treatment and diagnosis of a wide range of benign and  
CC malignant tumours and of viral infections (including HIV, influenza,  
CC hepatitis and Epstein-Barr virus). The present sequence represents human  
CC DNA related to REIC.

SQ Sequence 266 BP; 64 A; 76 C; 60 G; 66 T; 0 other;

Query Match 9.6%; Score 248; DB 22; Length 266;  
Best Local Similarity 100.0%; Pred. No. 9.7e-87;

Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1775 CATTTCATATCCAAAGATCAATTCCTCTCTCAGACAGCCTGGGAGGGGTCATTGTT 1834

Db 1 CATTTCATATCCAAAGATCAATTCCTCTCTCAGACAGCCTGGGAGGGGTCATTGTT 60

QY 1835 CTCCTGCTCATCAGGAGATCTCAGAGGCTCAGAGACTGCAAGCTGCTGCCCAAGTCACA 1894

Db 61 CTCCTGCTCATCAGGAGATCTCAGAGGCTCAGAGACTGCAAGCTGCTGCCCAAGTCACA 120

QY 1895 CAGTAGTAGAAGACCAAGAGATTCATCTGTTGACTCTTAAGCTCAGTGCCTCTCC 1954

Db 121 CAGTAGTAGAAGACCAAGAGATTCATCTGTTGACTCTTAAGCTCAGTGCCTCTCC 180

QY 1955 ACTACCCCAACACAGCTTGGTGGCCAAAGTCTCTCCCAAAAGAGAGAAATGGGA 2014

Db 181 ACTACCCCAACACAGCTTGGTGGCCAAAGTCTCTCCCAAAAGAGAGAAATGGGA 240

QY 2015 TTTTCTT 2022

Db 241 TTTTCTT 248

## RESULT 39

AAH41559  
ID AAH41559 standard; cDNA; 247 BP.

AC AAH41559;

DT 21-AUG-2000 (first entry)

DE Human secreted expressed sequence tag SEQ ID NO:299.

KW Human; mouse; xenopus; rat; secreted expressed sequence tag; SEST;  
KW expressed sequence tag; EST; probe; chemotactic; proliferative;  
KW immunomodulatory; haematopoietic; chemokine; analgesic; haemostatic;  
KW thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;  
KW antiviral; antidiabetic; antiasclerotic; vulnary; antiparkinsonian;  
KW anticancer; osteoprotective; neuroprotective; nocotropic; antiproliferative;  
KW cerebroprotective; anticonvulsant; antidepressant; gene therapy;  
KW vaccine; autoimmune disorder; multiple sclerosis; allergic condition;  
KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;  
KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;  
KW central nervous system disorder; Alzheimer's disease; stroke;  
KW Parkinson's disease; Huntington's disease; coagulation disorder;  
KW hemophilia; thrombosis; inflammatory disorder; Crohn's disease;  
KW tumour; infection; depression; psoriasis; ss.

OS Homo sapiens.

PN WO200021990-A1.

PD 20-Apr-2000.

PF 15-OCT-1999; 99WO-US24205.

PR 15-OCT-1998; 98US-0104435.

PA (GENMY ) GENETICS INST INC.

PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
PI Merberg D, Treacy M;

PI WPI; 2000-317937/27.

PT Isolated polynucleotides, and encoded proteins, comprising secreted  
PT expressed sequence tags (SESTs), useful for treating various disorders  
PT such as autoimmune, infectious, and central nervous system disorders -

PS Claim 1; Page 238; 618pp; English.

CC AAA41261 to AAA43419 represent specifically claimed secreted expressed  
CC sequence tags (SESTs), isolated from human, mouse, xenopus and rat  
CC tissue sources. The SESTs can have a range of activities depending on  
CC the tissues they were isolated from. The activities include:  
CC chemotactic; proliferative; immunomodulatory; haematopoietic;  
CC chemokine; analgesic; haemostatic; thrombolytic; antiinflammatory;  
CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;  
CC antiasclerotic; vulnary; anticancer; osteoprotective; neuroprotective;  
CC nocotropic; antiparkinsonian; antiproliferative; cerebroprotective;  
CC anticonvulsant; and antidepressant. The SESTs can be used for gene  
CC therapy and in vaccines. The SESTs are useful as probes for the  
CC identification and isolation of full-length cDNAs and genomic DNA  
CC molecules which correspond to the SESTs. Proteins encoded by the SESTs  
CC are useful in assays for determining biological activity and raising  
CC antibodies. They may be useful for treatment of autoimmune disorders  
CC (multiple sclerosis, insulin dependent diabetes), allergic conditions  
CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,  
CC osteoporosis, osteoarthritis, central nervous system disorders  
CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation  
CC disorders (hemophilia, thrombosis), inflammatory disorders (Crohn's  
CC disease), tumours, bacterial, fungal or viral infections, depression and  
CC psoriasis. AAA43420 to AAA43425 represent linker variants which are given  
CC in the exemplification of the present invention.

XX Sequence 247 BP; 75 A; 50 C; 58 G; 64 T; 0 other;

Query Match 8.5%; Score 219; DB 21; Length 247;

Best Local Similarity 100.0%; Pred. No. 1.9e-75;

Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2038 GGAATTAAGGTCAAACATTAATTCATCATCCCTTAAAGTAACATCTGTAGGAACAGC 2097

22 GGAATTAAGGTCAAACATTAATTCATCATCCCTTAAAGTAACATCTGTAGGAACAGC 81

2038 AGGTTTTCACAGTGTGGGCGACCCCTCTTAAAGTAACATTAATTCATCATCTGTG 2157

82 AGGTTTTCACAGTGTGGGCGACCCCTCTTAAAGTAACATTAATTCATCATCTGTG 141

2158 CCTCTTGGCAGTTGCTAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2217

142 CCTCTTGGCAGTTGCTAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 201

2218 TAACTTCAGAAACAGTACTTAAGTAATTTGTAGGCGAG 2256

202 TAACTTCAGAAACAGTACTTAAGTAATTTGTAGGCGAG 240

# RESULT 40

AAQ59652 standard; cDNA; 447 BP.

AAQ59652;

25-MAR-2003 (updated)

16-MAR-1994 (first entry)

Human brain Expressed Sequence Tag EST01499.

Gene transcription product; genetic markers; tagging; in vivo;

transcription; mapping; locations; chromosomes; chromosomal; ss.

Homo sapiens.

MO9316178-A2.

19-AUG-1993.

12-FEB-1993; 93WO-US01294.

12-FEB-1992; 92US-0837195.

(USSH ) US DEPT HEALTH & HUMAN SERVICE.

Adams MD, Moreno RF, Venter CJ;

WPI; 1993-272882/34.

Enriched oligonucleotides and corresp. sequences - used as

markers for human genes transcribed in-vivo, facilitate tagging

of most human genes

Example 4; Page 210; 500bp; English.

The Expressed Sequence Tag was isolated from a human brain cDNA

library as part of a large set of ESTs which can be used as markers

for human genes transcribed in vivo. They can be used to facilitate

tagging of most human genes, for mapping locations of expressed genes

on chromosomes, for individual or forensic identification, for mapping

locations of disease-associated genes, for identification of tissue

type, and for prepn. of antisense sequences, probes and constructs.

EST01499 has a "good" coding probability as evaluated using the

coding-region prediction program CRM. See also AAQ59041-Q61440.

(Updated on 25-MAR-2003 to correct PN field.)

Query Match 8.2%; Score 213; DB 14; Length 447;

Best Local Similarity 100.0%; Pred. No. 3.7e-73;

Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1800 CTCCTCAGGACACACCTGGGAGGGGTCATTTGTTCTCCCTGTCATCAGGATCTGAGA 1859

1 CTCCTCAGGACACACCTGGGAGGGGTCATTTGTTCTCCCTGTCATCAGGATCTGAGA 60

1860 GAGTCAGAGACTGCAAGTGTCTTCCCAAGTCACACAGCTAGTAAAGCAGAGCACTTT 1919

61 GAGTCAGAGACTGCAAGTGTCTTCCCAAGTCACACAGCTAGTAAAGCAGAGCACTTT 120

1920 CATCTGTTGTGATCTTAAGTCTAGTCTCTCTCCACTATCCCAACAGCTGTGGTCC 1979

121 CATCTGTTGTGATCTTAAGTCTAGTCTCTCTCCACTATCCCAACAGCTGTGGTCC 180

1980 ACCAAAGTGTCTCCCAAGAGAGAGATG 2012

181 ACCAAAGTGTCTCCCAAGAGAGAGATG 213

# RESULT 41

AAV52117 standard; cDNA; 356 BP.

AAV52117;

09-NOV-1998 (first entry)

Homo sapiens CESP gene related EST clone.

CESP; cerebellum and embryo specific protein; restenosis;

myocardial infarction; arrhythmia; heart disease;

atherosclerosis; expressed sequence tag; ds.

Homo sapiens.

MO9827932-A2.

02-JUL-1998.

18-DEC-1997; 97WO-US23518.

20-DEC-1996; 96US-0033870.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Soppet DR;

WPI; 1998-377366/32.

New isolated cerebellum and embryo specific polypeptide - used to

develop products for treating e.g. coronary restenosis, myocardial

infarction, heart disease and artery or venous thrombosis

Disclosure; Page 56-57; 77pp; English.

The sequence is that of an EST clone related to the cerebellum and

embryo specific protein (CESP) gene.

Sequence 356 BP; 66 A; 106 C; 113 G; 67 T; 4 other;

Query Match 8.0%; Score 207; DB 19; Length 356;

Best Local Similarity 99.6%; Pred. No. 8.3e-71;

Matches 257; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

591 TGCATCATGACGACGAGCTGTGGGCCCAAGCATGATGCGCACTTCCAGCTTCAATAC 650

1 TGCATCATGACGACGAGCTGTGGGCCCAAGCATGATGCGCACTTCCAGCTTCAATAC 60

651 ACCGTGACGACCATGCGGGGCGAGAGATGCTGTGACCCCGGACAGTGAAGTGTGTGA 710

61 ACCGTGACGACCATGCGGGGCGAGAGATGCTGTGACCCCGGACAGTGAAGTGTGTGA 120

QY 711 GACCACTGTGTGTGTGGGTCACTGCACCAAAATGGCCAGGGGACCAATGGAC 770  
DB 121 GACCACTGTGTGTGTGGGTCACTGCACCAAAATGGCCAGGGGACCAATGGAC 180  
QY 771 ATCTGTGACACACAGAGGAGTCCAGCCGGGGCTGTGTGTGCTTCCAGAGAGGCTTG 830  
DB 181 ATCTGTGACACACAGAGGAGTCCAGCCGGGGCTGTGTGTGCTTCCAGAGAGGCTTG 240  
QY 831 CTGTTCCCTGTGTGACA 848  
DB 241 CTGTTCCCTGTGTGACA 258  
RESULT 42  
AAV52120  
ID AAV52120 standard; cDNA, 302 BP.  
XX  
XX AAV52120;  
XX  
DT 09-NOV-1998 (first entry)  
XX  
DE Homo sapiens CESP gene related EST clone.  
XX  
XX CESP, cerebellum and embryo specific protein; restenosis;  
XX myocardial infarction; arrhythmia; heart disease;  
XX atherosclerosis; expressed sequence tag; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO9827932-A2.  
XX  
PD 02-JUL-1998.  
XX  
PF 18-DEC-1997; 97WO-US23518.  
XX  
PR 20-DEC-1996; 96US-0033870.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Soppet DR;  
XX  
XX WPI; 1998-377366/32.  
XX  
DR WPI; 1998-377366/32.  
XX  
XX New isolated cerebellum and embryo specific polypeptide - used to  
XX develop products for treating e.g. coronary restenosis, myocardial  
XX infarction, heart disease and artery or venous thrombosis  
XX  
PS Disclosure; Page 58; 77pp; English.  
XX  
XX The sequence is that of an EST clone related to the cerebellum and  
XX embryo specific protein (CESP) gene.  
XX  
XX Sequence 302 BP; 97 A; 77 C; 76 G; 50 T; 2 other;  
XX  
XX  
XX Query Match 7.4%; Score 191; DB 19; Length 302;  
XX Best Local Similarity 100.0%; Pred. No. 1.4e-64;  
XX Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 358 TGGAGAGATGAGAGGAGAGAGCTGTCTAAAGCATCATCAAGAGTGAACCTTGACA 417  
DB 112 TGGAGAGATGAGAGGAGAGAGCTGTCTAAAGCATCATCAAGAGTGAACCTTGACA 171  
QY 418 ACTTACTCCAGCTATCACAAATGAGACCAACAGACAGAGAGTTGAAATATATACCA 477  
DB 172 ACTTACTCCAGCTATCACAAATGAGACCAACAGACAGAGTTGAAATATATACCA 231  
QY 478 TCCATGTGACACGAGAAATTCACAAATTAACCAACCAAGCTGACCAATGCTCTTT 537  
DB 232 TCCATGTGACACGAGAAATTCACAAATTAACCAACCAAGCTGACCAATGCTCTTT 291  
QY 538 CAGAGACAGTT 548

DB 292 CAGAGACAGTT 302  
RESULT 43  
AAO60267  
ID AAO60267 standard; DNA; 386 BP.  
XX  
XX AAO60267;  
XX  
DT 25-MAR-2003 (updated)  
DT 16-MAR-1994 (first entry)  
XX  
XX Human brain Expressed Sequence Tag EST02264.  
XX  
XX Gene transcription product; genetic markers; tagging; in vivo;  
XX transcription; mapping; locations; chromosomes; chromosomal; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9316178-A2.  
XX  
XX 19-AUG-1993.  
XX  
PF 12-FEB-1993; 93WO-US01294.  
XX  
PR 12-FEB-1992; 92US-0837195.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.  
XX  
XX Adams MD, Moreno RF, Venter CJ;  
XX  
XX WPI; 1993-272882/34.  
XX  
DR WPI; 1993-272882/34.  
XX  
XX Enriched oligonucleotides and corresp. sequences - used as  
XX markers for human genes transcribed in-vivo, facilitate tagging  
XX of most human genes  
XX  
PS Example 4; Page 307-308; 500pp; English.  
XX  
XX The Expressed Sequence Tag was isolated from a human brain cDNA  
XX library as part of a large set of ESTs which can be used as markers  
XX for human genes transcribed in vivo. They can be used to facilitate  
XX tagging of most human genes, for mapping locations of expressed genes  
XX on chromosomes, for individual or forensic identification, for mapping  
XX locations of disease-associated genes, for identification of tissue  
XX type, and for prepn. of antisense sequences, probes and constructs.  
XX EST02264 has a "poor" coding probability as evaluated using the  
XX coding-region prediction program CRM. See also AAO59041-Q61440.  
XX (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 386 BP; 85 A; 108 C; 95 G; 97 T; 1 other;  
XX  
XX Query Match 6.9%; Score 178; DB 14; Length 386;  
XX Best Local Similarity 100.0%; Pred. No. 1.6e-59;  
XX Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1835 CTCCCTGCATCAGGATCTCAGAGGCTCAGAGACTGCAAGCTGTTGCCCAAGTCACA 1894  
DB 36 CTCCCTGCATCAGGATCTCAGAGGCTCAGAGACTGCAAGCTGTTGCCCAAGTCACA 95  
QY 1895 CAGCTAGTGAAGACCAAGCAAGTTTCACTGTGTGACTTAAGCTCAGAGCTCTCC 1954  
DB 96 CAGCTAGTGAAGACCAAGCAAGTTTCACTGTGTGACTTAAGCTCAGAGCTCTCC 155  
QY 1955 ACTACCCACACAGCTTGTGTGCACCAAAAGTCTCCCAAAAGAGAGGAATGG 2012  
DB 156 ACTACCCACACAGCTTGTGTGCACCAAAAGTCTCCCAAAAGAGGAATGG 213  
RESULT 44  
AAV38808  
ID AAV38808 standard; cDNA; 480 BP.  
XX

AC AAV28808;  
 XX  
 DT 09-NOV-1998 (first entry)  
 XX  
 DE Homo sapiens CESP gene related clone HHPDB95R.  
 XX  
 DE CESP; cerebellum and embryo specific protein; restenosis;  
 KM myocardial infarction; arrhythmia; heart disease;  
 XX atherosclerosis; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9827932-A2.  
 XX  
 PD 02-JUL-1998.  
 XX  
 PF 18-DEC-1997; 97MO-US23518.  
 XX  
 PR 20-DEC-1996; 96US-003870.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Soppet DR;  
 XX  
 DR WPI; 1998-377366/32.  
 XX  
 PT New isolated cerebellum and embryo specific polypeptide - used to  
 PT develop products for treating e.g. coronary restenosis, myocardial  
 PT infarction, heart disease and artery or venous thrombosis  
 XX  
 PS Disclosure; Page 53-54; 77pp; English.  
 XX  
 CC The sequence is that of a cDNA clone related to extensive portions  
 CC of the coding region of the cerebellum and embryo specific protein  
 CC (CESP) gene. CESP is involved in: (i) the regulation of collateral  
 CC circulation (particularly in the heart), coronary artery restenosis  
 CC following a revascularization procedure, apoptosis in myocytes; (ii) the  
 CC modulation of myocyte development in the developing heart; (iii) the  
 CC regulation of circulating blood volume, vascular tone, blood pressure and  
 CC cardiac output, diuresis, natriuresis; (iv) facilitation of transudation  
 CC of plasma water to the interstitium, and (iv) inhibition of the release  
 CC or action of hormones such as aldosterone, angiotensin II, endothelins,  
 CC renin and vasopressin. The products can be used in the diagnosis and  
 CC treatment of CESP related disorders, e.g. coronary restenosis following  
 CC coronary revascularisation, coronary artery thrombus or occlusion,  
 CC myocardial infarction, atrial and/or ventricular arrhythmias, heart  
 CC block, hereditary medial necrosis of small coronary arteries, athero-  
 CC cardiomyopathy, arrhythmogenic right ventricular dysplasia, athero-  
 CC sclerotic heart disease, venous thrombosis or Reynaud's syndrome.  
 XX  
 SQ Sequence 480 BP; 124 A; 107 C; 111 G; 111 T; 27 other;  
 XX  
 Query Match 6.5%; Score 169; DB 19; Length 480;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-56;  
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 353 CGGGTGAAGAGATGAGGACAGAGAAAGCTGCTAAAGCATGATGAGAGTGAACCT 412  
 DB 64 CGGGTGAAGAGATGAGGACAGAGAAAGCTGCTAAAGCATGATGAGAGTGAACCT 123  
 QY 413 GGGAACTTACCTCCCAAGCTATCACAATGAGACCAACAGACAGAGGTTGGAAATTA 472  
 DB 124 GGGAACTTACCTCCCAAGCTATCACAATGAGACCAACAGACAGAGGTTGGAAATTA 183  
 QY 473 TACCATCATGTGACCGAGAAATTCACAAGATTAACCAACACAGACT 521  
 DB 184 TACCATCATGTGACCGAGAAATTCACAAGATTAACCAACACAGACT 232

RESULT 45  
 AA060722/c  
 ID AA060722 standard; cDNA; 337 BP.  
 XX

AC AA060722;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 16-MAR-1994 (first entry)  
 XX  
 DE Human brain Expressed Sequence Tag EST00846.  
 XX  
 DE Gene transcription product; genetic markers; tagging; in vivo;  
 KM transcription; mapping; locations; chromosomes; chromosomal; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9316178-A2.  
 XX  
 PD 19-AUG-1993.  
 XX  
 PF 12-FEB-1993; 93MO-US01294.  
 XX  
 PR 12-FEB-1992; 92US-0837195.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.  
 XX  
 PI Adams MD, Moreno RF, Venter CJ;  
 XX  
 DR WPI; 1993-272882/34.  
 XX  
 PT Enriched oligonucleotides and corresp. sequences - used as  
 PT markers for human genes transcribed in-vivo, facilitate tagging  
 PT of most human genes  
 XX  
 PS Example 4; Page 379; 500bp; English.  
 XX  
 CC The Expressed Sequence Tag was isolated from a human brain cDNA  
 CC library as part of a large set of ESTs which can be used as markers  
 CC for human genes transcribed in vivo. They can be used to facilitate  
 CC tagging of most human genes, for mapping locations of expressed genes  
 CC on chromosomes, for individual or forensic identification, for mapping  
 CC locations of disease-associated genes, for identification of tissue  
 CC type, and for prep. of antisense sequences, probes and constructs.  
 CC EST00846 has a "poor" coding probability as evaluated using the  
 CC coding-region prediction program CRM. See also AA059041-Q61440.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 337 BP; 91 A; 69 C; 78 G; 92 T; 7 other;  
 XX  
 Query Match 6.1%; Score 157; DB 14; Length 337;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-51;  
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1866 GAGACTGCAAGCTGCTTGGCCCAAGTCAACAGCTAGTGAAGACAGACAGATTTCATCTG 1925  
 DB 337 GAGACTGCAAGCTGCTTGGCCCAAGTCAACAGCTAGTGAAGACAGACAGATTTCATCTG 278  
 QY 1926 GTTGAGCTTAAGCTCAGTGTCTCTCCACATACCCCAACAGCCTTGTCACCAAA 1985  
 DB 277 GTTGAGCTTAAGCTCAGTGTCTCTCCACATACCCCAACAGCCTTGTCACCAAA 218  
 QY 1986 AGTGCTCCCAAGAGAGAGAAATGGATTTTCTT 2022  
 DB 217 AGTGCTCCCAAGAGAGAGAAATGGATTTTCTT 181

RESULT 46  
 AA052119  
 ID AA052119 standard; cDNA; 298 BP.  
 XX  
 AC AA052119;  
 XX  
 DT 09-NOV-1998 (first entry)  
 XX  
 DE Homo sapiens CESP gene related EST clone.  
 DE CESP; cerebellum and embryo specific protein; restenosis;  
 XX



KW myocardial infarction; arrhythmia; heart disease;  
 KW atherosclerosis; expressed sequence tag; ds.  
 XX Homo sapiens.  
 OS WO9827932-A2.  
 XX 02-JUL-1998.  
 PD 18-DEC-1997; 97WO-US23518.  
 PF 20-DEC-1996; 96US-0033870.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Ruben SM, Soppet DR;  
 PI WPI; 1998-377366/32.  
 DR New isolated cerebellum and embryo specific polypeptide - used to  
 PT develop products for treating e.g. coronary restenosis, myocardial  
 PT infarction, heart disease and artery or venous thrombosis  
 XX Disclosure; Page 57; 77pp; English.  
 PS The sequence is that of an EST clone related to the cerebellum and  
 CC embryo specific protein (CESP) gene.  
 XX Sequence 298 BP; 55 A; 68 C; 98 G; 75 T; 2 other;  
 SQ  
 Query Match 6.0%; Score 155; DB 19; Length 298;  
 Best Local Similarity 99.5%; Pred. No. 1.4e-50;  
 Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1180 CACTGCTGGGAGGAGAGATTAGATCTGACACGAGCTGTGATGTGAATAGA 1239  
 DB 93 CACTGCTGGGAGGAGAGATTAGATCTGACACGAGCTGTGATGTGAATAGA 152  
 OY 1240 AATAGCTAATTTATTTCCCGAGGTGTGCTTTAGGCGTGGCTGACAGGCTTTCTTCT 1299  
 DB 153 AATAGCTAATTTATTTCCCGAGGTGTGCTTTAGGCGTGGCTGACAGGCTTTCTTCT 212  
 OY 1300 ACATCTTCTTCCCGAGTATGTTCCCTCTGCTGACAGCATGAGGTTGTGCAATTGT 1359  
 DB 213 ACATCTTCTTCCCGAGTATGTTCCCTCTGCTGACAGCATGAGGTTGTGCAATTGT 272  
 OY 1360 TCAGCTCCCCCAGGCTGTTCTCCAGG 1385  
 DB 273 TCAGCTCCCCCAGGCTGTTCTCCAGG 298  
 RESULT 47  
 ID AAV52127 standard; cDNA; 344 BP.  
 XX AAV52127;  
 AC AAV52127;  
 XX 09-NOV-1998 (first entry)  
 DT Homo sapiens CESP gene related EST clone.  
 DE Homo sapiens CESP gene related EST clone.  
 KW CESP; cerebellum and embryo specific protein; restenosis;  
 KW myocardial infarction; arrhythmia; heart disease;  
 KW atherosclerosis; expressed sequence tag; ds.  
 XX Homo sapiens.  
 OS WO9827932-A2.  
 XX 02-JUL-1998.  
 PD 18-DEC-1997; 97WO-US23518.  
 PF 20-DEC-1996; 96US-0033870.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Ruben SM, Soppet DR;  
 PI WPI; 1998-377366/32.  
 DR New isolated cerebellum and embryo specific polypeptide - used to  
 PT develop products for treating e.g. coronary restenosis, myocardial  
 PT infarction, heart disease and artery or venous thrombosis  
 XX Disclosure; Page 57; 77pp; English.  
 PS The sequence is that of an EST clone related to the cerebellum and  
 CC embryo specific protein (CESP) gene.  
 XX Sequence 344 BP; 60 A; 106 C; 108 G; 68 T; 2 other;  
 SQ

PR 20-DEC-1996; 96US-0033870.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Ruben SM, Soppet DR;  
 PI WPI; 1998-377366/32.  
 DR New isolated cerebellum and embryo specific polypeptide - used to  
 PT develop products for treating e.g. coronary restenosis, myocardial  
 PT infarction, heart disease and artery or venous thrombosis  
 XX Disclosure; Page 60-61; 77pp; English.  
 PS The sequence is that of an EST clone related to the cerebellum and  
 CC embryo specific protein (CESP) gene.  
 XX Sequence 344 BP; 60 A; 106 C; 108 G; 68 T; 2 other;  
 SQ  
 Query Match 5.9%; Score 153; DB 19; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-50;  
 Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 713 CCAGCTGTGTCTCTGCGGTCACTGACCAAAATGGCCACGAGGCGACCAATGGGACCAT 772  
 DB 1 CCAGCTGTGTCTCTGCGGTCACTGACCAAAATGGCCACGAGGCGACCAATGGGACCAT 60  
 OY 773 CTGTGACAACAGAGAGAGACTGCCAGCCGAGCTGTGCTGTGCTTCCAGAGAGGCTGCT 832  
 DB 61 CTGTGACAACAGAGAGAGACTGCCAGCCGAGCTGTGCTGTGCTTCCAGAGAGGCTGCT 120  
 OY 833 GTTCCCTGTGTGACACACCCCTTGCCCTGTGAGGG 865  
 DB 121 GTTCCCTGTGTGACACACCCCTTGCCCTGTGAGGG 153  
 RESULT 48  
 ID AAV52126 standard; cDNA; 236 BP.  
 XX AAV52126;  
 AC AAV52126;  
 XX 09-NOV-1998 (first entry)  
 DT Homo sapiens CESP gene related EST clone.  
 DE Homo sapiens CESP gene related EST clone.  
 KW CESP; cerebellum and embryo specific protein; restenosis;  
 KW myocardial infarction; arrhythmia; heart disease;  
 KW atherosclerosis; expressed sequence tag; ds.  
 XX Homo sapiens.  
 OS WO9827932-A2.  
 XX 02-JUL-1998.  
 PD 18-DEC-1997; 97WO-US23518.  
 PF 20-DEC-1996; 96US-0033870.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Ruben SM, Soppet DR;  
 PI WPI; 1998-377366/32.  
 DR New isolated cerebellum and embryo specific polypeptide - used to  
 PT develop products for treating e.g. coronary restenosis, myocardial  
 PT infarction, heart disease and artery or venous thrombosis  
 XX Disclosure; Page 60; 77pp; English.  
 PS The sequence is that of an EST clone related to the cerebellum and  
 CC

CC embryo specific protein (CESP) gene.  
XX  
SQ Sequence 236 BP, 68 A; 60 C; 62 G; 44 T; 2 other;  
Query Match 5.8%; Score 151; DB 19; Length 236;  
Best Local Similarity 99.5%; Pred. No. 5.3e-49;  
Matches 201; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 463 TTGGAATATATACATCATGTCGACCGAGAAATTCACAAAGATTAACCAACAGACAGCTG 522  
DB 1 TTGGAATATATACATCATGTCGACCGAGAAATTCACAAAGATTAACCAACAGACAGCTG 60  
QY 523 GACAAATGCTCTTTTCAGAGACAGTTATCACTCTGTGGAGACGAAAGAGCAGAGGA 582  
DB 61 GACAAATGCTCTTTTCAGAGACAGTTATCACTCTGTGGAGACGAAAGAGCAGAGGA 120  
QY 583 GCCACGAGTCATCATGTCGACCGAGAGCTGTGGCCGACATGTCTGSCCAGTTGCCAGCT 642  
DB 121 GCCACGAGTCATCATGTCGACCGAGAGCTGTGGCCGACATGTCTGSCCAGTTGCCAGCT 180  
QY 643 TCCAGTACACCTGCGCAGCCATG 664  
DB 181 TCCAGTACACCTGCGCAGCCATG 202  
RESULT 49  
AAV3807  
ID AAV38807 standard; cDNA; 384 BP.  
XX  
XX AAV38807;  
XX  
DT 09-NOV-1998 (first entry)  
XX  
DE Homo sapiens CESP gene related clone HFB155fa.  
XX  
XX CESP; cerebellum and embryo specific protein; restenosis;  
KM myocardial infarction; arrhythmia; heart disease;  
KM atherosclerosis; da.  
XX  
OS Homo sapiens.  
XX  
XX WO9827932-A2.  
PN  
XX  
PD 02-JUL-1998.  
XX  
XX 18-DEC-1997; 97MO-US23518.  
PF  
XX 20-DEC-1996; 96US-0033870.  
PR  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX Ruben SM, Soppet DR;  
PI  
XX WPI; 1998-377366/32.  
DR  
XX  
XX New isolated cerebellum and embryo specific polypeptide - used to  
PT develop products for treating e.g. coronary restenosis, myocardial  
PT infarction, heart disease and artery or venous thrombosis  
XX  
XX  
PS Disclosure; Page 53; 77pp; English.  
XX  
XX The sequence is that of a cDNA clone related to extensive portions  
CC of the coding region of the cerebellum and embryo specific protein  
CC (CESP) gene. CESP is involved in: (i) the regulation of collateral  
CC circulation (particularly in the heart), coronary artery restenosis  
CC following a revascularisation procedure, apoptosis in myocytes; (ii) the  
CC modulation of myocyte development in the developing heart; (iii) the  
CC regulation of circulating blood volume, vascular tone, blood pressure and  
CC cardiac output, diuresis, natriuresis; (iv) Facilitation of transudation  
CC of plasma water to the interstitium; and (iv) inhibition of the release  
CC or action of hormones such as aldosterone, angiotensin II, endothelins,  
CC renin and vasopressin. The products can be used in the diagnosis and  
CC treatment of CESP related disorders, e.g. coronary restenosis following

CC coronary revascularisation, coronary artery thrombus or occlusion,  
CC myocardial infarction, atrial and/or ventricular arrhythmias, heart  
CC block, hereditary medial necrosis of small coronary arteries,  
CC cardiomyopathy, arrhythmogenic right ventricular dysplasia, athero-  
CC sclerotic heart disease, venous thrombosis or Reynaud's syndrome.  
SQ Sequence 384 BP, 73 A; 87 C; 106 G; 106 T; 12 other;  
Query Match 5.7%; Score 148; DB 19; Length 384;  
Best Local Similarity 100.0%; Pred. No. 7.3e-48;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1178 TGCACTGCTGGAGGAGGAGATTTAGATCTGACACGAGCTGTGATATGTCATA 1237  
DB 59 TGCACTGCTGGAGGAGGAGATTTAGATCTGACACGAGCTGTGATATGTCATA 118  
QY 1238 GAAATAGCTAATTTATTTCCCGAGGTGTGCTTTAGACGCGGCTGACAGGCTTCTTC 1297  
DB 119 GAAATAGCTAATTTATTTCCCGAGGTGTGCTTTAGACGCGGCTGACAGGCTTCTTC 178  
QY 1298 CTACATCTTCTTCCGAGTAAGTTTCCCC 1325  
DB 179 CTACATCTTCTTCCGAGTAAGTTTCCCC 206  
RESULT 50  
AAX56832  
ID AAX56832 standard; cDNA; 432 BP.  
XX  
XX AAX56832;  
XX  
AC  
XX  
XX 14-JUL-1999 (first entry)  
XX  
XX Human phdkk-3 cDNA.  
XX  
XX  
XX Signal pathway; wnt; inhibitor; secreted glycoprotein; receptor;  
XX therapy; diagnosis; treatment; cancer; breast; carcinoma; melanoma;  
XX colon; cell proliferation; differentiation; ss.  
XX  
XX  
XX Homo sapiens.  
XX  
XX WO9922000-A1.  
PN  
XX  
XX 06-MAY-1999.  
PD  
XX  
XX 27-OCT-1998; 98MO-DE03155.  
PF  
XX 27-OCT-1997; 97DE-1047418.  
PR  
XX (DEMR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA  
XX  
XX Glinka A, Niehrs C;  
PI  
XX  
XX WPI; 1999-303017/25.  
DR  
XX  
XX Protein that inhibits wnt signalling  
PT  
XX  
XX Claim 4a; Fig 2; 39pp; German.  
PS  
XX  
XX This invention describes an inhibitory protein of the wnt signalling  
CC pathway (which comprises secreted glycoproteins and their associated  
CC receptors). The products of the invention are useful as therapeutic  
CC and diagnostic agents, e.g. to treat cancer (e.g. carcinoma of breast  
CC and colon, or melanoma) and for studying processes associated with wnt  
CC signalling (cell proliferation and differentiation). Primers derived  
CC from the nucleic acid of the invention are used to detect the expression  
CC of the gene. AAX56827-X26833 are sequences used in the method of the  
CC invention.  
SQ  
XX  
XX Sequence 432 BP, 102 A; 131 C; 135 G; 64 T; 0 other;  
SQ  
Query Match 5.6%; Score 144; DB 20; Length 432;  
Best Local Similarity 100.0%; Pred. No. 2.6e-46;



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2004, 23:46:36 ; Search time 5325 Seconds  
(without alignments)

11803.075 Million cell updates/sec

Title: US-10-063-671-7

Perfect score: 2586

Sequence: 1 cgcgcgcctccaccaccgc.....aaaaaaaaaaaaaaaaa 2586

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 10

Total number of hits satisfying chosen parameters: 33952573

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_esthm:\*  
4: em\_estmu:\*  
5: em\_estm:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hnc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hnc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_esthm:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_piro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrt:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	786	30.4	936	13	BQ690088 AGENCOURT
2	778	30.1	951	13	BQ690888 AGENCOURT
3	763	29.5	977	9	AL535720 AL535720
4	760	29.4	1201	13	BX418715 BX418715

5	758	29.3	936	13	BQ879213 AGENCOURT
6	752	29.1	949	13	BQ149689 AGENCOURT
7	741	28.7	985	13	BQ196879 AGENCOURT
8	734	28.4	870	13	BQ689208 AGENCOURT
9	734	28.4	885	13	BQ230646 AGENCOURT
10	717	27.7	931	13	BQ722575 AGENCOURT
11	715	27.6	883	13	BQ897953 AGENCOURT
12	715	27.6	1065	13	BQ162929 AGENCOURT
13	711	27.5	892	13	BQ889489 AGENCOURT
14	708	27.4	932	13	BQ868792 AGENCOURT
15	706	27.3	878	13	BQ890463 AGENCOURT
16	698	27.0	922	13	BX391733 AGENCOURT
17	693	26.8	867	13	BQ689483 AGENCOURT
18	690	26.7	852	13	BQ894810 AGENCOURT
19	690	26.7	1002	13	BQ157365 AGENCOURT
20	685	26.5	906	13	BQ897122 AGENCOURT
21	684	26.5	841	13	BQ174805 AGENCOURT
22	684	26.5	877	13	BQ686534 AGENCOURT
23	684	26.5	915	13	BQ686811 AGENCOURT
24	684	26.5	952	13	BQ690443 AGENCOURT
25	678	26.2	898	13	BQ687864 AGENCOURT
26	676	26.1	893	13	BQ146050 AGENCOURT
27	676	26.1	901	13	BQ691090 AGENCOURT
28	673	26.0	760	12	B1553362 AGENCOURT
29	672	26.0	869	13	BQ888956 AGENCOURT
30	672	26.0	1043	13	BQ196397 AGENCOURT
31	671	25.9	905	13	BQ196968 AGENCOURT
32	671	25.9	912	13	BQ691927 AGENCOURT
33	668	25.8	880	13	BQ888730 AGENCOURT
34	668	25.8	887	13	BQ191090 AGENCOURT
35	668	25.8	921	13	BQ149760 AGENCOURT
36	668	25.8	996	13	BQ689566 AGENCOURT
37	667	25.8	858	13	BQ689791 AGENCOURT
38	667	25.8	940	13	BQ688783 AGENCOURT
39	665	25.7	871	13	BQ191108 AGENCOURT
40	656	25.4	923	13	BQ876718 AGENCOURT
41	653	25.3	905	13	BQ185743 AGENCOURT
42	652	25.2	883	13	BQ718036 AGENCOURT
43	651	25.2	883	13	BQ688234 AGENCOURT
44	651	25.2	916	13	BQ691372 AGENCOURT
45	648	25.1	889	13	BQ163369 AGENCOURT
46	648	25.1	908	13	BQ157606 AGENCOURT
47	643	24.9	879	13	BQ686410 AGENCOURT
48	643	24.9	883	13	BQ687171 AGENCOURT
49	640	24.7	871	13	BQ878479 AGENCOURT
50	640	24.7	926	13	BQ688559 AGENCOURT
51	640	24.7	1007	13	BQ190800 AGENCOURT
52	637	24.6	877	13	BQ897670 AGENCOURT
53	637	24.6	882	13	BQ686370 AGENCOURT
54	634	24.5	855	13	BQ688328 AGENCOURT
55	627	24.2	879	13	BQ688185 AGENCOURT
56	627	24.2	934	13	BQ163436 AGENCOURT
57	626	24.2	933	13	BQ892630 AGENCOURT
58	625	24.2	854	13	BQ163255 AGENCOURT
59	625	24.2	907	13	BQ897519 AGENCOURT
60	622	24.1	795	10	BQ697212 AGENCOURT
61	617	23.9	886	13	BQ185935 AGENCOURT
62	611	23.6	730	12	B1547921 AGENCOURT
63	610	23.6	901	13	BQ169116 AGENCOURT
64	609	23.5	714	14	BQ684552 AGENCOURT
65	609	23.5	816	14	CD242188 AGENCOURT
66	605	23.4	605	13	CB152156 AGENCOURT
67	600	23.2	919	13	BQ687539 AGENCOURT
68	599	23.2	913	13	BQ174886 AGENCOURT
69	595	23.0	952	13	BQ684750 AGENCOURT
70	590	22.8	581	9	AL134569 AGENCOURT
71	588	22.7	935	13	BQ185540 AGENCOURT
72	580	22.4	924	14	CD513993 AGENCOURT
73	579	22.4	597	10	BQ702538 AGENCOURT
74	575	22.2	1201	13	BX440690 AGENCOURT
75	574	22.2	842	13	BQ688035 AGENCOURT
76	573	22.2	573	14	CB152654 AGENCOURT
77	572	22.1	617	10	AM950947 AGENCOURT

C	78	571	22.1	737	13	EO185014	151	463	17.9	1211	13	BU169105
	79	568	22.0	967	13	EO185014	C 152	462	17.9	467	9	AA779346
	80	563	21.8	563	9	BU279954	C 153	460	17.8	462	9	AA704905
	81	562	21.7	903	13	BU147482	C 154	459	17.7	466	9	AA022551
	82	561	21.7	854	13	BO898374	C 155	456	17.6	526	14	CB306212
C	83	558	21.6	581	13	BU677657	C 156	456	17.6	689	12	BM704826
	84	555	21.5	947	13	BO685825	C 157	455	17.6	455	9	AI199529
	85	555	21.5	971	13	BU150570	C 158	452	17.5	580	13	BO327404
	86	551	21.3	972	13	BO690627	C 159	451	17.4	533	12	BM006716
	87	550	21.3	934	13	BO696834	C 160	451	17.4	354	10	BG700049
C	88	545	21.1	853	13	BO230977	C 161	451	17.4	78	14	CD299059
	89	544	21.0	685	10	BG701274	C 162	451	17.4	915	13	BO687319
	90	544	21.0	902	13	BU168697	C 163	447	17.3	724	12	BI667633
	91	541	20.9	930	13	BO685822	C 164	446	17.2	457	9	AA931636
	92	540	20.9	607	13	BO685822	C 165	446	17.2	516	9	AA719365
	93	540	20.9	607	13	BO685822	C 166	445	17.2	1201	9	AA572550
	94	540	20.9	607	13	BO685822	C 167	445	17.2	1201	9	AA572550
	95	539	20.8	814	10	BO674624	C 168	441	17.1	551	13	BO638944
	96	538	20.8	862	13	BO691532	C 169	439	17.0	443	9	AI141896
	97	537	20.8	893	12	BU488296	C 170	439	17.0	443	9	AI141896
	98	537	20.8	893	12	BU488296	C 171	438	16.9	593	14	CB153230
	99	534	20.6	962	13	BU149818	C 172	434	16.8	616	13	BO638484
	100	534	20.6	962	13	BU149818	C 173	433	16.7	733	14	CA434995
	101	533	20.6	856	13	BO687064	C 174	432	16.7	932	10	BE877367
	102	533	20.6	822	12	BO155372	C 175	431	16.7	727	13	BU736663
	103	532	20.6	941	13	BO719517	C 176	426	16.5	727	10	BG029262
	104	531	20.5	963	13	BU180392	C 177	423	16.4	638	10	BG327672
	105	531	20.5	1026	13	BU174087	C 178	423	16.4	710	12	BI763173
	106	530	20.5	943	13	BO685823	C 179	422	16.3	558	9	AI146840
	107	528	20.4	544	9	AM022685	C 180	421	16.3	420	9	AI304820
	108	528	20.4	933	13	BU157967	C 181	418	16.2	420	9	AA041360
	109	518	20.0	1002	13	BO878024	C 182	416	16.1	439	9	AI023381
C	110	516	20.0	562	13	BO879647	C 183	416	16.1	768	14	CB963043
	111	515	19.9	928	10	BO326091	C 184	415	16.0	964	13	BO886866
	112	514	19.9	541	12	BO008298	C 185	413	16.0	465	14	H99266
	113	512	19.8	572	12	BM511891	C 186	410	15.9	585	14	CB155251
	114	512	19.8	573	13	BU948926	C 187	410	15.9	461	9	AI174722
	115	510	19.7	1110	13	BU196372	C 188	407	15.7	443	9	AI580909
	116	508	19.6	508	14	CA930508	C 189	404	15.6	416	9	AI055888
	117	507	19.6	1046	13	BO670374	C 190	403	15.6	1007	12	BI763092
	118	505	19.5	1118	13	BU190780	C 191	400	15.5	400	9	AI1298778
	119	504	19.5	520	13	BO639623	C 192	399	15.4	409	9	AI1343544
	120	504	19.5	675	10	BE910066	C 193	399	15.4	407	9	AI751921
	121	502	19.4	1154	13	BU174766	C 194	399	15.4	595	10	BF567954
	122	501	19.4	922	13	BO689655	C 195	397	15.4	542	9	AI870872
	123	495	19.1	546	12	BM531088	C 196	396	15.3	959	9	AI566024
	124	494	19.1	494	10	BF724383	C 197	395	15.3	401	9	AI1291566
	125	492	19.0	923	13	BO692841	C 198	394	15.2	336	9	AA701551
	126	491	19.0	666	10	BO679946	C 199	394	15.2	336	9	AA654450
	127	490	18.9	958	13	BU185705	C 200	392	15.2	506	9	AA628979
	128	489	18.9	776	12	BT599926	C 201	392	15.2	901	9	AI519269
	129	488	18.9	555	13	BO327344	C 202	390	15.1	391	9	AA425947
	130	488	18.9	728	9	AL046115	C 203	387	15.0	1018	13	BO888214
	131	486	18.8	551	9	AL046115	C 204	385	14.9	925	13	BO685695
	132	484	18.7	601	12	BM895547	C 205	383	14.8	390	9	AI751922
	133	484	18.7	617	13	BU689372	C 206	383	14.8	409	12	BM693391
	134	484	18.7	635	9	AL145570	C 207	383	14.8	411	12	BM668665
	135	482	18.6	587	14	CB045353	C 208	382	14.8	411	12	BM668665
	136	480	18.6	499	14	CB045352	C 209	382	14.8	524	9	AI028240
	137	480	18.6	533	14	CA438305	C 210	380	14.7	505	9	AA071168
	138	479	18.5	916	13	BU145154	C 211	380	14.7	565	14	CB156451
	139	478	18.5	654	14	CB156678	C 212	378	14.6	678	10	BG715341
	140	477	18.4	495	9	AM301027	C 213	376	14.6	883	14	CD359926
	141	477	18.4	889	10	BB880937	C 214	373	14.4	723	9	AA119449
	142	476	18.4	478	9	AI149005	C 215	372	14.4	429	9	AA119449
	143	474	18.3	613	14	CB121677	C 216	371	14.3	371	9	AA368870
	144	472	18.3	965	13	BU180395	C 217	371	14.3	435	14	WA55126
	145	471	18.2	671	12	BU1835184	C 218	370	14.3	440	12	BM61871
	146	469	18.1	966	9	AL534481	C 219	369	14.3	596	13	BQ344606
	147	465	18.0	465	9	BF057318	C 220	367	14.2	670	9	AV727184
	148	463	17.9	601	12	BI45074	C 221	362	14.0	508	14	H71273
	149	463	17.9	947	13	BU149391	C 222	361	14.0	410	9	AA349552
	150	463	17.9	992	13	BU163532	C 223	361	14.0	547	9	AI871488

C 224	357	13.8	454	9	A1185662	A1185662 qe5d02.x	C 297	254	9.8	381	9	AA662378	AA662378 mu91a07.s
C 225	357	13.8	450	13	EX282247	EX282247	C 298	254	9.8	625	9	AM393112	AM393112 RCO-ST028
C 226	356	13.8	356	10	BG059953	BG059953 na6f4d03.	C 299	253	9.8	330	10	BE702752	BE702752 QVO-NM107
C 227	356	13.8	361	9	AA878917	AA878917 c1254d04.s	C 300	252	9.7	1003	13	BQ718638	BQ718638 AGENCOURT
C 228	356	13.8	362	9	AA677835	AA677835 z113b04.s	C 301	251	9.7	251	9	AA652462	AA652462 ns64g04.s
C 229	356	13.7	1201	13	EX358350	EX358350 BX358350	C 302	250	9.7	386	12	BQ022961	BQ022961 UI-1-BB1P
C 230	354	13.7	420	13	BQ327394	BQ327394 MR4-HR100	C 303	250	9.7	387	14	H70874	H70874
C 231	353	13.7	525	12	BQ024501	BQ024501 UI-1-BB1P	C 304	250	9.7	713	12	BM006330	BM006330 603615020
C 232	353	13.7	549	9	AM839123	AM839123 CM0-LT006	C 305	245	9.5	687	10	BM715216	BM715216 602675685
C 233	350	13.5	400	9	A1087068	A1087068 c271a03.x	C 306	244	9.4	352	9	AM630030	AM630030 hb74c11.y
C 234	345	13.3	348	9	AA836954	AA836954 c0e97f07.s	C 307	244	9.4	395	12	BM928436	BM928436 AGENCOURT
C 235	340	13.1	516	9	A1837142	A1837142 w962b09.x	C 308	242	9.4	260	12	BI335757	BI335757
C 236	338	13.1	608	12	BM006362	BM006362 603615062	C 309	239	9.2	334	10	BF364430	BF364430 QVO-NM107
C 237	338	13.1	1095	13	BO691349	BO691349 AGENCOURT	C 310	239	9.2	348	9	A1422538	A1422538 t186c01.x
C 238	336	13.0	449	9	A1421536	A1421536 t126b10.x	C 311	238	9.2	346	9	AA666013	AA666013 ag71h06.s
C 239	335	13.0	391	9	AA759247	AA759247 a84g04.s	C 312	237	9.2	329	9	AM839844	AM839844 RCI-LT007
C 240	335	13.0	448	10	BF440011	BF440011 nac52a12.	C 313	237	9.2	781	13	BUS70629	BUS70629 AGENCOURT
C 241	334	12.9	896	9	AL565532	AL565532 AL565532	C 314	237	9.2	1246	13	BQ899292	BQ899292 AGENCOURT
C 242	333	12.9	410	14	RS4473	RS4473 y979d06.s1	C 315	233	9.0	363	14	T97718	T97718
C 243	332	12.8	336	9	AA971440	AA971440 Op81a10.s	C 316	229	8.9	447	9	AM190213	AM190213 x160b10.x
C 244	331	12.8	500	12	BM819152	BM819152 K-EST0086	C 317	227	8.8	428	14	H49280	H49280 Y19509.r1
C 245	329	12.7	331	9	A1249754	A1249754 q164g12.x	C 318	227	8.8	590	13	BQ575512	BQ575512 UI-H-BZ1
C 246	329	12.7	331	9	A1686056	A1686056 t191g08.x	C 319	226	8.7	308	9	AM369055	AM369055 IL2-HT020
C 247	329	12.7	440	10	BF432358	BF432358 nac33c11.	C 320	225	8.7	1201	9	AL542758	AL542758
C 248	326	12.6	355	9	AA633601	AA633601 aae6811.s	C 321	223	8.6	223	9	AM305945	AM305945
C 249	326	12.6	553	9	AU148057	AU148057	C 322	221	8.5	411	12	BM689841	BM689841 UI-E-CX1
C 250	325	12.6	371	9	AM368850	AM368850 IL5-HT019	C 323	220	8.5	526	9	AA155928	AA155928 z047c06.x
C 251	325	12.6	507	12	BM688974	BM688974 UI-E-CQ1-9	C 324	219	8.5	427	14	T80210	T80210 y03a04.r1
C 252	324	12.5	405	9	AM368873	AM368873 IL5-HT019	C 325	218	8.4	707	10	BE274073	BE274073 601104422
C 253	322	12.5	332	9	A1954144	A1954144 wx80c06.x	C 326	217	8.4	355	14	F134409	F134409 HSCMH091.n
C 254	321	12.5	481	14	N16746	N16746 yx06f08.r1	C 327	213	8.2	225	9	A1972358	A1972358 w17g10.x
C 255	321	12.4	321	9	AM517066	AM517066 x06f08.x	C 328	213	8.2	343	10	BE702746	BE702746 QVO-NM107
C 256	318	12.3	360	12	BM694674	BM694674 UI-E-C11-	C 329	213	8.2	362	9	AA386106	AA386106 EST07518
C 257	317	12.3	1164	9	AL547689	AL547689	C 330	213	8.2	447	14	M77915	M77915 EST01499.Fe
C 258	315	12.2	342	10	BE702755	BE702755 QVO-NM107	C 331	213	8.2	1351	13	BU174747	BU174747 AGENCOURT
C 259	315	12.2	517	14	H18569	H18569 ym35f04.r1	C 332	212	8.2	212	9	AA773948	AA773948 ab67c05.x
C 260	309	11.9	370	14	T33293	T33293 EST56233.Hu	C 333	211	8.2	885	9	AL519268	AL519268
C 261	308	11.9	468	10	BE855681	BE855681 7907g06.x	C 334	208	8.0	309	10	AA849836	AA849836
C 262	307	11.8	308	10	BE702754	BE702754 QVO-NM107	C 335	207	8.0	356	9	AA351624	AA351624
C 263	306	11.8	376	9	AM368856	AM368856 IL5-HT019	C 336	207	8.0	457	14	T97821	T97821
C 264	305	11.8	359	9	A1146923	A1146923 o254d02.s	C 337	203	7.8	929	13	BA434739	BA434739
C 265	305	11.8	466	9	AA779309	AA779309 z153f03.s	C 338	200	7.7	375	10	AM900181	AM900181 CM0-NM100
C 266	301	11.6	423	12	BI496659	BI496659 df127a09.	C 339	198	7.7	294	10	BF196256	BF196256 7448g10.x
C 267	301	11.6	433	14	CA436217	CA436217 UI-H-DT0-	C 340	196	7.6	238	9	AA909223	AA909223 cchp0673.
C 268	298	11.5	796	12	BG831984	BG831984 602764968	C 341	196	7.6	345	14	CA950860	CA950860 i195b09.x
C 269	297	11.5	565	10	BF305953	BF305953 601889245	C 342	193	7.5	440	14	W39572	W39572
C 270	292	11.3	557	14	W61032	W61032 zc54d12.r1	C 343	192	7.4	414	14	AA424416	AA424416 zv82h04.s
C 271	291	11.3	373	10	AM905104	AM905104	C 344	192	7.4	946	10	BF525914	BF525914 60206876
C 272	288	11.1	316	9	A1720797	A1720797 a874h01.x	C 345	191	7.4	284	14	T03648	T03648 IB666.Infan
C 273	287	11.1	810	12	BI596318	BI596318 603243040	C 346	191	7.4	302	9	AA324686	AA324686 EST27557
C 274	286	11.1	372	14	H07080	H07080 y181f11.s1	C 347	190	7.3	332	14	R15488	R15488 HH393-F.Adu
C 275	285	11.0	945	9	BO877349	BO877349 AGENCOURT	C 348	189	7.3	217	13	BU075731	BU075731 im83e12.x
C 276	282	11.0	266	13	EA041143	EA041143 z109g05.r	C 349	189	7.3	591	10	BF223276	BF223276
C 277	282	10.9	1050	13	BU151131	BU151131 AGENCOURT	C 350	186	7.2	616	10	BG700918	BG700918
C 278	281	10.9	910	13	BQ962557	BQ962557 AGENCOURT	C 351	181	7.0	395	9	AA683017	AA683017 aee1c02.s
C 279	280	10.8	352	10	BF844913	BF844913 RCI-HT097	C 352	178	6.9	183	9	A1383694	A1383694 tC46h03.x
C 280	279	10.8	441	9	A1041039	A1041039 c0v6d03.x	C 353	178	6.9	386	14	M85745	M85745 EST02264.Fe
C 281	277	10.7	277	9	A1620833	A1620833 t086d06.x	C 354	176	6.8	262	12	BM662647	BM662647 UI-E-CQ1-
C 282	275	10.6	442	9	AA018255	AA018255 z441p12.r	C 355	176	6.8	493	9	AL057596	AL057596 ovi31d05.x
C 283	271	10.5	530	12	BM827626	BM827626 K-EST0100	C 356	176	6.8	945	13	BQ227791	BQ227791 AGENCOURT
C 284	270	10.4	305	9	AM239560	AM239560 XB32h05.y	C 357	175	6.8	247	10	BE836668	BE836668 CM3-FN007
C 285	267	10.4	321	9	AM103477	AM103477 xD36h05.x	C 358	174	6.7	252	12	BM711878	BM711878 UI-E-CL1-
C 286	266	10.3	317	9	A1567663	A1567663 t164a02.x	C 359	174	6.7	252	12	BM930095	BM930095 UI-E-BJ1-
C 287	266	10.3	451	13	BO640482	BO640482 he29c06.y	C 360	169	6.5	221	14	F10394	F10394 HSCMH092.n
C 288	266	10.2	377	10	AM805102	AM805102 QVO-NM107	C 361	169	6.5	248	9	AM839788	AM839788 RCI-LT007
C 289	264	10.2	418	14	H43281	H43281 yq19g09.s1	C 362	167	6.5	303	14	D54360	D54360 HUM137D01B
C 290	263	10.2	548	9	AA209468	AA209468 z884c12.s	C 363	164	6.3	222	13	BQ345772	BQ345772 PW3-WT031
C 291	262	10.1	365	10	BE702761	BE702761 QVO-NM107	C 364	164	6.3	403	14	W44526	W44526 zc20b04.s1
C 292	262	10.1	688	9	AV729560	AV729560 AV729560	C 365	161	6.2	673	12	BM006658	BM006658 603615361
C 293	262	10.0	354	9	AM523086	AM523086 UI-R-BOO-	C 366	159	6.2	324	14	F13452	F13452 HSC37E101.r1
C 294	258	10.0	384	9	AA668448	AA668448 ab85f10.s	C 367	157	6.1	137	13	M78698	M78698 EST00846.H1
C 295	257	9.9	357	9	AA668448	AA668448	C 368	156	6.0	1121	14	BU145340	BU145340 AGENCOURT
C 296	255	9.9	465	14	T78829	T78829 yc96f09.r1	C 369	155	6.0	298	14	T33818	T33818 EST59370.Hu



C 370	155	6.0	308	9	A1929307	aus9909.x	443	67	2.6	517	12	BM006523	BM006523	603615481
C 371	153	5.9	344	14	R14945	YF94G06.r1	444	65	2.5	156	14	Z19902	Z19902	HSAAAZFT.P
C 372	153	5.9	412	14	T33827	EST58418.Hu	445	65	2.5	1113	12	BM007075	BM007075	603615481
C 373	151	5.8	203	14	Z38477	HSC0CH082.n	446	63	2.4	800	14	CB111336	CB111336	AGENCOURT
C 374	151	5.8	236	14	T08793	EST06685.in	447	59	2.3	190	14	Z20312	Z20312	HSAAEMXS.P
C 375	150	5.8	403	9	AA88511	am75e01.s	448	54	2.1	529	13	BQ426205	BQ426205	UMNB8A11-
C 376	148	5.7	267	10	BF954624	RC6-NN116	449	53	2.0	151	14	R57834	R57834	FS953.Fetal
C 377	147	5.7	359	9	A1249686	qx50G12.x	450	53	1.9	233	14	T03598	T03598	IBS68.inten
C 378	147	5.7	253	12	BM684732	UI-E-EJ1-	451	48	1.3	123	12	BM482687	BM482687	PM2-CT080
C 379	147	5.7	325	9	AM190135	x159G04.x	452	47	1.8	86	9	AA911546	AA911546	oe77n12.s
C 380	147	5.7	473	14	N26110	yx90G01.s1	453	46	1.8	331	14	L48824	L48824	HUM060625P
C 381	146	5.6	146	9	AA844276	a194e04.s	454	45	1.7	150	10	BF076133	BF076133	225637.MA
C 382	141	5.5	750	12	BM007284	603615062	455	45	1.7	121	12	BM482966	BM482966	536073.MA
C 383	140	5.4	359	9	AA226979	z118G10.r	456	45	1.7	161	12	BM482970	BM482970	536073.MA
C 384	139	5.4	309	14	T32418	EST48217.Hu	457	45	1.7	144	12	BM482687	BM482687	535672.MA
C 385	139	5.4	426	9	AM078717	xb32h05.x	458	45	1.7	350	9	AU231600	AU231600	AU231600
C 386	136	5.3	238	14	T31076	EST27168.Hu	459	45	1.7	560	13	BO091916	BO091916	UMN17C01
C 387	131	5.1	314	14	T20942	H8AADERK.P	460	45	1.7	576	13	BO091454	BO091454	UMN 17C02
C 388	129	5.0	361	14	T30528	H8AADERK.P	461	44	1.7	582	14	CB586647	CB586647	AMGNNUC.N
C 389	127	4.9	491	10	BE812829	RCO-AN006	462	43	1.7	383	12	BI397424	BI397424	UMN38A11-
C 390	124	4.8	187	9	AM794562	RC6-UM001	463	42	1.6	640	12	BM006880	BM006880	603615361
C 391	124	4.8	300	14	N86855	LI235F.Huma	464	41	1.6	477	12	BG988742	BG988742	MR2-HT116
C 392	123	4.8	396	14	T33817	EST59369.Hu	465	39	1.5	379	9	AL631296	AL631296	AL631296
C 393	122	4.7	424	14	H18461	YM43f04.s1	466	38	1.5	245	14	C14023	C14023	C14023
C 394	120	4.6	349	12	BI497458	dfi36h02.	467	35	1.4	268	14	BO960784	BO960784	AGENCOURT
C 395	119	4.6	124	14	Z19631	HSAAADXT.J	468	35	1.4	255	9	AA807015	AA807015	oc29h09.s
C 396	118	4.6	148	13	AI351552	qf06f08.x	469	35	1.4	576	9	AI673820	AI673820	fc03902.x
C 397	117	4.5	1058	13	BU941114	AGENCOURT	470	35	1.4	1010	14	CD117119	CD117119	AGENCOURT
C 398	116	4.5	218	9	AA031480	2k16b05.s	471	35	1.4	1056	10	BF678927	BF678927	602153554
C 399	116	4.5	221	9	AA322156	EST24750	472	35	1.4	1239	12	BM560285	BM560285	AGENCOURT
C 400	115	4.4	160	12	BI496658	dfi27a09.	473	34	1.4	222	10	BI775230	BI775230	467635.MA
C 401	114	4.4	255	12	BM665688	UI-E-CL1-	474	34	1.3	232	10	BE752573	BE752573	204995.MA
C 402	113	4.4	334	12	BG45256	PMO-AN008	475	34	1.3	230	12	BI775295	BI775295	467719.MA
C 403	112	4.3	451	10	BE812783	RCO-AN006	476	34	1.3	337	10	BF601715	BF601715	266750.MA
C 404	112	4.3	210	14	C05296	C05296.Huma	477	34	1.3	439	9	AV734888	AV734888	AV734888
C 405	111	4.3	255	14	F09872	HSC37E102.n	478	34	1.3	611	14	CB448740	CB448740	702900.MA
C 406	110	4.3	118	9	AI146938	cy24c09.s	479	34	1.3	1370	12	BM924462	BM924462	AGENCOURT
C 407	110	4.3	174	14	T18925	g12048t.Tes	480	33	1.3	148	9	AI251982	AI251982	qy57d12.x
C 408	110	4.3	263	14	T10923	HSC24807.Hu	481	33	1.3	171	9	AI733956	AI733956	qy57d12.x
C 409	110	4.3	109	14	Z19623	HSAAAMBR.P	482	33	1.3	177	9	AI739863	AI739863	qy57d12.y
C 410	107	4.1	279	14	Z42237	HSC0CH081.n	483	33	1.3	184	9	AI345909	AI345909	qy57d12.x
C 411	107	4.1	664	12	BM021491	UI-H-DH1-	484	33	1.3	219	9	AI141711	AI141711	oc08h05.x
C 412	105	4.1	247	9	AA424460	zvr2h04.r	485	33	1.3	230	12	BI976333	BI976333	485174.MA
C 413	103	4.0	175	14	T65270	yc79c10.r1	487	33	1.3	243	9	AI345202	AI345202	l667501.x
C 414	103	4.0	166	10	BG223349	naef9h03.	488	33	1.3	294	12	BM541506	BM541506	AGENCOURT
C 415	99	3.9	163	13	BM072865	CV1-FM016	489	33	1.3	320	9	AM479635	AM479635	26635.MAR
C 416	99	3.8	605	12	BM006260	603614924	490	33	1.3	324	11	BC018864	BC018864	HOMO.SAPI
C 417	99	3.8	647	13	BO807940	NISC_KK12	491	33	1.3	336	9	AA222318	AA222318	mm19h09.r
C 418	95	3.7	325	14	WA5085	zc20c09.r1	492	33	1.3	351	9	AA768369	AA768369	oc17c05.s
C 419	94	3.6	330	9	AA360054	EST69206	493	33	1.3	384	9	AI097316	AI097316	qy57d03.x
C 420	94	3.6	451	10	BE812783	RCO-AN006	494	33	1.3	397	14	CA910323	CA910323	PCS05676F
C 421	93	3.6	491	10	BE812829	RCO-AN006	495	33	1.3	478	14	CB344206	CB344206	CA48EN000
C 422	93	3.6	404	12	BI703415	PM3-NN022	496	33	1.3	478	9	AI378748	AI378748	lc18f05.x
C 423	92	3.6	742	10	BE807724	601497757	497	33	1.3	486	14	CB344266	CB344266	CA48EN000
C 424	91	3.5	91	12	BE829903	602764307	498	33	1.3	487	14	CB344044	CB344044	CA48EN000
C 425	90	3.5	183	10	BF944464	RC6-NN116	499	33	1.3	505	14	CA666143	CA666143	wiki.pk00
C 426	90	3.5	189	14	T65229	yc79c10.r1	500	33	1.3	587	14	CA666143	CA666143	wiki.pk00
C 427	89	3.4	328	14	CB297787	12822015	501	33	1.3	86	9	AA911546	AA911546	oe77n12.s
C 428	89	3.4	397	14	RS2311	yg79d06.r1-	502	33	1.3	150	10	BF076133	BF076133	225637.MA
C 429	87	3.4	398	14	CO1001	HTMG5000386	503	33	1.3	161	12	BM482966	BM482966	536073.MA
C 430	87	3.4	179	14	Z19659	HSAAAEVM.P	504	33	1.3	184	12	BM482687	BM482687	535672.MA
C 431	84	3.2	303	14	RS6671	G4596.Fetal	505	33	1.3	350	9	AU231600	AU231600	AU231600
C 432	84	3.2	181	9	AA376024	EST88391	506	33	1.3	383	12	BI397424	BI397424	UMN38A11-
C 433	82	3.2	458	9	AI394169	cg6h03.x	507	33	1.3	478	14	CB344206	CB344206	CA48EN000
C 434	81	3.1	708	14	CB311290	AGENCOURT	508	33	1.3	478	9	AI378748	AI378748	lc18f05.x
C 435	81	3.1	796	14	CB308228	AGENCOURT	509	33	1.3	486	14	CB344266	CB344266	CA48EN000
C 436	81	3.1	185	10	BE718913	CM3-HT080	510	33	1.3	505	14	CA666143	CA666143	wiki.pk00
C 437	79	3.1	576	9	AU146754	AU146754	511	33	1.3	587	14	CA666143	CA666143	wiki.pk00
C 438	79	3.1	129	10	BM058190	na12h06.	512	33	1.3	587	14	CA666143	CA666143	wiki.pk00
C 439	76	2.9	139	10	BM058190	na12h06.	513	33	1.3	587	14	CA666143	CA666143	wiki.pk00
C 440	71	2.7	439	9	AI929384	PM3-NN022	514	33	1.3	587	14	CA666143	CA666143	wiki.pk00
C 441	70	2.7	438	9	AI929384	PM3-NN022	515	33	1.3	587	14	CA666143	CA666143	wiki.pk00
C 442	69	2.7	1455	12	BM006928	603615632	516	33	1.3	587	14	CA666143	CA666143	wiki.pk00

## ALIGNMENTS

RESULT 1  
LOCUS BQ690088 936 bp mRNA  
DEFINITION AGENCOURT 8034033 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6208328  
5', mRNA sequence.  
ACCESSION BQ690088  
VERSION BQ690088.1 GI:21815404  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens



BASE COUNT 191 a 239 c 276 g 244 t 1 others

ORIGIN

Query Match 30.1%; Score 778; DB 13; Length 951;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 878; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

849 CCCCTGCCCTGGAGGCGAGCTTTGCCATGACCCCGCAGCCGCTTGGACCTCATC 908  
 1 CCCCTGCCCTGGAGGCGAGCTTTGCCATGACCCCGCAGCCGCTTGGACCTCATC 60

909 ACCTGGAGAGTAAAGCTGATGAGACCTTGGACCCATGCCCTTGTCCACGTGCTCTC 968  
 61 ACCTGGAGAGTAAAGCTGATGAGACCTTGGACCCATGCCCTTGTCCACGTGCTCTC 120

969 TGCAGCCGCCACAGCCACACCTGTGTATGTGTGCAAGCCGACTTCTGGGAGCCGT 1028  
 121 TGCAGCCGCCACAGCCACACCTGTGTATGTGTGCAAGCCGACTTCTGGGAGCCGT 180

1029 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGGTCCCGATGATGATGAGTGGAC 1088  
 181 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGGTCCCGATGATGATGAGTGGAC 240

1089 TTCAATGAGAGAGGAGCGCAGAGAGTGGAGACCTGGAGAGAGGCTGACTGAAGAG 1148  
 241 TTCAATGAGAGAGGAGCGCAGAGAGTGGAGACCTGGAGAGAGGCTGACTGAAGAG 300

1149 GCGCTGGGAGAGCTCTGCGGCTGCCCGCGCTGCACTGCTGGAGAGGAGATTTAGATC 1208  
 301 GCGCTGGGAGAGCTCTGCGGCTGCCCGCGCTGCACTGCTGGAGAGGAGATTTAGATC 360

1209 TGACACCGGCTGTGGGAGATGAGCAATAGAAATAGCTAATTTATTTCCCGAGGTGTG 1268  
 361 TGACACCGGCTGTGGGAGATGAGCAATAGAAATAGCTAATTTATTTCCCGAGGTGTG 420

1269 CTTTGGCGCTGGGCTGACACAGGCTTCTTCCATACCTTCTTCCAGTAAATTTCCCTCT 1328  
 421 CTTTGGCGCTGGGCTGACACAGGCTTCTTCCATACCTTCTTCCAGTAAATTTCCCTCT 480

1329 GCGCTGACAGATGAGGTGTGTGTGATTTGTTCAGCTGCCCGAGGCTGTCTTCAGGCTT 1388  
 481 GCGCTGACAGATGAGGTGTGTGTGATTTGTTCAGCTGCCCGAGGCTGTCTTCAGGCTT 540

1389 CACAGTGTGTGCTTGGAGAGTGCAGGCAAGGTTAACTGCAGAGCAAGTTGCCACCCC 1448  
 541 CACAGTGTGTGCTTGGAGAGTGCAGGCAAGGTTAACTGCAGAGCAAGTTGCCACCCC 600

1449 TGTCCAGATTAATTTGGCTGCTTGTCTTACCAAGTTGSCAGACAGCGTTTGTCTAATG 1508  
 601 TGTCCAGATTAATTTGGCTGCTTGTCTTACCAAGTTGSCAGACAGCGTTTGTCTAATG 660

1509 GCTTGTGAATTTGTTTGAAGGAGAGAGATGAAAACAATGTGAGTCTCCCTCTGATTTG 1568  
 661 GCTTGTGAATTTGTTTGAAGGAGAGAGATGAAAACAATGTGAGTCTCCCTCTGATTTG 720

1569 TTTTGGGGAATTTGTGAGAGAGAGTGCCTGCTTGGCAAAACATCAACTGGGCAAAATGCA 1628  
 721 TTTTGGGGAATTTGTGAGAGAGAGTGCCTGCTTGGCAAAACATCAACTGGGCAAAATGCA 780

1629 CAATGGAATTTTGCAGCGAGTCTTTCATGAGGAGATGATGAGTGTGCTTGAAGTGT 1688  
 781 CAATGGAATTTTGCAGCGAGTCTTTCATGAGGAGATGATGAGTGTGCTTGAAGTGT 840

1689 GCAGATGAATTTGTTCTGTTCACTCTGCAATTAACATGTGTT 1728  
 841 GCAGATGAATTTGTTCTGTTCACTCTGCAATTAACATGTGTT 880

RESULT 3  
 AL535720 977 bp RNA linear EST 31-MAY-2003  
 LOCUS AL535720 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
 DEFINITION CS0DF016VJ11 5-PRIME, mRNA sequence.

ACCESSION AL535720  
 VERSION AL535720.2 GI:1260722  
 KEYWORDS EST  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1 (bases 1 to 977)  
 Li, W.-B., Gruber, C., Jesses, J., and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished

COMMENT  
 On Feb 13, 2001 this sequence version replaced gi:12799213.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6027.r For more information about this cluster, see  
 http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF016CE06QPicluster=6027.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Paraday Avenue Genoscope sequence ID : CS0DF016CE06Q1.

FEATURES  
 source  
 Location/Qualifiers  
 1..977  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DF016VJ11"  
 /tissue\_type="FETAL BRAIN"  
 /dev\_stage="fetal"  
 /clone\_lib="Homo sapiens FETAL BRAIN"  
 /note="Organ: Brain; Vector: pCMVSPORT\_6; 1st strand cDNA was primed with a NotI-0.150 (nt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

BASE COUNT 222 a 294 c 296 g 165 t

ORIGIN

Query Match 29.5%; Score 763; DB 9; Length 977;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 883; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

126 GCGCGGCGCTGCGGCGCGAGAGCGAGATGACGCGCTTGGGCGCACCTGCTGCTG 185  
 95 GCGCGGCGCTGCGGCGCGAGAGCGAGATGACGCGCTTGGGCGCACCTGCTGCTG 154

186 CTGCTGGGCGGCGCGGTCGCCAGCGGCCCGCGCTCCGACGCGGACTCGGCTTCCA 245  
 155 CTGCTGGGCGGCGCGGTCGCCAGCGGCCCGCGCTCCGACGCGGACTCGGCTTCCA 214

246 GTCAAGCCCGCGCGGCTCTGAGCTACCGGAGAGAGCCACCTCAATGAGATGTT 305  
 215 GTCAAGCCCGCGCGGCTCTGAGCTACCGGAGAGAGCCACCTCAATGAGATGTT 274

306 CGCGAGTTGAGGAACTGATGAGAGACACGAGACAAATTTGCGAGCGCGGTGAGAG 365  
 275 CGCGAGTTGAGGAACTGATGAGAGACACGAGACAAATTTGCGAGCGCGGTGAGAG 333

366 ATGAGGCGAGAGAGCTGCTGCTAAAGCATCATCAGAGTGAAGTGAAGTGAAGTGA 425  
 334 ATGAGGCGAGAGAGCTGCTGCTAAAGCATCATCAGAGTGAAGTGAAGTGAAGTGA 393

426 CCAGCTATCAATAGAGACCAACAGACAGAGGTGGAAATTAATACATCATGTG 485  
 394 CCAGCTATCAATAGAGACCAACAGACAGAGGTGGAAATTAATACATCATGTG 453

486 CACCGAATTTCCAAATATTAACCAACCAAGAGTGAAGTGAAGTGAAGTGAAGTGA 545  
 454 CACCGAATTTCCAAATATTAACCAACCAAGAGTGAAGTGAAGTGAAGTGAAGTGA 513

QY 546 GTTATCATCTGTGGAGACGAAGAAGGACGACGATCATTCACGAG 605  
 Db 514 GTTATCATCTGTGGAGACGAAGAAGGACGACGATCATTCACGAG 573  
 QY 606 GACTGTGGAGACGATGTGCTGACGATTTGACGCTTCCAGTACCTCCAGCCATGC 665  
 Db 574 GACTGTGGAGACGATGTGCTGACGATTTGACGCTTCCAGTACCTCCAGCCATGC 633  
 QY 666 CGGGGACGAGATGTGCTGACGATTTGACGCTTCCAGTACCTCCAGCCATGC 725  
 Db 634 CGGGGACGAGATGTGCTGACGATTTGACGCTTCCAGTACCTCCAGCCATGC 693  
 QY 726 TGGAGTCACTGACCAAAATGACCAAGGAGGAGCAATGGACCATCTGTGACCAAG 785  
 Db 694 TGGAGTCACTGACCAAAATGACCAAGGAGGAGCAATGGACCATCTGTGACCAAG 753  
 QY 786 AGGAGTCACTGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 845  
 Db 754 AGGAGTCACTGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 813  
 QY 846 ACACCCCTGCGCGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 905  
 Db 814 ACACCCCTGCGCGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 873  
 QY 906 ATCACTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 965  
 Db 874 ATCACTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 933  
 QY 966 CTCTGCGAGCCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1009  
 Db 934 CTCTGCGAGCCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 977

RESULT 4  
 LOCUS BX418715  
 DEFINITION BX418715 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
 CS0DF008YN12 5-PRIME, mRNA sequence.  
 VERSION BX418715  
 KEYWORDS BX418715.1 GI:30769505  
 SOURCE EST.  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 1201)  
 Full-length cDNA libraries and normalization  
 Unpublished  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 6027.r. For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cot-bin/cluster.cgi?seq=CS0DF008YN12&OP1=cluster=6027.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0DF008YN12

FEATURES  
 source  
 1..1201  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DF008YN12"  
 /tissue\_type="FETAL BRAIN"  
 /dev\_stage="fetal"  
 /clone\_id="Homo sapiens FETAL BRAIN"  
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-strand cDNA was digested with Not I and

BASE COUNT 266 a 347 c 379 g 195 t 14 others  
 ORIGIN  
 Query Match 29.4%; Score 760; DB 13; Length 1201;  
 Best Local Similarity 59.8%; Pred. No. 0;  
 Matches 1000; Conservative 0; Mismatches 0; Indels 2; Gaps 2;  
 QY 55 CGCAGCCGCGGCGCTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 114  
 Db 67 CGCAGCCGCGGCGCTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 126  
 QY 115 GGTTCAGTCCGCGGCGGCGCTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 174  
 Db 127 GGTTCAGTCCGCGGCGGCGCTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 186  
 QY 175 TGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 234  
 Db 187 TGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 246  
 QY 235 CCTGGCTCCAGTCAAGCGCGCGCGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 294  
 Db 247 CCTGGCTCCAGTCAAGCGCGCGCGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 305  
 QY 295 ATGAGATGTTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 354  
 Db 306 ATGAGATGTTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 364  
 QY 355 CGGTGGAAGAGATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 414  
 Db 365 CGGTGGAAGAGATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 424  
 QY 415 CAACTTACCTTCCAGCTATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 474  
 Db 425 CAACTTACCTTCCAGCTATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 484  
 QY 475 CCATCATGTGCAACGAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAAT 534  
 Db 485 CCATCATGTGCAACGAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAAT 544  
 QY 535 TTTCAGAGACAGTTATCATATCTGTGGAGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 594  
 Db 545 TTTCAGAGACAGTTATCATATCTGTGGAGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 604  
 QY 595 TCATGAGAGAG 654  
 Db 605 TCATGAGAGAG 664  
 QY 655 GCCAGCCATGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 714  
 Db 665 GCCAGCCATGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 724  
 QY 715 AGCTGTGTGCTGGGAGTCACTGACCAAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 774  
 Db 725 AGCTGTGTGCTGGGAGTCACTGACCAAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 784  
 QY 775 GTGACACGAGAG 834  
 Db 785 GTGACACGAGAG 844  
 QY 835 TCCCTGTGTGCAACCCCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 894  
 Db 845 TCCCTGTGTGCAACCCCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 904  
 QY 895 TTCTGAGCTCATCACTGTGAGAGTGAAGCTGTGAGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 954  
 Db 905 TTCTGAGCTCATCACTGTGAGAGTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 964  
 QY 955 CCAGTGGCTCTCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1014  
 Db 965 CCAGTGGCTCTCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1024

QY 1015 TCGTGGGAGAGCCGTRACCAAGATGGGAGATCTCTGCTGCCA 1056  
 Db 1025 TCGTGGGAGAGCCGTRACCAAGATGGGAGATCTCTGCTGCCA 1066

RESULT 5  
 B0879213 936 bp mRNA linear EST 16-AUG-2002  
 DEFINITION AGENCOURT 8229317 lupski\_dorsal\_root\_ganglion Homo sapiens cDNA  
 LOCUS clone IMAGE:6183568 5', mRNA sequence.

ACCESSION B0879213  
 VERSION B0879213  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/1 (bases 1 to 936)  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: Dr. James R. Lupski  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: L14M13571 row: f column: 17  
 High quality sequence stop: 708.

FEATURES  
 source  
 1..936  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6183568"  
 /sex="male"  
 /tissue\_type="dorsal root ganglia"  
 /dev\_stage="adult, 36 yr"  
 /lab\_host="DH10B"  
 /clone\_lib="lupski\_dorsal\_root\_ganglion"  
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:  
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.  
 Directionally cloned using the following adaptors:  
 5'-TCGACCCAGCGCGTCCG-3' and  
 5'-GACTAGTCTAGATCGGAGCGCGCCCTT(15)-3'. Size selected >  
 1 kb for average insert length 1.7 kb. This is a primary  
 library, non-amplified. Library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine) and is available through Life  
 Technologies."

BASE COUNT 213 a 249 c 289 g 185 t  
 ORIGIN

Query Match 29.3%; Score 758; DB 13; Length 936;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 758; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 AGAAGTGAACCTGGCAACTTACCTCCAGCTATCAACATGAGACCAACAGACAGCA 460  
 Db 1 AGAAGTGAACCTGGCAACTTACCTCCAGCTATCAACATGAGACCAACAGACAGCA 60

QY 461 GGTGGAAATTAATCAATCATGAGACCGAGAAATTCACAAATTAACCAACACAGAC 520  
 Db 61 GGTGGAAATTAATCAATCATGAGACCGAGAAATTCACAAATTAACCAACACAGAC 120

QY 521 TGGCAAAATGCTCTTTTCAGAGACAGTATCACTCTGTGGAGACGAGAGAGCGAAG 580  
 Db 121 TGGCAAAATGCTCTTTTCAGAGACAGTATCACTCTGTGGAGACGAGAGAGCGAAG 180

QY 581 GAGCCAGAGTGCATCATGAGAGAGACTGTGGGCCCAAGATGTACGACAGTTGCCAG 640

Db 181 GAGCCAGAGTGCATCATGAGAGAGACTGTGGGCCCAAGATGTACGACAGTTGCCAG 240  
 QY 641 CTTCAGATCACTCTGAGAGCCATGCGGGGCGAGAGATGCTCTGCAACCGGGAGATGA 700  
 Db 241 CTTCAGATCACTCTGAGAGCCATGCGGGGCGAGAGATGCTCTGCAACCGGGAGATGA 300  
 QY 701 GTGCTGTGAGAGACCAAGCTGTGTCTGTGGGCTCACTGACCAAAATGACCAAGGGGCGAG 760  
 Db 301 GTGCTGTGAGAGACCAAGCTGTGTCTGTGGGCTCACTGACCAAAATGACCAAGGGGCGAG 360

QY 761 CAATGAGACCAATCTGTGAGACCAAGAGGAGCTGCCAGCGGGGCTGTGTGCTTCCA 820  
 Db 361 CAATGAGACCAATCTGTGAGACCAAGAGGAGCTGCCAGCGGGGCTGTGTGCTTCCA 420

QY 821 GAGAGGCTGTGCTGCTTCTCTGTGTGACACACCCCTGCCGTGAGAGGCGACCTTGCCATGA 880  
 Db 421 GAGAGGCTGTGCTGCTTCTCTGTGTGACACACCCCTGCCGTGAGAGGCGACCTTGCCATGA 480

QY 881 CCCCCGAGCGGCTTCTGACCTCTATCACTGTGAGAGCTGAGAGCTGATGAGACCTTGA 940  
 Db 481 CCCCCGAGCGGCTTCTGACCTCTATCACTGTGAGAGCTGAGAGCTGATGAGACCTTGA 540

QY 941 CCGATGCGCTTGTGCGAGTGGCTCTCTGCGAGCCCAAGCCCAAGCCTGTGTATGT 1000  
 Db 541 CCGATGCGCTTGTGCGAGTGGCTCTCTGCGAGCCCAAGCCTGTGTATGT 600

QY 1001 GTGCAGAGCCGACCTTGTGTGGGAGCGGTGACCAAGATGGGAGATCTCTGCGCAGAGA 1060  
 Db 601 GTGCAGAGCCGACCTTGTGTGGGAGCGGTGACCAAGATGGGAGATCTCTGCGCAGAGA 660

QY 1061 GGTGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1120  
 Db 661 GGTGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720

QY 1121 CTTGAGAGAGGCGCTGACTGAAAGATGCGCTGGGCG 1158  
 Db 721 CTTGAGAGAGGCGCTGACTGAAAGATGCGCTGGGCG 758

RESULT 6  
 BUI49689 949 bp mRNA linear EST 03-SEP-2002  
 LOCUS AGENCOURT 8049944 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6083782  
 DEFINITION 5', mRNA sequence.  
 BUI49689  
 BUI49689 1 GI:22663221  
 VERSION BUI49689.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/1 (bases 1 to 949)  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: L14M2314 row: h column: 23  
 High quality sequence start: 19  
 High quality sequence stop: 678.

FEATURES  
 source  
 1..949  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"

/clone="IMAGE:6083782"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_id="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI;  
 Site\_2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAAGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC library."

BASE COUNT 188 a 236 c 288 g 237 t  
 ORIGIN

Query Match 29.1%; Score 752; DB 13; Length 949;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 802; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

848 ACCCTGCCCCGTTGGAGGGGAGGCTTTGCCATGACCCCGGACCGGCTTTGACCTCAT 907  
 31 ACCCTGCCCCGTTGGAGGGGAGGCTTTGCCATGACCCCGGACCGGCTTTGACCTCAT 90  
 908 CACCTGGAGACTAGAGCTGATGAGACCTTGGACCGATGCCCTTGTGGCAGTGGCCCTCT 967  
 91 CACCTGGAGACTAGAGCTGATGAGACCTTGGACCGATGCCCTTGTGGCAGTGGCCCTCT 150  
 968 CTGCGACCCCGACAGCCAGCCTGTGTATGTGTGCAAGCCGACCTTGTGGGAGCCG 1027  
 151 CTGCGACCCCGACAGCCAGCCTGTGTATGTGTGCAAGCCGACCTTGTGGGAGCCG 210  
 1028 TGAACAAGTGGGGAGATCCTGCTGCCAGAGGCTCCCGAGTGAATGAAGTTGGCAG 1087  
 211 TGAACAAGTGGGGAGATCCTGCTGCCAGAGGCTCCCGAGTGAATGAAGTTGGCAG 270  
 1088 CTTCATGAGAGAGTGGCCGACAGAGCTGGAGACCTGGAGAGAGCTTGAAGAGAT 1147  
 271 CTTCATGAGAGAGTGGCCGACAGAGCTGGAGAGCTGGAGAGAGCTTGAAGAGAT 330  
 1148 GGGCGTGGGGAGCCCTGGCGCTGGCCCGCTGACATGCTGGAGAGGAGAGATTTAGT 1207  
 331 GGGCGTGGGGAGCCCTGGCGCTGGCCCGCTGACATGCTGGAGAGGAGAGATTTAGT 390  
 1208 CTGACACAGGCTGTGGGTAGATGTGCAATGAATAGTAAATTTATTTCCAGGTGTGT 1267  
 391 CTGACACAGGCTGTGGGTAGATGTGCAATGAATAGTAAATTTATTTCCAGGTGTGT 450  
 1268 GCTTTAGGGCTGGGCTGACAGGCTTCTTCTCAATCTTCTTCCAGTAAGTTCCCTTC 1327  
 451 GCTTTAGGGCTGGGCTGACAGGCTTCTTCTCAATCTTCTTCCAGTAAGTTCCCTTC 510  
 1328 TGGCTTGAACAGATGAGGTGTGTGCAATTTGTTCAGCTCCCGAGGCTTTCTCCAGGT 1387  
 511 TGGCTTGAACAGATGAGGTGTGTGCAATTTGTTCAGCTCCCGAGGCTTTCTCCAGGT 570  
 1388 TCACAGTCTGTGCTTGGAGAGTCAAGCAAGGTTAACTGACAGAGCAGTTTGCACCC 1447  
 571 TCACAGTCTGTGCTTGGAGAGTCAAGCAAGGTTAACTGACAGAGCAGTTTGCACCC 630  
 1448 CTGTCCAGATTTATTTGGCTGCTTGGCTTCAACAGTTGGCAGAGCAGTTTGTCTCAT 1507  
 631 CTGTCCAGATTTATTTGGCTGCTTGGCTTCAACAGTTGGCAGAGCAGTTTGTCTCAT 690  
 1508 GGGCTTTGATTAATTTGTTGAGGGAGAGATGAAACAATGTGAGTCTCTCTGATTTGG 1567  
 691 GGGCTTTGATTAATTTGTTGAGGGAGAGATGAAACAATGTGAGTCTCTCTGATTTGG 750  
 1568 TTTTGGGGAATTTGAGAGAGATGTGCTGCTTGGCAACATCAACTGGCAAAAATGCA 1627  
 751 TTTTGGGGAATTTGAGAGAGATGTGCTGCTTGGCAACATCAACTGGCAAAAATGCA 810  
 1628 ACAATGAATTTTCCACGAGTT 1650

Db 811 ACAATGAATTTTCCACGAGTT 833

RESULT 7  
 BU196879 985 bp mRNA linear EST 04-SEP-2002  
 LOCUS AGENCOURT\_8076102 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6084891  
 DEFINITION 5', mRNA sequence.  
 ACCESSION BU196879  
 VERSION BU196879.1 GI:22710863  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM

REFERENCE  
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: gga@ds-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: L10M2317 row: 9 column: 04  
 High quality sequence stop: 644.  
 Location/Qualifiers

#### FEATURES

1..985  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6084891"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_id="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI;  
 Site\_2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAAGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC library."

BASE COUNT 199 a 256 c 282 g 248 t  
 ORIGIN

Query Match 28.7%; Score 741; DB 13; Length 985;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 791; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

849 CCCCTGCCCCGTTGGAGGGGAGGCTTTGGCATGACCCCGGACCGGCTTTGAGACTCATC 908  
 1 CCCCTGCCCCGTTGGAGGGGAGGCTTTGGCATGACCCCGGACCGGCTTTGAGACTCATC 60  
 909 ACTGAGAGCTAGAGCTGATGAGAGCTTGGACCGATGCCCTTGTGCGAGTGGCTCTC 968  
 61 ACTGAGAGCTAGAGCTGATGAGAGCTTGGACCGATGCCCTTGTGCGAGTGGCTCTC 120  
 969 TGGCAGCCCCCAGACCCAGAGCTGTGTATGTGTGCAAGCGACCTTGTGGGAGGCGT 1028  
 121 TGGCAGCCCCCAGACCCAGAGCTGTGTATGTGTGCAAGCGACCTTGTGGGAGGCGT 180  
 1029 GACCAAGTGGGAGAGATCTGTGCTGCCAGAGAGGTCCCGCATGATGAATGAGTTGGCAGC 1088  
 181 GACCAAGTGGGAGAGATCTGTGCTGCCAGAGAGGTCCCGCATGATGAATGAGTTGGCAGC 240  
 1089 TTCTATGAGAGAGTGGCGCCAGAGACTGGAGAGCTTGGAGAGAGCTTGAAGAGATG 1148  
 241 TTCTATGAGAGAGTGGCGCCAGAGACTGGAGAGCTTGAAGAGAGCTTGAAGAGATG 300



QY 1149 GCGCTGGGGAGAGCTGCGGCTGCGCGCTGCTGCTGAGGAGGAGATTTAGATC 1208  
 DB 301 GCGCTGGGGAGAGCTGCGGCTGCGCGCTGCTGCTGAGGAGGAGATTTAGATC 360  
 QY 1209 TGGACGAGGCTGTGGGTGATGTGCAATGAAATGCTAATTTATTTCCCGAGGTGTG 1268  
 DB 361 TGGACGAGGCTGTGGGTGATGTGCAATGAAATGCTAATTTATTTCCCGAGGTGTG 420  
 QY 1269 CTTTGGGCTGGGCTGAGCAGGCTCTCTCAATCTCTCCAGTAAGTTCCCTCT 1328  
 DB 421 CTTTGGGCTGGGCTGAGCAGGCTCTCTCAATCTCTCCAGTAAGTTCCCTCT 480  
 QY 1329 GCGCTGAGCAGATGAGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1388  
 DB 481 GCGCTGAGCAGATGAGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 QY 1389 CACAGCTGTGCTGTGGAGAGTCAAGGAGGTTAACTGAGAGGAGTGTGCACTCC 1448  
 DB 541 CACAGCTGTGCTGTGGAGAGTCAAGGAGGTTAACTGAGAGGAGTGTGCACTCC 600  
 QY 1449 TGTCCAGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1508  
 DB 601 TGTCCAGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
 QY 1509 GCTTGGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1568  
 DB 661 GCTTGGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
 QY 1569 TTTGGGAAATGTGGAGAGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1628  
 DB 721 TTTGGGAAATGTGGAGAGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 QY 1629 CAAATGATTTT 1640  
 DB 781 CAAATGATTTT 792

RESULT 8  
 B0689208  
 LOCUS  
 DEFINITION AGNCOURT\_8063939 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6207819  
 5', mRNA sequence.  
 ACCESSION B0689208.1 GI:21814524  
 VERSION B0689208  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 870)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 Contract: Robert Strausberg, Ph.D.  
 Email: rgs@bbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov/  
 Plate: L10M2364 row: 1 column: 04  
 High quality sequence stop: 691.  
 Location/Qualifiers  
 1..870

FEATURES  
 source  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6207819"  
 /issue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"

/clone.lib="NIH MGC 110"  
 /note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GCGACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH MGC Library."

BASE COUNT 170 a 217 c 267 g 216 t  
 ORIGIN

Query Match 28.4%; Score 734; DB 13; Length 870;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 784; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 849 CCCTGCCCCGAGAGGAGAGCTTGGCATGACCCCGAGCCGCTTGTGACCTCATC 908  
 DB 1 CCCTGCCCCGAGAGGAGAGCTTGGCATGACCCCGAGCCGCTTGTGACCTCATC 60  
 QY 909 ACCTGGAGCTAGAGCTTATGAGAGCTTGAACCGATGCCCTTGTGCAAGTGGCCCTC 968  
 DB 61 ACCTGGAGCTAGAGCTTATGAGAGCTTGAACCGATGCCCTTGTGCAAGTGGCCCTC 120  
 QY 969 TGGCAGCCCCCAGAGCAGAGCTGATGTGTGTGCAAGCCGACCTTCGTGGGAGCCGT 1028  
 DB 121 TGGCAGCCCCCAGAGCAGAGCTGATGTGTGTGCAAGCCGACCTTCGTGGGAGCCGT 180  
 QY 1029 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGATGATGAGTGGCAGC 1088  
 DB 181 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGATGATGAGTGGCAGC 240  
 QY 1089 TTCTATGAGAGAGGTGGGAGAGAGCTGAGAGAGCTGAGAGAGAGCTGAGAGAGATG 1148  
 DB 241 TTCTATGAGAGAGGTGGGAGAGAGCTGAGAGAGCTGAGAGAGAGCTGAGAGAGATG 300  
 QY 1149 GCGCTGGGAGAGCTGCGGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1208  
 DB 301 GCGCTGGGAGAGCTGCGGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 QY 1209 TGGACGAGGCTGTGGGTGATGTGCAATGAAATGCTAATTTATTTCCCGAGGTGTG 1268  
 DB 361 TGGACGAGGCTGTGGGTGATGTGCAATGAAATGCTAATTTATTTCCCGAGGTGTG 420  
 QY 1269 CTTTGGGCTGGGCTGAGCAGGCTCTCTCAATCTCTCCAGTAAGTTCCCTCT 1328  
 DB 421 CTTTGGGCTGGGCTGAGCAGGCTCTCTCAATCTCTCCAGTAAGTTCCCTCT 480  
 QY 1329 GCGCTGAGCAGATGAGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1388  
 DB 481 GCGCTGAGCAGATGAGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 QY 1389 CACAGCTGTGCTGTGGAGAGTCAAGGAGGTTAACTGAGAGGAGTGTGCACTCC 1448  
 DB 541 CACAGCTGTGCTGTGGAGAGTCAAGGAGGTTAACTGAGAGGAGTGTGCACTCC 600  
 QY 1449 TGTCCAGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1508  
 DB 601 TGTCCAGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
 QY 1509 GCTTGGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1568  
 DB 661 GCTTGGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
 QY 1569 TTTGGGAAATGTGGAGAGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1628  
 DB 721 TTTGGGAAATGTGGAGAGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 QY 1629 CAAAT 1633  
 DB 781 CAAAT 785

```

RESULT 9
BQ230646      885 bp      mRNA      linear      EST 02-MAY-2002
LOCUS         AGENCOURT 7273720 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6016827
DEFINITION    5', mRNA sequence.
ACCESSION     BQ230646
VERSION       BQ230646.1 GI:20412046
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 885)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM13215 row: c column: 04
High quality sequence stop: 665.
Location/Qualifiers
1..885
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6016827"
/tissue_type="epitheloid carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_70"
/note="Organ: pancreas; Vector: pCMV-Sport6; Site: 1; NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
BASE COUNT    184 a      212 c      251 g      234 t      4 others
ORIGIN
Query Match      28.4%; Score 734; DB 13; Length 885;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1082  TGGCAGTTCATGAGAGAGGTGGCCAGAGCTGGAGAGACCTGGAGAGAGGCTGCTGA 1141
DB      1   TGGCAGTTCATGAGAGAGGTGGCCAGAGCTGGAGAGACCTGGAGAGAGGCTGCTGA 60

QY      1142  AGAGATGGCGCTGGGGAGGCTGGCGGCTGCCGCGCTGCACTGCTGGAGAGGAGAGAT 1201
DB      61  AGAGATGGCGCTGGGGAGGCTGGCGGCTGCCGCGCTGCACTGCTGGAGAGGAGAGAT 120

QY      1202  TTAGATCTGAGACCAAGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCGAG 1261
DB      121  TTAGATCTGAGACCAAGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCGAG 180

QY      1262  GTGTGTCCTTAGAGCGTGGGCTGACCAAGGCTTCTTCTACATCTTCTCCAGTAAGTTT 1321
DB      181  GTGTGTCCTTAGAGCGTGGGCTGACCAAGGCTTCTTCTTCTACATCTTCTCCAGTAAGTTT 240

QY      1322  CCCCTCTGGCTTGACAGCATGAGAGTGTGGCATTTTGTTCAGCTCCCCAGAGCTGTTC 1381
DB      241  CCCCTCTGGCTTGACAGCATGAGAGTGTGGCATTTTGTTCAGCTCCCCAGAGCTGTTC 300

QY      1382  CAGGCTTCACAGTCTGTGCTGGAGAGTCAAGGAGGCTTAATGCAAGAGACAGTTTG 1441
DB      301  CAGGCTTCACAGTCTGTGCTGGAGAGTCAAGGAGGCTTAATGCAAGAGACAGTTTG 360

QY      1442  CCACCCCTGTCCAGATTATGGCTGCTTGGCTCTTACAGTTGGCAGACAGCCGTTTGT 1501

```

```

DB      361  CCACCCCTGTCCAGATTATTTGGCTGCTTGGCTCTTACAGTTGGCAGACAGCCGTTTGT 420
QY      1502  CTACATGGCTTTGATTAATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCTCT 1561
DB      421  CTACATGGCTTTGATTAATTTGTTGAGGGGAGAGATGAAACAATGTGAGTCTCCTCT 480
QY      1562  GATTGTTTTGGGAAATGTGGAGAAAGAGGCGCTGTTTGGCAAACTCAACCTGGCAA 1621
DB      481  GATTGTTTTGGGAAATGTGGAGAAAGAGTGCCTGTTTGGCAAACTCAACCTGGCAA 540
QY      1622  AATCAACAATGAATTTTCCACGACAGTCTTTCATAGGAGCATAGTAACCTGTGCTTC 1681
DB      541  AATCAACAATGAATTTTCCACGACAGTCTTTCATAGGAGCATAGTAACCTGTGCTTC 600
QY      1682  AGCTGTGGCAGATGAATGTTCCTGTTTCACTTCACTTCACTTCACTTCACTTCACT 1741
DB      601  AGCTGTGGCAGATGAATGTTCCTGTTTCACTTCACTTCACTTCACTTCACTTCACT 660
QY      1742  TGTGCTCAGCTCTACCTCTGTGCGCAGGAGCATTTTCATATCCAAATCAATTCCT 1801
DB      661  TGTGCTCAGCTCTACCTCTGTGCGCAGGAGCATTTTCATATCCAAATCAATTCCT 720
QY      1802  CTCTCAGCAGACGCC 1815
DB      721  CTCTCAGCAGACGCC 734

RESULT 10
BQ722575      931 bp      mRNA      linear      EST 16-JUL-2002
LOCUS         AGENCOURT 8304969 Lupski_sympathetic_trunk Homo sapiens cDNA clone
DEFINITION    IMAGE:6133228 5', mRNA sequence.
ACCESSION     BQ722575
VERSION       BQ722575.1 GI:21861472
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 931)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM13596 row: i column: 05
High quality sequence stop: 642.
Location/Qualifiers
1..931
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6133228"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult", 16 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sympathetic trunk"
/note="Vector: pCMV-Sport6 (Life Technologies); Site: 1;
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGGTCG-3' and
5'-GACTAGTCTGATGCGAGCGGCGGCTT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor

```



Db 541 CACAGTCTGGTCTTGGAGAGATGAGGAGGGTTAACTGACGAGGAGGATTGGACACCC 600  
QY 1449 TGTCCAGATTATGGCTGCTTGGCTCTTACGATTGGAGAGAGCCGTTGTTCAATG 1508  
Db 601 TGTCCAGATTATGGCTGCTTGGCTCTTACGATTGGAGAGAGCCGTTGTTCAATG 660  
QY 1509 GCTTGTATATTTGTTGAGGAGAGAGATGAAACATGTGAGTCTCCCTCTGATTGGT 1568  
Db 661 GCTTGTATATTTGTTGAGGAGAGAGATGAAACATGTGAGTCTCCCTCTGATTGGT 720  
QY 1569 TTTGGGAAATGTGAGAAAGATGCCCTGCTTTCACAAATCAACC 1614  
Db 721 TTTGGGAAATGTGAGAAAGATGCCCTGCTTTCACAAATCAACC 766  
RESULT 12  
BUI62929 1065 bp mRNA linear EST 04-SEP-2002  
LOCUS AGENCOURT\_6910849 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:5952242  
DEFINITION 5', mRNA sequence.  
ACCESSION BUI62929  
VERSION BUI62929.1 GI:22676839  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1065)  
NIH-MGC http://mgs.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLCM2139 row: P column: 03  
High quality sequence stop: 647.  
Location/Qualifiers  
1. 1065  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5952242"  
/tissue="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 110"  
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-CDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC library."

Db 61 ACCTGGAGCTTAAGCCTGATGAGACCTTGGACCCATGCCCTTGTGCTGAGTGGCTTC 120  
QY 969 TGCAGAGCCCAACAGCAGACCTGATGATGTGAGAGCCGCTTGTGAGGAGCCGT 1028  
Db 121 TGCAGAGCCCAACAGCAGACCTGATGATGTGAGAGCCGCTTGTGAGGAGCCGT 180  
QY 1029 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGGATGAGATGAGATGGAGC 1088  
Db 181 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCGGATGAGATGAGATGGAGC 240  
QY 1089 TTCATGAGAGAGGTGCGCCAGAGAGCTGAGAGACCTGAGAGAGAGCTGAGAGAGATG 1148  
Db 241 TTCATGAGAGAGGTGCGCCAGAGAGCTGAGAGACCTGAGAGAGAGCTGAGAGAGATG 300  
QY 1149 GCGCTGGAGAGAGCTGCGGCTGCGCCGCTGCGCACTGTGGAGAGGAGAGATTTAGATC 1208  
Db 301 GCGCTGAGAGAGAGCTGCGGCTGCGCCGCTGCGCACTGTGGAGAGGAGAGATTTAGATC 360  
QY 1209 TGAACAGAGCTGTGGATGATGTCATATGATGATGATGATGATGATGATGATGATG 1268  
Db 361 TGAACAGAGCTGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
QY 1269 CTTTACGCTGAGCTGACACAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1328  
Db 421 CTTTACGCTGAGCTGACACAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 480  
QY 1329 GCGTTGACAGATGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1388  
Db 481 GCGTTGACAGATGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 540  
QY 1389 CACAGTCTGATGCTTGGAGAGTCAAGGAGGTTAACTGACAGAGATTTGACACCC 1448  
Db 541 CACAGTCTGATGCTTGGAGAGTCAAGGAGGTTAACTGACAGAGATTTGACACCC 600  
QY 1449 TGTCCAGATTATGGCTGCTTGGCTCTTACAGATTGGAGAGAGCCGTTTGTCAATG 1508  
Db 601 TGTCCAGATTATGGCTGCTTGGCTCTTACAGATTGGAGAGAGCCGTTTGTCAATG 660  
QY 1509 GCTTGTATATTTGTTGAGGAGAGAGATGAAACATGTGAGTCTCCCTGATTGGT 1568  
Db 661 GCTTGTATATTTGTTGAGGAGAGAGATGAAACATGTGAGTCTCCCTGATTGGT 720  
QY 1569 TTTGGGAAATGTGAGAAAGATGCCCTGCTTTCACAAATCAACC 1614  
Db 721 TTTGGGAAATGTGAGAAAGATGCCCTGCTTTCACAAATCAACC 766  
RESULT 13  
BQ889489 892 bp mRNA linear EST 16-AUG-2002  
LOCUS AGENCOURT\_8061866 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6208646  
DEFINITION 5', mRNA sequence.  
ACCESSION BQ889489  
VERSION BQ889489.1 GI:22281503  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 892)  
NIH-MGC http://mgs.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLCM2366 row: K column: 15

High quality sequence stop: 680.  
Location/Qualifiers

source  
1. .892  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6208646"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."  
BASE COUNT 179 a 223 c 269 g 221 t  
ORIGIN

Query Match 27.5%; Score 711; DB 13; Length 892;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 761; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

849 CCCCTGCCCCGTGAGGAGGAGCTTTGCCATGACCCGCCAGCCGCTTGTGACCTCATC 908  
1 CCCCTGCCCCGTGAGGAGGAGCTTTGCCATGACCCGCCAGCCGCTTGTGACCTCATC 60  
909 ACCGTGGAGGTAGAGCTGATGAGAGCTTGGACCGATGACCTTGTGACCTCATC 968  
61 ACCGTGGAGGTAGAGCTGATGAGAGCTTGGACCGATGACCTTGTGACCTCATC 120  
969 TGGCAGGCCCAACAGCCAGCCTGTGTATGTGTGCAAGCCGACTTGTGGAGAGCCGT 1028  
121 TGGCAGGCCCAACAGCCAGCCTGTGTATGTGTGCAAGCCGACTTGTGGAGAGCCGT 180  
1029 GACCAAGATGGAGAGATCTCTGCTGCCAGAGAGTCCCGCATAGATAGATTTGGCAGC 1088  
181 GACCAAGATGGAGAGATCTCTGCTGCCAGAGAGTCCCGCATAGATAGATTTGGCAGC 240  
1089 TTCAATGAGAGAGGTGCGCCAGAGAGCTTGAAGACCTTGAAGAGAGCTTGAAGAGATG 1148  
241 TTCAATGAGAGAGGTGCGCCAGAGAGCTTGAAGACCTTGAAGAGAGCTTGAAGAGATG 300  
1149 GCGCTGGAGAGCTTGGCGCTGCGCCGCTGCACTGCTGGAGAGAGAGATTTAGATC 1208  
301 GCGCTGGAGAGCTTGGCGCTGCGCCGCTGCACTGCTGGAGAGAGAGATTTAGATC 360  
1209 TGAACCAAGGCTGTGGATAGATGTGCAATAGATAATTAATTTATTTCCCAAGTGTGTG 1268  
361 TGAACCAAGGCTGTGGATAGATGTGCAATAGATAATTAATTTATTTCCCAAGTGTGTG 420  
1269 CTTAAGCGTGGCTGACCAAGCTTCTTCTCAATCTTCTTCCCAAGTATTTCCCTCTC 1328  
421 CTTAAGCGTGGCTGACCAAGCTTCTTCTCAATCTTCTTCCCAAGTATTTCCCTCTC 480  
1329 GCGTTGACAGATGAGGTGTGATTTGTCATTTGTCAGCTCCCAAGGCTTCTCAAGCTT 1388  
481 GCGTTGACAGATGAGGTGTGATTTGTCATTTGTCAGCTCCCAAGGCTTCTCAAGCTT 540  
1389 CACAGTCTGTGCTTGGAGAGTCAAGAGAGGTTAACTGCAAGAGAGAGTTGGCACTCC 1448  
541 CACAGTCTGTGCTTGGAGAGTCAAGAGAGGTTAACTGCAAGAGAGAGTTGGCACTCC 600  
1449 TGTCCAGATTATGGCTGTGCTTGTGCTCTCAACAGTTGGCAAGAGCTTTGTTCAATG 1508  
601 TGTCCAGATTATGGCTGTGCTTGTGCTCTCAACAGTTGGCAAGAGCTTTGTTCAATG 660  
1509 GCTTGAATTAATTTGTTGAGGAGAGATGAGAACTAATGTGAGTCTTCTGATTTGAT 1568  
661 GCTTGAATTAATTTGTTGAGGAGAGATGAGAACTAATGTGAGTCTTCTGATTTGAT 720

QY 1569 TTGGGGAATGTGAGAGAGTCCCTGCTTTCACACATC 1610  
DB 721 TTGGGGAATGTGAGAGAGTCCCTGCTTTCACACATC 762

RESULT 14  
B0686792  
LOCUS  
DEFINITION  
5', mRNA sequence.  
AGENCOURT 8343587 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6250382  
B0686792.1 GI:21812108  
EST.  
Homo sapiens (human)  
SOURCE  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 932)  
NIH-MGC http://img.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cga@dcf-remail.nih.gov  
Tissue Procurement: ATCC  
DNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LMNL at:  
http://image.llnl.gov  
Plate: L1CM2393 row: f column: 15  
High quality sequence stop: 710.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

1. .932  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6250382"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."  
BASE COUNT 184 a 235 c 279 g 234 t  
ORIGIN

Query Match 27.4%; Score 708; DB 13; Length 932;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 758; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

847 CACCCCTGCGGTGAGAGGCGAGCTTTCACATGACCCCGAGCGGCTTGTGACCTCA 906  
18 CACCCCTGCGGTGAGAGGCGAGCTTTCACATGACCCCGAGCGGCTTGTGACCTCA 77  
907 TCACCTGGAGCTAGAGCTGATGAGAGCTTGAACCGATGACCTTGTGACCTCACTCC 966  
78 TCACCTGGAGCTAGAGCTGATGAGAGCTTGAACCGATGACCTTGTGACCTCACTCC 137  
967 TGTGCAAGCCCAACAGCCAGCCTGTGTGTGTGTGAAACCACTTGTGGGAGACC 1026  
138 TGTGCAAGCCCAACAGCCAGCCTGTGTGTGTGTGAAACCACTTGTGGGAGACC 197  
1027 GTGACCAAGATGGAGAGATCTGCTGCCAGAGAGTCCCGATGATGATGAGTTGGCA 1086  
198 GTGACCAAGATGGAGAGATCTGCTGCCAGAGAGTCCCGATGATGATGAGTTGGCA 257  
1087 GCTTATGAGAGAGTGTGCGCCAGAGAGCTGTGAGAGACTGTGAGAGAGAGCTGATGAGAG 1146

Db 258 GCTTCAATGAGAGAGCTGCGCCAGAGCTGAGAGACCTGAGAGAGAGCTGAGAGAGAGA 317  
 QY 1147 TGGCGCTGGGGGAGCTTGGCGCTGGCGCCGCTCACTGCTGGAGAGGAGAGATTAGA 1206  
 Db 318 TGGCGCTGAGGGAGCTTGGCGCTGGCGCCGCTCACTGCTGGAGAGGAGAGATTAGA 377  
 QY 1207 TCTGAGACAGAGCTGAGAGAGTATGATGCAATAGATTAATTATTTCCAGAGTGTG 1266  
 Db 378 TCTGAGACAGAGCTGAGAGAGTATGATGCAATAGATTAATTATTTCCAGAGTGTG 437  
 QY 1267 TGGTTAGAGAGCTGAGAGAGTATGATGCAATAGATTAATTATTTCCAGAGTGTG 1326  
 Db 438 TGGTTAGAGAGCTGAGAGAGTATGATGCAATAGATTAATTATTTCCAGAGTGTG 497  
 QY 1327 TGGTTAGAGAGCTGAGAGAGTATGATGCAATAGATTAATTATTTCCAGAGTGTG 1386  
 Db 498 TGGTTAGAGAGCTGAGAGAGTATGATGCAATAGATTAATTATTTCCAGAGTGTG 557  
 QY 1387 TTTCAAGCTGAGAGAGTATGATGCAATAGATTAATTATTTCCAGAGTGTG 1446  
 Db 558 TTTCAAGCTGAGAGAGTATGATGCAATAGATTAATTATTTCCAGAGTGTG 617  
 QY 1447 CCGTCCAGATTAATGCTGCTGCTTGGCTCTACAGATTTGGAGAGAGCTTTGCTTACA 1506  
 Db 618 CCGTCCAGATTAATGCTGCTGCTTGGCTCTACAGATTTGGAGAGAGCTTTGCTTACA 677  
 QY 1507 TGGCTTGAATATTTGTTGAGAGAGAGATGAGAAACAATGAGAGTCTCCCTGATTTG 1566  
 Db 678 TGGCTTGAATATTTGTTGAGAGAGAGATGAGAAACAATGAGAGTCTCCCTGATTTG 737  
 QY 1567 GTTTTGGGAAATGTGAGAGAGAGTGGCTTGTGCTTTGCA 1605  
 Db 738 GTTTTGGGAAATGTGAGAGAGAGTGGCTTGTGCTTTGCA 776

RESULT 15  
 B0890463 878 bp mRNA linear EST 16-AUG-2002  
 LOCUS AGENCOURT\_8064243 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6207928  
 DEFINITION 5', mRNA sequence.  
 B0890463  
 VERSION B0890463.1 GI:22282477  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 NIH-MGC http://mgs.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: gsp@biml.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov  
 Plate: LNCM364 row: m column: 17  
 High quality sequence stop: 677.  
 Location/Qualifiers  
 1..878  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6207928"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_id="NIH MGC 110"  
 /note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI;

Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH MGC Library."

Query Match 27.3% Score 706; DB 13; Length 878;  
 Best Local Similarity 99.9% Pred. No. 0;  
 Matches 756; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 849 CCCCCTGCGTGGAGAGGAGCTTTGGCATGACCCCGCAGCCGCTTGTGACCTATC 908  
 Db 1 CCCCCTGCGTGGAGAGGAGCTTTGGCATGACCCCGCAGCCGCTTGTGACCTATC 60  
 QY 909 ACCTGGAGCTAGAGAGCTGATGAGAGCTTGGACCGATGCTTGTGCAAGTGGCTCTC 968  
 Db 61 ACCTGGAGCTAGAGAGCTGATGAGAGCTTGGACCGATGCTTGTGCAAGTGGCTCTC 120  
 QY 969 TGGCAGCCCAAGCAGCAGAGCTGATGAGAGCTTGGACCGATGCTTGTGCAAGTGGCTCTC 1028  
 Db 121 TGGCAGCCCAAGCAGCAGAGCTGATGAGAGCTTGGACCGATGCTTGTGCAAGTGGCTCTC 180  
 QY 1029 GACCAAGATGGGGAGAGTCTGCTGCTCCAGAGAGTCCCGATGATGAAAGTTGGCAGC 1088  
 Db 181 GACCAAGATGGGGAGAGTCTGCTGCTCCAGAGAGTCCCGATGATGAAAGTTGGCAGC 240  
 QY 1089 TTCAATGAGAGAGTGGCGCAGAGAGTGGAGAGCTTGGAGAGAGCTGATGAGAGATG 1148  
 Db 241 TTCAATGAGAGAGTGGCGCAGAGAGTGGAGAGCTTGGAGAGAGCTGATGAGAGATG 300  
 QY 1149 GCGCTGGGGAGAGCTTGGCTGCTCCGCGCTGCACTGCTGGAGAGAGATTTAGTC 1208  
 Db 301 GCGCTGGGGAGAGCTTGGCTGCTCCGCGCTGCACTGCTGGAGAGAGATTTAGTC 360  
 QY 1209 TGGACAGAGCTGAGAGAGTGGATGCAATAGATTAATTATTTCCAGAGTGTG 1268  
 Db 361 TGGACAGAGCTGAGAGAGTGGATGCAATAGATTAATTATTTCCAGAGTGTG 420  
 QY 1269 CTTTGGAGTGGAGCTGAGCAGAGCTTCTTCTTCAATCTTTCCAGTAAAGTTCCCTCT 1328  
 Db 421 CTTTGGAGTGGAGCTGAGCAGAGCTTCTTCTTCAATCTTTCCAGTAAAGTTCCCTCT 480  
 QY 1329 GCGTTGAGAGAGTGGAGTGTGATTTTTCAGCTCCCGCAGAGCTTCCAGAGCTT 1388  
 Db 481 GCGTTGAGAGAGTGGAGTGTGATTTTTCAGCTCCCGCAGAGCTTCCAGAGCTT 540  
 QY 1389 CACAGTCTGAGCTTGGAGAGAGTGGAGAGGTTAACTGAGAGAGAGTTGGCAGCC 1448  
 Db 541 CACAGTCTGAGCTTGGAGAGAGTGGAGAGGTTAACTGAGAGAGAGTTGGCAGCC 600  
 QY 1449 TGTCCAGATTAATGCTGCTCTTGGCTCTTCAACAGTTGGAGAGAGCTTGTCTTCAAGT 1508  
 Db 601 TGTCCAGATTAATGCTGCTCTTGGCTCTTCAACAGTTGGAGAGAGCTTGTCTTCAAGT 660  
 QY 1509 GCTTGTATTAATTTTGGAGAGAGAGTGGAAACAATGAGAGTCTCCCTGATTTGT 1568  
 Db 661 GCTTGTATTAATTTTGGAGAGAGAGTGGAAACAATGAGAGTCTCCCTGATTTGT 720  
 QY 1569 TTTGGGAAATGTGAGAGAGAGTGGCTTGTGCTTTGCA 1605  
 Db 721 TTTGGGAAATGTGAGAGAGAGTGGCTTGTGCTTTGCA 757

RESULT 16  
 BX391733/c 922 bp mRNA linear EST 13-MAY-2003  
 LOCUS BX391733 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 DEFINITION clone CS01036YNI1 3-PRIME, mRNA sequence.  
 ACCESSION BX391733





Db	61	ACCTGGAGCTAGACCTGATGAGACCTTGGACCGATGCTTGTGCCAGTGGCCCTCTC	120			
Qy	969	TGCCAGCCCCCAACCCACAGCCCTGGTGTATGTGCAAGCCGACCTTGTGGGGAGCCGT	1028			
Db	121	TGCCAGCCCCCAACCCACAGCCCTGGTGTATGTGCAAGCCGACCTTGTGGGGAGCCGT	180			
Qy	1029	GACCAAGATGGGGAGATCTCTGCTGCCCGAAGAGGTCGCCGATGAGTATGAGATTGGACG	1088			
Db	181	GACCAAGATGGGGAGATCTCTGCTGCCCGAAGAGGTCGCCGATGAGTATGAGATTGGACG	240			
Qy	1089	TTCAATGAGAGAGTGTCCGCCAGAGCTGGAGGACCTGGAGAGAGCTGTACTGAAGAGATG	1148			
Db	241	TTCAATGAGAGAGTGTCCGCCAGAGCTGGAGGACCTGGAGAGAGCTGTACTGAAGAGATG	300			
Qy	1149	GCGCTGGGGGAGCTGTCCGCTGTCCGCCCTGTCACTGCTGGAGGGGAAAGAAATTAAATC	1208			
Db	301	GCGCTGGAGGAGCCCTGCGGCTGTCCGCCCTGTCACTGCTGGAGGGGAAAGAAATTAAATC	360			
Qy	1209	TGACACAGCTGTGGGTGATGTGTCAATAGAAATGACTAATTTATTTCCGAGGTGTG	1268			
Db	361	TGACACAGCTGTGGGTGATGTGTCAATAGAAATGACTAATTTATTTCCGAGGTGTG	420			
Qy	1269	CTTAAAGCGTGGGCTGACCAAGCTTCTTCTTCAATCTTCTTCCAGTAAGTTTCCCTCT	1328			
Db	421	CTTAAAGCGTGGGCTGACCAAGCTTCTTCTTCAATCTTCTTCCAGTAAGTTTCCCTCT	480			
Qy	1329	GCGCTGACAGATAGAGGTGTGTGCAATTTGTTCACGCTCCCCAGGCTGTCTCCAGGCTT	1388			
Db	481	GCGCTGACAGATAGAGGTGTGTGCAATTTGTTCACGCTCCCCAGGCTGTCTCCAGGCTT	540			
Qy	1389	CACAGTCTGTGTCTTGGAGAGTCAAGCAGGGTTAACTGACAGAGCAGTTCGCCACCC	1448			
Db	541	CACAGTCTGTGTCTTGGAGAGTCAAGCAGGGTTAACTGACAGAGCAGTTCGCCACCC	600			
Qy	1449	TGTCCAGATTAATGGCTGCTTGTCTTCAACGATGGGAGACAGCCGTTTGTCTCAATG	1508			
Db	601	TGTCCAGATTAATGGCTGCTTGTCTTCAACGATGGGAGACAGCCGTTTGTCTCAATG	660			
Qy	1509	GCTTGTATTAATTGTTTGAAGGGAGAGATGAAACAAATGTGAGTCTCCCTCAATTGT	1568			
Db	661	GCTTGTATTAATTGTTTGAAGGGAGAGATGAAACAAATGTGAGTCTCCCTCAATTGT	720			
Qy	1569	TTTGGGGAATGTGGAGAAAGATG 1592				
Db	721	TTTGGGGAATGTGGAGAAAGATG 744				
RESULT 18						
BQ894810 852 bp mRNA linear EST 16-AUG-2002						
BQ894810						
LOCUS						
DEFINITION AGENCOURT_8121849_lupsk1_dorsal_root_ganglion Homo sapiens cDNA						
clone IMAGE:6181825 5', mRNA sequence.						
BQ894810						
BQ894810.1 GI:22286824						
VERSION						
KEYWORDS EST.						
SOURCE Homo sapiens (human)						
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.						
REFERENCE 1 (bases 1 to 852)						
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.						
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)						
JOURNAL Unpublished						
COMMENT Contact: Robert Strausberg, Ph.D.						
Email: cga@bbs-remail.nih.gov						
Tissue Procurement: Dr. James R. Lupski						
cDNA Library Preparation: Life Technologies, Inc.						
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)						
Clone distribution: MGC clone distribution information can be						
found through the I.M.A.G.E. Consortium/LLNL at:						
http://image.llnl.gov						

Plate: L1AM13566 row: n column: 02  
High quality sequence stop: 655.  
location/Qualifiers

Plate: LIAM13566 row: n column: 02  
High quality sequence stop: 655.

FEATURES	LOCATION/QUANTITIES
SOURCE	1. .852

```
/organism="Homo sapiens"  
/mol_type="mRNA"
```

```

/db_xref="taxon:9606"
/clone="IMAGE:6181825"

```

```

/sex="male"
/tissue_type="dorsal" root c

```

```
/dev_stage="adult, 36 yr"
```

```
/lab_host="DH10B"
/clone_lib="lupski_dorsal_r
```

```

/Note="Vector: pCMV-Sport6
NotI; Site 2: SalI; CDNA ma

```

Directionally cloned using 5'-TCGACCCACGGGTCCG-3' and

5'-GACTAGTTCTAGATCGCAGCGGC  
1 kb for average insert lat

library, non-amplified. Like

technologies and donated by College of Medicine) and is

BASE COUNT	189 a	286 c	264 g	113 t
	Technologies."			

ORIGIN

Query Match	Score	DE
26.7%	690	
100.0%	NO	

```

Best Local Similarity 100.0%; Free: No. 0;
Matches 690; Conservative 0; Mismatches

```

QY 1 CGCCGCGCTCCCCGACCCGCGGCCCGCCCAACCGG

Db 21 CGCCGCGCTCCCGCACCCGCGGCCCGCCCAACCGC

51 CCGGCGGCTCCCGGCGGAGCGAGCAGATCCAC

[illegible]

81 CCCCCCCCCCCCAACAAAAA

DB -----

121 GTCGGGCGCGCTGCGGGCGCAGAGCGGAGAT

Db 141 GTCCGGGCGGCTGCGGGCGCAGAGCGGAGAT

181 GCCTGCTGCGCGCGCGGTCCCAAGGCC

Db 201 GCCTGCTGCTGGCGGCGCGGTCCCCCAGCGCCCC

241 CTC CAGTCAAGCCCGGCCCGGCTCTCAGCTACCG

Db 261 CTCAGTCAAGCCCGGCCCGGCTCTCAGCTACCC

301 TGTTCGCGAGGTGAGGA<sup>CTGATGGAGGACAC</sup>

221 TCTTCCGCGGCGCTTGAAGAACTGATGGAGGACAA

[illegible]

QY 361 AACGAGATGGAGCAGAGAGAGCTGCATCCATTACG

Db 381 AAGAGATGGAGGCAGAAAGAAGCTGCTGCTAAAGG

QY 421 TACCTCCAGCTATCACAATGAGACCAACACAGAG

Db 441 TACCTCCAGCTATCACAATGAGACCAACACAGAG

481 ATGTGCACCGAGAAATTCACAAGATAACCAACA

Db 501 ATGTGACCGAGAATTCAAGAATAACCAACA

541 AGACACTTATCACATCTGTGGGAGACGAGAAGC

561 AGACAGTTATCACA TCTGTGGAGACGAA GAAGC

[illegible]

**DY**

**B01** ACGAGGACGGTGCCATGTCCTGCCTCCTT  
|||||  
|||TTTGTCTGCACTACTCTGCTGCCAATT

Db 621 ACGAGACIGTGGCCAGCAIGTACGCCAGT

[illegible]

QY 661 CATGCCGGGGCCAGAGATGCTCTGCACCC 690  
 DB 681 CATGCCGGGGCCAGAGATGCTCTGCACCC 710  
 RESULT 19  
 LOCUS BU157365 1002 bp mRNA linear EST 04-SEP-2002  
 DEFINITION AGENCOURT\_6937229 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:5952261  
 5', mRNA sequence.  
 BU157365  
 ACCESSION BU157365.1 GI:22670897  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 NIH-MGC http://mgs.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgsbbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 Tissue Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LNC2139 row: p column: 22  
 High quality sequence stop: 743.  
 Location/Qualifiers  
 1. 1002  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5952261"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_1lb="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pORF7; Site\_1: XhoI;  
 Site\_2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAAGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH-MGC library."  
 BASE COUNT 204 a 258 c 288 g 252 t  
 ORIGIN  
 Query Match 26.7%; Score 690; DB 13; Length 1002;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 740; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 849 CCCCTGCCCCGTGAGAGGCGAGCTTTGCCATGACCCCGCAGCCGGCTTCTGAACTCAGC 908  
 DB 1 CCCCTGCCCCGTGAGAGGCGAGCTTTGCCATGACCCCGCAGCCGGCTTCTGAACTCAGC 60  
 QY 909 ACCTGGAGACTAGAGAGCTGAGAGCTTGAACCGATGCGCTTGTGCGCAGTGGCCTCTC 968  
 DB 61 ACCTGGAGACTAGAGAGCTGAGAGCTTGAACCGATGCGCTTGTGCGCAGTGGCCTCTC 120  
 QY 969 TGGCAGCCCCCAAGCAGAGCTTGTGTATGTGTGCAACCGACCTCTGTGGAGAGCCGT 1028  
 DB 121 TGGCAGCCCCCAAGCAGAGCTTGTGTATGTGTGCAACCGACCTCTGTGGAGAGCCGT 180  
 QY 1029 GACCAAGATGGGAGATCTCTGCTGACCAAGAGATCCCGCAGTATGATGATTTGACAGC 1088  
 DB 181 GACCAAGATGGGAGATCTCTGCTGACCAAGAGATCCCGCAGTATGATGATTTGACAGC 240

QY 1089 TTGATGAGAGAGTGGCGCCAGAGAGCTGAGAGACCTTGAGAGAGAGGCTGATGAAAGATG 1148  
 DB 241 TTGATGAGAGAGTGGCGCCAGAGAGCTGAGAGACCTTGAGAGAGAGGCTGATGAAAGATG 300  
 QY 1149 GCGCTGGGAGAGCTGCGGCTGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1208  
 DB 301 GCGCTGAGAGAGCTGCGGCTGCGCGCTGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 360  
 QY 1209 TGGACCAAGCTGTGGTATGATGCAATGAAATGATGATTTATTTTCCCGAGGTGTG 1268  
 DB 361 TGGACCAAGCTGTGGTATGATGCAATGAAATGATGATTTATTTTCCCGAGGTGTG 420  
 QY 1269 CTTTACGCGGAGCTGACAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1328  
 DB 421 CTTTACGCGGAGCTGACAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 480  
 QY 1329 GAGTTACAGCATGAGATGATGATTTGCTATTTGCTAGCTCCCGAGGCTGCTTCCAGGCTT 1388  
 DB 481 GAGTTACAGCATGAGATGATGATTTGCTATTTGCTAGCTCCCGAGGCTGCTTCCAGGCTT 540  
 QY 1389 CACAGTCTGGTCTTGGAGAGATCAGGAGGTTAACTGACAGAGCACTTGGCCACCC 1448  
 DB 541 CACAGTCTGGTCTTGGAGAGATCAGGAGGTTAACTGACAGAGCACTTGGCCACCC 600  
 QY 1449 TGTCCAGATTTATGCTGCTTGTCTTACCAAGTGGCAGAGCCGTTTGTCTTACATG 1508  
 DB 601 TGTCCAGATTTATGCTGCTTGTCTTACCAAGTGGCAGAGCCGTTTGTCTTACATG 660  
 QY 1509 GCTTTGATATTTGTTGAGAGGAGAGATGGAACAATGAGATGCTCCCTGATGATG 1568  
 DB 661 GCTTTGATATTTTGAAGAGAGAGATGGAACAATGAGATGCTCCCTGATGATG 720  
 QY 1569 TTGGGGAAATGTGAGAAAG 1589  
 DB 721 TTGGGGAAATGTGAGAAAG 741  
 RESULT 20  
 LOCUS BQ897122 906 bp mRNA linear EST 16-AUG-2002  
 DEFINITION AGENCOURT\_8074293 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6085612  
 5', mRNA sequence.  
 BQ897122  
 ACCESSION BQ897122.1 GI:22269136  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 NIH-MGC http://mgs.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgsbbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 Tissue Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LNC2139 row: e column: 05  
 High quality sequence stop: 607.  
 Location/Qualifiers  
 1. 906  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6085612"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_1lb="NIH\_MGC\_110"

/note="Organ: pancreas"; Vector: pOT7; Site:1: XhoI; Site:2: EcoRI. cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAC(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC library."

BASE COUNT	183 a	227 c	271 g	225 t
ORIGIN				

Query Match	26.5%	Score 685	DB 13	Length 906
Best Local Similarity	99.9%	Pred. No. 0		
Matches 735	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	849	CCCTGCCCGTGGAGGCGAGCTTTGCCATGACCCCGCAGCGGCTTCTGAGCTATC	908	
Db	1	CCCCGTGCGCGTGGAGGCGAGCTTTGCCATGACCCCGCAGCGGCTTCTGAGCTATC	60	
QY	909	ACCTGGAGAGCTAGAGCCCTGATGAGACCTTTGAGCCGATCCCTTGGCCAGTGACCTCTC	968	
Db	61	ACCTGGAGAGCTAGAGCCCTGATGAGACCTTTGAGCCGATCCCTTGGCCAGTGACCTCTC	120	
QY	969	TGCCAGCCCCACAGCCAGCGCTGTGTATGTGTGCAAGCGGACCTTGTGTGGAGACCGT	1028	
Db	121	TGCCAGCCCCACAGCCAGCGCTGTGTATGTGTGCAAGCGGACCTTGTGTGGAGACCGT	180	
QY	1029	GACCAAGATGGAGGAGATCTCTGTGCGCCAGAGAGGTCGCCGATGATGAAGTTGGCAGC	1088	
Db	181	GACCAAGATGGAGGAGATCTCTGTGCGCCAGAGAGGTCGCCGATGATGAAGTTGGCAGC	240	
QY	1089	TTCAATGAGAGAGGTGTGCGCCAGAGGCTGAGGACCTTGAAGAGGCTGATGAAGATG	1148	
Db	241	TTCAATGAGAGAGGTGTGCGCCAGAGGCTGAGGACCTTGAAGAGGCTGATGAAGATG	300	
QY	1149	GGCGTGGGGAGGCGCTGCGGCTGCGCGCTGCACTGCTGGAGGGGAGAGATTAGATC	1208	
Db	301	GGCGTGGGGAGGCGCTGCGGCTGCGCGCTGCACTGCTGGAGGGGAGAGATTAGATC	360	
QY	1209	TGAGACAGGCTGTGGGTAGATGTGCAATGAAATGCTAATTTATTTCCCAAGGTGTGTG	1268	
Db	361	TGAGACAGGCTGTGGGTAGATGTGCAATGAAATGCTAATTTATTTCCCAAGGTGTGTG	420	
QY	1269	CTTTAGGGGTGGGAGTCAACAGGCTCTTCTCAACCTTTCCAGATGATTTCCCGCT	1328	
Db	421	CTTTAGGGGTGGGAGTCAACAGGCTCTTCTCAACCTTTCCAGATGATTTCCCGCT	480	
QY	1329	GGCTTTGACAGCATGAGGTGTGTGTGCAATTTTTCAGCTTCCCCAGGCTTTTCCAGGCTT	1388	
Db	481	GGCTTTGACAGCATGAGGTGTGTGTGCAATTTTTCAGCTTCCCCAGGCTTTTCCAGGCTT	540	
QY	1389	CACAGTCTGGGTCTTGGAGAGTCAAGGAGGGTTAACTGACAGAGAGAGTTTGCACACCC	1448	
Db	541	CACAGTCTGGGTCTTGGAGAGTCAAGGAGGGTTAACTGACAGAGAGAGTTTGCACACCC	600	
QY	1449	TGTCCAGATTATGTGCTGCTTTTGCCTCTTACACAGTTGGCAGACAGCCGTTTGTCTACATG	1508	
Db	601	TGTCCAGATTATGTGCTGCTTTTGCCTCTTACACAGTTGGCAGACAGCCGTTTGTCTACATG	660	
QY	1509	GCTTTGATTAATTTGTTGAGAGGAGAGATGAGAAACAATGTGAGTCTCCCTGATTTGCT	1568	
Db	661	GCTTTGATTAATTTGTTGAGAGGAGAGATGAGAAACAATGTGAGTCTCCCTGATTTGCT	720	
QY	1569	TTTGGGGAATGTGGA 1584		
Db	721	TTTGGGGAATGTGGA 736		

ACCESSION	E0174805
VERSION	E0174805.1
KEYWORDS	GI:22688776
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 841)
JOURNAL	NIH-MGC <a href="http://mgc.nhl.nih.gov/">http://mgc.nhl.nih.gov/</a> .
COMMENT	Unpublished
	Contact: Robert Strassberg, Ph.D.

BASE COUNT	168 a	210 c	254 g	209 t
Query Match	26.5%; Score 684; DB 13; Length 841;			
Best Local Similarity	99.9%; Pred. No. 0;			
Matches 734; Conservative	0; Mismatches 1; Indels 0; Gaps 0;			
Dy	849	CCCCTGCCCGTGGAGGGCGAGCTTTGGCCATGACCCCGCCAGCCGGCTTCTGGACCTTCATC	908	
Dg	1	CCCCTGCCCGTGGAGGGCGAGCTTTGGCCATGACCCCGCCAGCCGGCTTCTGGACCTTCATC	60	
Dy	909	ACCTGGGAGGTATAGAGCTGTATGGAGAGCTTTGGACCGATGCCCTTGTGGCAGTGGCTCTC	968	
Db	61	ACCTGGGAGGTATAGAGCTGTATGGAGAGCTTTGGACCGATGCCCTTGTGGCAGTGGCTCTC	120	
Dy	969	TGCCAGCCCCACAGCCACAGCCTTGTTATGTGTATGTGTGCAAGCTCGACCTTTCGTGGGAGCCGT	1028	
Db	121	TGCCAGCCCCACAGCCACAGCCTTGTTATGTGTATGTGTGCAAGCTCGACCTTTCGTGGGAGCCGT	180	
Dy	1029	GACCAAGATGGGGAGATCTCTGCTGCCAGAGAGGTCCCGATGATATGAAGTTGGCAGC	1088	
Db	181	GACCAAGATGGGGAGATCTCTGCTGCCAGAGAGGTCCCGATGATATGAAGTTGGCAGC	240	
Dy	1089	TTTCATGGAGGAGGTGCGCCACGAGCTGGAGAGCTTGGAGAGAGCCTGACTGAAGAATG	1148	
Db	241	TTTCATGGAGGAGGTGCGCCACGAGCTGGAGAGCTTGGAGAGAGCCTGACTGAAGAATG	300	
Dy	1149	GCGGTGGGGAGAGCTTGCGGCTGCGCGCTGCATCTGTGGAGAGGGAAGATTTAGATC	1208	
Db	301	GCGGTGGGGAGAGCTTGCGGCTGCGCGCTGCATCTGTGGAGAGGGAAGATTTAGATC	360	
Dy	1209	TGGACCAAGGCTGTGGGTAGATGTGCATATAGAAATAGTAATTTATTTCCCAAGGTGTGTG	1268	
Db	361	TGGACCAAGGCTGTGGGTAGATGTGCATATAGAAATAGTAATTTATTTCCCAAGGTGTGTG	420	

QY 1269 CTTTAGGGGCTGGGCTGACCAAGGCTTCTCCATCTTCTTCCAGTAGTTCCCTCT 1328  
Db 421 CTTTAGGGGCTGGGCTGACCAAGGCTTCTCCATCTTCTTCCAGTAGTTCCCTCT 480  
QY 1329 GGCTTGACAGCATGAGCTGTGTGATTTGTTCAAGTCCGCCAGGCTGTCTCCAGGCTT 1388  
Db 481 GGCTTGACAGCATGAGCTGTGTGATTTGTTCAAGTCCGCCAGGCTGTCTCCAGGCTT 540  
QY 1389 CACAGCTGTGTGTGGGAGAGTCAGGAGGCTTAACTGACAGGAGCTTTGCCACCCC 1448  
Db 541 CACAGCTGTGTGTGGGAGAGTCAGGAGGCTTAACTGACAGGAGCTTTGCCACCCC 600  
QY 1449 TGTCCAGATTATTTGCTGTGCTTCTCTAACAATTGGACAGACCGTTTGTCTACATG 1508  
Db 601 TGTCCAGATTATTTGCTGTGCTTCTCTAACAATTGGACAGACCGTTTGTCTACATG 660  
QY 1509 GCTTTGATTAATTTGTTGAGGGAGAGATGAAACAATGGAGTCCCTCTGATTTGAT 1568  
Db 661 GCTTTGATTAATTTGTTGAGGGAGAGATGAAACAATGGAGTCCCTCTGATTTGAT 720  
QY 1569 TTTGGGGAATGTGG 1583  
Db 721 TTTGGGGAATGTGG 735

RESULT 22  
B0686534 877 bp mRNA linear EST 15-JUN-2002  
LOCUS AGENCOURT 8034689 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6207169  
DEFINITION 5', mRNA sequence.  
ACCESSION B0686534 GI:21811850  
VERSION B0686534.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LNCM2362 row: n column: 02  
High quality sequence stop: 692.  
Location/Qualifiers  
1. 877  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6207169"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1lib="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOTB7, Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library." 1 others

BASE COUNT 179 a 213 c 265 g 219 t

Query Match 26.5%; Score 684; DB 13; Length 877;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 734; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 849 CCCCTGCCCTGGAGAGGCGAGCTTTGCAATGACCCCGCACCGGCTTCTGACCTTCATC 908  
Db 1 CCCCTGCCCTGGAGAGGCGAGCTTTGCAATGACCCCGCACCGGCTTCTGACCTTCATC 60  
QY 909 ACCGTGGAGCTAGAGCCTGATGAGCCTTGAACCGATGCGCTTGTGCTGAGCTCTC 968  
Db 61 ACCGTGGAGCTAGAGCCTGATGAGCCTTGAACCGATGCGCTTGTGCTGAGCTCTC 120  
QY 969 TGGCAGCCCAACAGCCCAAGCCTGTGTATGTGTGCAAGCCACTTCTGTGGGAGCCCT 1028  
Db 121 TGGCAGCCCAACAGCCCAAGCCTGTGTATGTGTGCAAGCCACTTCTGTGGGAGCCCT 180  
QY 1029 GACCAAGATGGGAGATCCTGTGCCAGAGAGTCCCGATGATGATGATGAGCAGC 1088  
Db 181 GACCAAGATGGGAGATCCTGTGCCAGAGAGTCCCGATGATGATGATGAGCAGC 240  
QY 1089 TTCAATGAGAGAGGTGGCCAGAGCTGAGAGCCTGAGAGAGAGCTGACTGAGAGATG 1148  
Db 241 TTCAATGAGAGAGGTGGCCAGAGCTGAGAGCCTGAGAGAGAGCTGACTGAGAGATG 300  
QY 1149 GCGCTGGGAGAGCTGTGCGCTGCGCGCTGCACTGCTGGGAGGAGAGATTTAGATC 1208  
Db 301 GCGCTGGGAGAGCTGTGCGCTGCGCGCTGCACTGCTGGGAGGAGAGATTTAGATC 360  
QY 1209 TGACACAGGCTGTGGAGTGAATGCAATAGAAATAGCTAATTTATTTCCACAGTGTG 1268  
Db 361 TGACACAGGCTGTGGAGTGAATGCAATAGAAATAGCTAATTTATTTCCACAGTGTG 420  
QY 1269 CTTTAGGCGTGGGCTGACCAAGCTTCTCTACATCTTCTCCAGTAATTTCCCTCT 1328  
Db 421 CTTTAGGCGTGGGCTGACCAAGCTTCTCTACATCTTCTCCAGTAATTTCCCTCT 480  
QY 1329 GCGCTTGACAGCATGAGGTGTGTGCAATTTGTTCAGCTCCCGAGGCTTCTCAAGCTT 1388  
Db 481 GCGCTTGACAGCATGAGGTGTGTGCAATTTGTTCAGCTCCCGAGGCTTCTCAAGCTT 540  
QY 1389 CACAGCTGTGTGTGGGAGAGTCAGGAGGCTTAACTGACAGGAGAGTTTGCACCCC 1448  
Db 541 CACAGCTGTGTGTGGGAGAGTCAGGAGGCTTAACTGACAGGAGAGTTTGCACCCC 600  
QY 1449 TGTCCAGATTATTTGCTGTGCTTCTCTAACAATTGGACAGACCGTTTGTCTACATG 1508  
Db 601 TGTCCAGATTATTTGCTGTGCTTCTCTAACAATTGGACAGACCGTTTGTCTACATG 660  
QY 1509 GCTTTGATTAATTTGTTGAGGGAGAGATGAAACAATGGAGTCCCTCTGATTTGAT 1568  
Db 661 GCTTTGATTAATTTGTTGAGGGAGAGATGAAACAATGGAGTCCCTCTGATTTGAT 720  
QY 1569 TTTGGGGAATGTGG 1583  
Db 721 TTTGGGGAATGTGG 735

RESULT 23  
B0686811 915 bp mRNA linear EST 15-JUN-2002  
LOCUS AGENCOURT 8345155 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6250117  
DEFINITION 5', mRNA sequence.  
ACCESSION B0686811 GI:21812127  
VERSION B0686811.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished





[illegible]

FEATURES		Location/Qualifiers
SOURCE		1..898
		/organism="Homo sapiens"
		/mol_type="mRNA"
		/db_xref="taxon:9606"
		/clone="IMAGE:6250987"
		/tissue_type="ductal carcinoma, cell line"
		/lab_host="DH10B (phage-resistant)"
		/clone_idb="NIH_MGC_110"
		/note="Organ: pancreas; Vector: pOT87; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT		181 a 222 c 267 g 227 t 1 others
ORIGIN		
Query Match	26.2%; Score 678; DB 13; Length 898;	
Best Local Similarity	99.9%; Pred. No. 0;	
Matches 728; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
QY	849	CCCCCTGCCCTGTGAGGGCGAGCTTTGGCATGACCCTCCGACGCGCTTTGAGACTATC 908
DB	1	CCCCCTGCCCTGTGAGGGCGAGCTTTGGCATGACCCTCCGACGCGCTTTGAGACTATC 60
QY	909	ACCTGGAGAGCTAGAGCCTGATGAGCCTTGAGCCGATGCGCTTGAGCAGTGGCCTCTC 968
DB	61	ACCTGGAGAGCTAGAGCCTGATGAGCCTTGAGCCGATGCGCTTTGCGCAGTGGCCTCTC 120
QY	969	TGCCAGCCCCACAGCCACAGCCTGTGTATGTGTGCAAGCCGACCTTGTGCGAGCCGT 1028
DB	121	TGCCAGCCCCACAGCCACAGCCTGTGTATGTGTGCAAGCCGACCTTGTGCGAGCCGT 180
QY	1029	GACCAAGATGGGGAGATCTGCTCCGCCAGAGAGGTCCCGCATGAGTGAAGTTGGCAGC 1088
DB	181	GACCAAGATGGGGAGATCTGCTCCGCCAGAGAGGTCCCGCATGAGTGAAGTTGGCAGC 240
QY	1089	TTCAATGAGAGAGGTGCCCCAGAGACTGAGAGACTCTGAGAGAGGCTGACTGMAAGATG 1148
DB	241	TTCAATGAGAGAGGTGCCCCAGAGACTGAGAGACTCTGAGAGAGGCTGACTGMAAGATG 300
QY	1149	GCGCTGGGGGAGCCTGGGGCTGCCCGCGCTCACTGCTGGGAGGGGAGAGATTGATGTC 1208
DB	301	GCGCTGGGGGAGCCTGGGGCTGCCCGCGCTCACTGCTGGGAGGGGAGAGATTGATGTC 360
QY	1209	TGAGCCAGGCTGTGGGTGATGTGCAATAGAAATAGCTAATTATTTCCCAAGTGTGTG 1268
DB	361	TGAGCCAGGCTGTGGGTGATGTGCAATAGAAATAGCTAATTATTTCCCAAGTGTGTG 420
QY	1269	CTTAAAGGCGTGGGTGACACAGGCTTCTCTCAACATCTTCTCCAGTAAGTTCCCTCT 1328
DB	421	CTTAAAGGCGTGGGTGACACAGGCTTCTCTCAACATCTTCTCCAGTAAGTTCCCTCT 480
QY	1329	GCGTTGACAGCATGAGGTGTGTGCAATTGTTCAAGCTCCCGCAGGCTTCTCCAGGCTT 1388
DB	481	GCGTTGACAGCATGAGGTGTGTGCAATTGTTCAAGCTCCCGCAGGCTTCTCCAGGCTT 540
QY	1389	CACAGTGTGGGTGAGAGAGTCAAGGAGGGTTAACTGCAGAGACGTTTGGCCACCC 1448
DB	541	CACAGTGTGGGTGAGAGAGTCAAGGAGGGTTAACTGCAGAGAGCGTTTGGCCACCC 600
QY	1449	TGTCCAGATTATTTGGCTGTCTTGGCTCTCAAGATTGGAGACAGCCGTTTGTCTACATG 1508
DB	601	TGTCCAGATTATTTGGCTGTCTTGGCTCTCAAGATTGGAGACAGCCGTTTGTCTACATG 660
QY	1509	GCTTTGATTAATTTGTTGAGGGAGAGATGAAACAATGTGAGAGTCCCTCTGATTTGT 1568
DB	661	GCTTTGATTAATTTGTTGAGGGAGAGATGAAACAATGTGAGAGTCCCTCTGATTTGT 720
QY	1569	TTTGGGAGA 1577

Db 721 TTTGGGGA 729

RESULT 26  
BUI46060  
LOCUS: BUI46060  
DEFINITION: AGENCOURT 8074271 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6085826  
5', mRNA sequence.

ACCESSION  
BUI46060  
VERSION  
BUI46060.1 GI:22659592  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 (bases 1 to 893)  
NIH-MGC <http://mgs.nci.nih.gov/>,  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Plate: LNCM2319 row: n column: 03  
High quality sequence stop: 644.  
Location/Qualifiers  
1. 893  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6085826"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1lb="NIH MGC 110"  
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

BASE COUNT 179 a 225 c 269 g 220 t

ORIGIN

Query Match 26.1%; Score 676; DB 13; Length 893;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 726; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 969 TGGCAGCCCCACAGCCAGCCTGTATGTGTGCAAGCCGACCTTCGTTGGGAGACCGT 1028  
121 TGGCAGCCCCACAGCCAGCCTGTATGTGTGCAAGCCGACCTTCGTTGGGAGACCGT 180  
1029 GACCAAGATGGGAGATCTGTCTGCCAGAGAGGTCCCGATGATGATGAAGTTGGACG 1088  
181 GACCAAGATGGGAGATCTGTCTGCCAGAGAGGTCCCGATGATGATGAAGTTGGACG 240  
1089 TTGATGAGAGGTGGCCAGAGAGCTGGAAGACTGAGAGAGCTGATGAAGATG 1148

Db 241 TTGATGAGAGGTGGCCAGAGAGCTGAGAGACCTGAGAGAGAGCTGATGAAGATG 300  
Qy 1149 GCGCTGGGGAGCCTGCGCGCTGCGCGCTGCACTGCTGGAGGGAGAAATTTATGTC 1208  
Db 301 GCGCTGAGGAGACCTGCGCGCTGCGCGCTGCACTGCTGGAGGGAGAAATTTATGTC 360  
Qy 1209 TGGACAGAGCTGTGGGTGATGTGCAATGAAATAGCTAATTTATTTCCAGAGTGTG 1268  
Db 361 TGGACAGAGCTGTGGGTGATGTGCAATGAAATAGCTAATTTATTTCCAGAGTGTG 420  
Qy 1269 CTTTAAAGGTGGGTGACACAGCTTTCTTCTACATCTTTCCAGTAAATTTCCCTCT 1328  
Db 421 CTTTAAAGGTGGGTGACACAGCTTTCTTCTACATCTTTCCAGTAAATTTCCCTCT 480  
Qy 1329 GCGTTGACAGATAGAGTGTGTGATTTGTACAGTCTCCAGAGCTTTCTCCAGGCT 1388  
Db 481 GCGTTGACAGATAGAGTGTGTGATTTGTACAGTCTCCAGAGCTTTCTCCAGGCT 540  
Qy 1389 CACAGCTGTGCTGTGGAGAGTCAGGAGGTTAACTGACAGAGAGATTGGCCACCC 1448  
Db 541 CACAGCTGTGCTGTGGAGAGTCAGGAGGTTAACTGACAGAGAGATTGGCCACCC 600  
Qy 1449 TGTCCAGTTATTTGGCTCTTGTGCTCTTACAGATGTCAGACAGCCGTTGTTACATG 1508  
Db 601 TGTCCAGTTATTTGGCTCTTGTGCTCTTACAGATGTCAGACAGCCGTTGTTACATG 660  
Qy 1509 GCTTGAATATTTGTTGAGGGAGAGATGAAACAATGTGAGTCTCTCTGATTTG 1568  
Db 661 GCTTGAATATTTGTTGAGGGAGAGATGAAACAATGTGAGTCTCTCTGATTTG 720  
Qy 1569 TTTGGGG 1575  
Db 721 TTTGGGG 727

RESULT 27  
B0691090 901 bp mRNA linear EST 15-JUL-2002  
LOCUS: AGENCOURT 8111705 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6251806  
5', mRNA sequence.

ACCESSION  
B0691090  
VERSION  
B0691090.1 GI:21816406  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 (bases 1 to 901)  
NIH-MGC <http://mgs.nci.nih.gov/>,  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Plate: LNCM2397 row: a column: 23  
High quality sequence stop: 601.  
Location/Qualifiers  
1. 901  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6251806"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1lb="NIH MGC 110"  
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming."

FEATURES  
source



QY 421 TACCTCCAGCTATCAATGAGACCAACAGACAGAGAGTTGGAATATACCATCC 480  
Db 465 TACCTCCAGCTATCAATGAGACCAACAGACAGAGAGTTGGAATATACCATCC 524  
QY 481 ATGTGACCGAGAAATTCACAGATTAACCAACACAGACTGACAAATGCTCTTTTCA 540  
Db 525 ATGTGACCGAGAAATTCACAGATTAACCAACACAGACTGACAAATGCTCTTTTCA 584  
QY 541 AGACAGTTATCATCTGTGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
Db 585 AGACAGTTATCATCATCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 644  
QY 601 AGAGAGAGCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
Db 645 AGAGAGAGCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 704  
QY 661 CATGCCGGGGCCA 673  
Db 705 CATGCCGGGGCCA 717

RESULT 29  
BQ888956 869 bp mRNA linear EST 16-AUG-2002  
LOCUS AGENCOURT 8049821 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:5083894  
DEFINITION 5', mRNA sequence.

ACCESSION BQ888956  
VERSION BQ888956  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 869)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM2314 row: m column: 15  
High quality sequence stop: 645.  
Location/Qualifiers

FEATURES  
Source  
1..869  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5083894"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_11b="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOPB7; Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

BASE COUNT 176 a 219 c 262 g 212 t  
ORIGIN

Query Match 26.0%; Score 672; DB 13; Length 869;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 849 CCCCTGCCGTGGAGGGCGAGCTTGCATGACCCCGCAGCCGCTTGTGACCTCATC 908  
Db 1 CCCCTGCCGTGGAGGGCGAGCTTGTGCATGACCCCGCAGCCGCTTGTGACCTCATC 60  
QY 909 ACTTGGAGAGCTAGAGCTGATGAGAGCTTGGAGCCGATGCCCTTGTGCGAGTGCCTC 968  
Db 61 ACTTGGAGAGCTAGAGCTGATGAGAGCTTGGAGCCGATGCCCTTGTGCGAGTGCCTC 120  
QY 969 TGCAGCCCCCAGCCCAAGAGCTGTGTATGTGTGCAAGCCGACTTGTGGAGAGCCGT 1028  
Db 121 TGCAGCCCCCAGCCCAAGAGCTGTGTATGTGTGCAAGCCGACTTGTGGAGAGCCGT 180  
QY 1029 GACCAAGATGGGAGATCTCTGCTGCCCAAGAGCTGCCGAGAGATGAAAGTTGGCAGC 1088  
Db 181 GACCAAGATGGGAGATCTCTGCTGCCCAAGAGCTGCCGAGAGATGAAAGTTGGCAGC 240  
QY 1089 TTCATGAGAGAGGTGCGCAAGAGCTGAGAGACCTGAGAGAGAGCTGATGAGAGATG 1148  
Db 241 TTCATGAGAGAGGTGCGCAAGAGCTGAGAGACCTGAGAGAGAGCTGATGAGAGATG 300  
QY 1149 GCGCTGGGGAGAGCTTGGGCTGCGCCGCTGCACTGCTGGAGAGGAGATTTAGATC 1208  
Db 301 GCGCTGGGGAGAGCTTGGGCTGCGCCGCTGCACTGCTGGAGAGGAGATTTAGATC 360  
QY 1209 TGGACCAAGGCTGTGGGATGATGCAATGAAATAGCTAATTTATTTCCCAAGTGTG 1268  
Db 361 TGGACCAAGGCTGTGGGATGATGCAATGAAATAGCTAATTTATTTCCCAAGTGTG 420  
QY 1269 CTTTAGGCGTGGGCTGACCAAGGCTTCTTCTACATCTTCTCCAGTAACTTCCCTCT 1328  
Db 421 CTTTAGGCGTGGGCTGACCAAGGCTTCTTCTACATCTTCTCCAGTAACTTCCCTCT 480  
QY 1329 GCGTTGACACATGAGGTGTGTGCAATTTGTGAGCTGCCCGCAGGCTCTCAGGCTT 1388  
Db 481 GCGTTGACACATGAGGTGTGTGCAATTTGTGAGCTGCCCGCAGGCTCTCAGGCTT 540  
QY 1389 CACAGCTGTGTGCTTGGAGAGAGTCAAGCAGAGGTTAACTGACAGAGAGAGTTGCCACCC 1448  
Db 541 CACAGCTGTGTGCTTGGAGAGAGTCAAGCAGAGGTTAACTGACAGAGAGAGTTGCCACCC 600  
QY 1449 TGTCCAGATTAATTTGGCTGCTTGTGCTTACCAAGTGGCAAGAGCGCTTGTCTACATG 1508  
Db 601 TGTCCAGATTAATTTGGCTGCTTGTGCTTACCAAGTGGCAAGAGCGCTTGTCTACATG 660  
QY 1509 GCTTGAATTAATTTGTTGAGGGAGAGAGATGAAACAAATGGAAGTCTCCTGTGATGCT 1568  
Db 661 GCTTGAATTAATTTGTTGAGGGAGAGAGATGAAACAAATGGAAGTCTCCTGTGATGCT 720  
QY 1569 TTT 1571  
Db 721 TTT 723

RESULT 30  
BU196397 1043 bp mRNA linear EST 04-SEP-2002  
LOCUS AGENCOURT 6910885 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:5952243  
DEFINITION 5', mRNA sequence.  
ACCESSION BU196397  
VERSION BU196397  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1043)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory

## FEATURES

source

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1CM2139 row: p column: 04  
 High quality sequence stop: 599.  
 Location/Qualifiers  
 1. 1043

BASE COUNT 207 a 264 c 308 g 263 t 1 others  
 ORIGIN

Query Match 26.0%; Score 672; DB 13; Length 1043;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

849 CCCCTGCCCCGAGAGGAGAGCTTGGCCATACCCCGCAGCCGCTTGGACCTATC 908  
 Db 1 CCCCTGCCCCGAGAGGAGAGCTTGGCCATACCCCGCAGCCGCTTGGACCTATC 60  
 QY 909 ACCTGGAGCTAGAGCTGTATGAGACCTTGAACCGATGCCCTTGTGCCAGTGGCCTCTC 968  
 Db 61 ACCTGGAGCTAGAGCTGTATGAGACCTTGAACCGATGCCCTTGTGCCAGTGGCCTCTC 120  
 QY 969 TGGCAGCCCCCAGACGACGCTGTGTATGTGTGCAAGCCGACTTGTGGGGAGCCGT 1028  
 Db 121 TGGCAGCCCCCAGACGACGCTGTGTATGTGTGCAAGCCGACTTGTGGGGAGCCGT 180  
 QY 1029 GACCAAGATGGGAGAGTCTGCTGACAGAGAGTCCCGATGAGTATGAAGTTGGACG 1088  
 Db 181 GACCAAGATGGGAGAGTCTGCTGACAGAGAGTCCCGATGAGTATGAAGTTGGACG 240  
 QY 1089 TTGATGAGAGAGTGTGCGCAGAGAGCTTGGAGAGAGCCCTGATCGAAGAGATG 1148  
 Db 241 TTGATGAGAGAGTGTGCGCAGAGAGCTTGGAGAGAGCCCTGATCGAAGAGATG 300  
 QY 1149 GGCCTGGGAGAGCTGCGGCTGCGCCGCTGCACTGTGGAGGGGAGAGATTAGATC 1208  
 Db 301 GGCCTGGGAGAGCTGCGGCTGCGCCGCTGCACTGTGGAGGGGAGAGATTAGATC 360  
 QY 1209 TGGACCAAGCTGTGGTATGATGTCAATAGAAATAGCTAATTATTTCCCGAGTGTG 1268  
 Db 361 TGGACCAAGCTGTGGTATGATGTCAATAGAAATAGCTAATTATTTCCCGAGTGTG 420  
 QY 1269 CTTTAAAGCGGGGTACACGAGCTTCTCTCATATTTCTTCCCAAGTATGTTCCCTCT 1328  
 Db 421 CTTTAAAGCGGGGTACACGAGCTTCTCTCATATTTCTTCCCAAGTATGTTCCCTCT 480  
 QY 1329 GAGCTTGAACAGATGAGGTGTGTGCAATTGTTCAGTCTCCCGAGGCTTCTTCACAGCTT 1388  
 Db 481 GAGCTTGAACAGATGAGGTGTGTGCAATTGTTCAGTCTCCCGAGGCTTCTTCACAGCTT 540  
 QY 1389 CACAGTCTGTGTGCTTGGAGAGAGTCAAGCAGAGTTAACTGACAGAGCAGTTGGCACC 1448  
 Db 541 CACAGTCTGTGTGCTTGGAGAGAGTCAAGCAGAGTTAACTGACAGAGCAGTTGGCACC 600  
 QY 1449 TGTCAGATTATTTGGCTTGTGCTTACAGTTGGCAGAGCCGTTTGTTCATG 1508

Db 601 TGTCAGATTATTTGGCTTGTGCTTACAGTTGGCAGAGCCGTTTGTTCATG 660  
 QY 1509 GCTTGAATATTTTGAAGGAGAGATGAAAACATGTGAGTCTTCCCTGATTTGT 1568  
 Db 661 GCTTGAATATTTTGAAGGAGAGATGAAAACATGTGAGTCTTCCCTGATTTGT 720

QY 1569 TTT 1571  
 Db 721 TTT 723

RESULT 31  
 BUI96968 905 bp mRNA linear EST 04-SEP-2002  
 LOCUS AGENCOURT\_7974356 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6082897  
 DEFINITION 5', mRNA sequence.  
 BUI96968  
 BUI96968.1 GI:22710952  
 EST.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 905)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL  
 COMMENT  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1CM2312 row: d column: 02  
 High quality sequence stop: 571.  
 Location/Qualifiers  
 1. 905

## FEATURES

source

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6082897"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;  
 Site 2: EcoRI; CDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-CDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

BASE COUNT 189 a 223 c 271 g 222 t  
 ORIGIN

Query Match 25.9%; Score 671; DB 13; Length 905;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

849 CCCCTGCCCCGAGAGGAGAGCTTGGCCATACCCCGCAGCCGCTTGGACCTATC 908  
 Db 1 CCCCTGCCCCGAGAGGAGAGCTTGGCCATACCCCGCAGCCGCTTGGACCTATC 60  
 QY 909 ACCTGGAGCTAGAGCTGTATGAGACCTTGAACCGATGCCCTTGTGCCAGTGGCCTCTC 968  
 Db 61 ACCTGGAGCTAGAGCTGTATGAGACCTTGAACCGATGCCCTTGTGCCAGTGGCCTCTC 120  
 QY 969 TGGCAGCCCCCAGACGACGCTGTGTATGTGTGCAAGCCGACTTGTGGGGAGCCGT 1028  
 Db 121 TGGCAGCCCCCAGACGACGCTGTGTATGTGTGCAAGCCGACTTGTGGGGAGCCGT 180

```

QY 1029 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCCGATGAGTATGAAGTTGGCAGC 1088
DB 181 GACCAAGATGGGAGATCTCTGCTGCCAGAGAGTCCCCGATGAGTATGAAGTTGGCAGC 240
QY 1089 TTCATGAGAGAGTGGCGCCAGAGAGCTGAGAGACCTGAGAGAGAGCTGAGAGAGATG 1148
DB 241 TTCATGAGAGAGTGGCGCCAGAGAGCTGAGAGAGCTGAGAGAGAGCTGAGAGAGATG 300
QY 1149 GCGCTGGGGAGCTTGGCGCTTCCGCCCTGCACTGCTGGAGGGGAAAGATTAGATC 1208
DB 301 GCGCTGAGGAGACCTTGGCGCTTCCGCCCTGCACTGCTGGAGGGGAAAGATTAGATC 360
QY 1209 TGGACCAAGCTGTGGGTAGATGTCATATGAATAGCTAATTATTTCCAGAGTGTG 1268
DB 361 TGGACCAAGCTGTGGGTAGATGTCATATGAATAGCTAATTATTTCCAGAGTGTG 420
QY 1269 CTTTAAAGCGTGGGCTGACCAAGAGCTTCTTCTACATCTTCTTCCAGTAAAGTTCCCTCT 1328
DB 421 CTTTAAAGCGTGGGCTGACCAAGAGCTTCTTCTACATCTTCTTCCAGTAAAGTTCCCTCT 480
QY 1329 GCGTTGACAGCATGAGAGTGTGTCATTTGTACCTCCCGAGGCTGTCCAGAGCTT 1388
DB 481 GCGTTGACAGCATGAGAGTGTGTCATTTGTACCTCCCGAGGCTGTCCAGAGCTT 540
QY 1389 CACAGCTGTGCTTGGAGAGATCAAGGAGGTTAACTGACAGAGAGAGTTGCCACCCC 1448
DB 541 CACAGCTGTGCTTGGAGAGATCAAGGAGGTTAACTGACAGAGAGAGTTGCCACCCC 600
QY 1449 TGTCCAGATTATTGGCTGCTTGTGCTCTTACAGATTGGCAGACAGCCGTTTGTCTACATG 1508
DB 601 TGTCCAGATTATTGGCTGCTTGTGCTCTTACAGATTGGCAGACAGCCGTTTGTCTACATG 660
QY 1509 GCGTTGATTAATGTTGAGAGGAGAGATGAGAAACATGTGAGTCTCCCTGTGATTGT 1568
DB 661 GCGTTGATTAATGTTGAGAGGAGAGATGAGAAACATGTGAGTCTCCCTGTGATTGT 720
QY 1569 TT 1570
DB 721 TT 722

```

RESULT 32

LOCUS B0691927 912 bp mRNA linear EST 15-JUL-2002

DEFINITION AGENCOURT 8034941 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6207089

ACCESSION B0691927

VERSION B0691927.1 GI:21817255

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1. (bases 1 to 912)

AUTHORS NIH-MGC <http://mgi.ncl.nih.gov/>

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished.

Contact: Robert Strausberg, Ph.D.

Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

plate: L16M2362 row: j column: 18

High quality sequence stop: 654.

location/Qualifiers

1..912

source

/organism="Homo sapiens"

/mol\_type="mRNA"

```

BASE COUNT 180 a 228 c 270 g 231 t 3 others
ORIGIN
Query Match 25.9%; Score 671; DB 13; Length 912;
Best Local Similarity 99.9%; Fred. No. 0;
Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 849 CCCTGCGCCGTGAGAGGCGAGCTTTCAGATGACCCCGCAGCCGCGCTTGTGACCTATC 908
DB 1 CCCTGCGCCGTGAGAGGCGAGCTTTCAGATGACCCCGCAGCCGCGCTTGTGACCTATC 60
QY 909 ACCTGGAGCTTAAGCTGATGAGAGCTTGGACCATGCTTGTGCAATGAGCTTCTC 968
DB 61 ACCTGGAGCTTAAGCTGATGAGAGCTTGGACCATGCTTGTGCAATGAGCTTCTC 120
QY 969 TGGCAGCCCGACAGCCACAGCTGTGTATGTGTGCAAGCCGACTTGTGGAGGCGCT 1028
DB 121 TGGCAGCCCGACAGCCACAGCTGTGTATGTGTGCAAGCCGACTTGTGGAGGCGCT 180
QY 1029 GACCAAGATGGGAGATCTGCTGCCAGAGAGTCCCGATAGATGAGATTGGCAGC 1088
DB 181 GACCAAGATGGGAGATCTGCTGCCAGAGAGTCCCGATAGATGAGATTGGCAGC 240
QY 1089 TTCATGAGAGAGTGGCGCCAGAGAGCTGAGAGACCTGAGAGAGAGCTGATGAGAGATG 1148
DB 241 TTCATGAGAGAGTGGCGCCAGAGAGCTGAGAGACCTGAGAGAGAGCTGATGAGAGATG 300
QY 1149 GCGCTGGGGAGAGCTGCGGCTGCGCGCTGCACTGCTGGAGAGGAGAGATTAGATC 1208
DB 301 GCGCTGGGGAGAGCTGCGGCTGCGCGCTGCACTGCTGGAGAGGAGAGATTAGATC 360
QY 1209 TGAACCAAGCTGTGGTGAATGTCATTAAGTAATAGCTAATTTATTTCCAGAGTGTG 1268
DB 361 TGAACCAAGCTGTGGTGAATGTCATTAAGTAATAGCTAATTTATTTCCAGAGTGTG 420
QY 1269 CTTTAAAGCGTGGGCTGACCAAGAGCTTCTTCTACATCTTCTCCAGTAAAGTTCCCTCT 1328
DB 421 CTTTAAAGCGTGGGCTGACCAAGAGCTTCTTCTACATCTTCTCCAGTAAAGTTCCCTCT 480
QY 1329 GCGTTGACAGCATGAGAGTGTGTCATTTGTGACGCTCCCGCAGGCTTCTCAGAGCTT 1388
DB 481 GCGTTGACAGCATGAGAGTGTGTCATTTGTGACGCTCCCGCAGGCTTCTCAGAGCTT 540
QY 1389 CACAGCTGTGCTTGGAGAGAGTCAAGGAGGTTAACTGACAGAGAGAGTTGGCACCCC 1448
DB 541 CACAGCTGTGCTTGGAGAGAGTCAAGGAGGTTAACTGACAGAGAGAGTTGGCACCCC 600
QY 1449 TGTCCAGATTATTGGCTGCTTGTGCTCTTACAGTGGCAGACAGCCGTTTGTCTACATG 1508
DB 601 TGTCCAGATTATTGGCTGCTTGTGCTCTTACAGTGGCAGACAGCCGTTTGTCTACATG 660
QY 1509 GCGTTGATTAATGTTTGAAGGAGAGAGATGAGAAACATGTGAGAGTCTCCCTGTGATTGT 1568
DB 661 GCGTTGATTAATGTTTGAAGGAGAGAGATGAGAAACATGTGAGAGTCTCCCTGTGATTGT 720
QY 1569 TT 1570
DB 721 TT 722

```

/db xref="taxon:9606"

/clone="IMAGE:6207089"

/csize="1088"

/issue="1"

/lab\_host="DH10B (phage-resistant)"

/clone\_1b="NIH\_MGC\_110"

/note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."



RESULT 33  
BO888730 880 bp mRNA linear EST 16-AUG-2002  
LOCUS BO888730  
DEFINITION AGENCOURT.8074455 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6085646  
5', mRNA sequence.  
ACCESSION BO888730  
VERSION BO888730.1 GI:22280744  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 880)  
NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: sgabbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCM2319 row: f column: 15  
High quality sequence stop: 652.  
Location/Qualifiers  
1. .880  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6085646"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

FEATURES  
source  
BASE COUNT 176 a 221 c 266 g 217 t  
ORIGIN  
Query Match 25.8%; Score 668; DB 13; Length 880;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 849 CCCCTGCCGTGGAGGGGAGCTTTGCAATGACCCCGCAGCGGCTTGTGACCTCATC 908  
DB 1 CCCCTGCCGTGGAGGGGAGCTTTGCAATGACCCCGCAGCGGCTTGTGACCTCATC 60  
QY 909 ACCTGGAGCTAGAGCTTATGAGAGCTTGAACCGATGCTTGTGCAATGAGTCTCTC 968  
DB 61 ACCTGGAGCTAGAGCTTATGAGAGCTTGAACCGATGCTTGTGCAATGAGTCTCTC 120  
QY 969 TGGCAGCCCAAGCAGCAGCTGTGTATGTGTGCAAGCCGACCTGTGTGGAGCGCT 1028  
DB 121 TGGCAGCCCAAGCAGCAGCTGTGTATGTGTGCAAGCCGACCTGTGTGGAGCGCT 180  
QY 1029 GACCAAGATGGGAGATCTGTGCTGCCAGAGAGTCCCGATGATGATGATGATGATG 1088  
DB 181 GACCAAGATGGGAGATCTGTGCTGCCAGAGAGTCCCGATGATGATGATGATGATG 240  
QY 1089 TTATATGAGAGAGTGGGAGAGAGTGGAGAGCTTGAAGAGAGAGAGAGAGAGATG 1148  
DB 241 TTATATGAGAGAGTGGGAGAGAGTGGAGAGAGCTTGAAGAGAGAGAGAGAGATG 300  
QY 1149 GCGCTGGGGAGAGCTGCGGCTGCGCGCTGCACTGCTGGAGAGAGATTTAGATC 1208

DB 301 GCGCTGAGGAGAGCTGCGGCTGCGCGCTGCACTGCTGGAGAGAGATTTAGATC 360  
QY 1209 TGGACCAAGCTGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1268  
DB 361 TGGACCAAGCTGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
QY 1269 CTTTAAAGCGGTGGGCTGACCAAGAGCTTCTTCAATCTTCTTCCAGTAAGTTCCCTCT 1328  
DB 421 CTTTAAAGCGGTGGGCTGACCAAGAGCTTCTTCAATCTTCTTCCAGTAAGTTCCCTCT 480  
QY 1329 GCGTTACAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1388  
DB 481 GCGTTACAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540  
QY 1389 CACAGCTGTGTGCTTGGAGAGAGTGCAGAGAGGTTAACTGCAGAGCAATTTGCCACCCC 1448  
DB 541 CACAGCTGTGTGCTTGGAGAGAGTGCAGAGAGGTTAACTGCAGAGCAATTTGCCACCCC 600  
QY 1449 TGTTCAGATTTATGCTGCTGCTTCCCTTACAGTTGGCAGACAGCGGTTGTTCTACATG 1508  
DB 601 TGTTCAGATTTATGCTGCTGCTTCCCTTACAGTTGGCAGACAGCGGTTGTTCTACATG 660  
QY 1509 GCTTTGATATTTGTTGAGAGAGAGATGAAACATGTGAGTCTCCCTGATTTG 1567  
DB 661 GCTTTGATATTTGTTGAGAGAGAGATGAAACATGTGAGTCTCCCTGATTTG 719

RESULT 34  
BUI91090 887 bp mRNA linear EST 04-SEP-2002  
LOCUS BUI91090  
DEFINITION AGENCOURT.8074903 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6086034  
5', mRNA sequence.  
ACCESSION BUI91090  
VERSION BUI91090.1 GI:22705074  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 887)  
NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: sgabbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCM2320 row: f column: 19  
High quality sequence stop: 592.  
Location/Qualifiers  
1. .887  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6086034"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

FEATURES  
source  
BASE COUNT 179 a 223 c 269 g 216 t  
ORIGIN

Query Match	Similarity	Score	DB	Length
Best Local	99.98%	99.98%	0	Indels
Matches	718	Conservative	0	Mismatches
			1	Indels
			0	Gaps
			0	
QY	849	CCCCCTGCCCTGAGAGGCGAGCTTTGGCCATGACCCCGCAGCCGGCTTCTGACCTTCATC	908	
Db	1	CCCCCTGCCCTGAGAGGCGAGCTTTGGCCATGACCCCGCAGCCGGCTTCTGACCTTCATC	60	
QY	909	ACCTGGAGAGCTAGAGCCCTGATGAGAGCCTTGGACCCGATGACCCCTTGTGCACTGGACCTTC	968	
Db	61	ACCTGGAGAGCTAGAGCCCTGATGAGAGCCTTGGACCCGATGACCCCTTGTGCACTGGACCTTC	120	
QY	969	TGCCAGCCCCACAGCCACAGCCTTGATGATGATGATGATGATGATGATGATGATGATGATGATG	1028	
Db	121	TGCCAGCCCCACAGCCACAGCCTTGATGATGATGATGATGATGATGATGATGATGATGATGATG	180	
QY	1029	GACCAAAATGAGGAGATCCTGCTGCGCCAGAGAGGCTCCCGATGATGATGATGATGATGATG	1088	
Db	181	GACCAAAATGAGGAGATCCTGCTGCGCCAGAGAGGCTCCCGATGATGATGATGATGATGATG	240	
QY	1089	TTCAATGAGAGAGTGTGCGCCACAGAGCTGAGAGCCTTGAGAGAGAGCTGAGAGAGATG	1148	
Db	241	TTCAATGAGAGAGTGTGCGCCACAGAGCTGAGAGCCTTGAGAGAGAGCTGAGAGAGATG	300	
QY	1149	GCGCTGGGGAGAGCTTGGCGCTGCGCGCGCTGCACTGCTGGAGAGGAGAGATTTAATC	1208	
Db	301	GCGCTGGGGAGAGCTTGGCGCTGCGCGCGCTGCACTGCTGGAGAGGAGAGATTTAATC	360	
QY	1209	TGACACAGAGCTGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1268	
Db	361	TGACACAGAGCTGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	420	
QY	1269	CTTTAGGCGTGGGCTGACACAGGCTTCTTCTCAATCTTCTTCCAGATGATTTCCCTCT	1328	
Db	421	CTTTAGGCGTGGGCTGACACAGGCTTCTTCTCAATCTTCTTCCAGATGATTTCCCTCT	480	
QY	1329	GGCTTGAACAGATAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1388	
Db	481	GGCTTGAACAGATAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	540	
QY	1389	CACAGCTGTGCTGCTTGGAGAGTACAGCAGAGGCTTAACTGACAGAGACATTTGCAACCC	1448	
Db	541	CACAGCTGTGCTGCTTGGAGAGTACAGCAGAGGCTTAACTGACAGAGACATTTGCAACCC	600	
QY	1449	TGTCAGATTTATGAGCTGCTTGGCTCTACAGATTGACAGACAGCCGTTTCTACATG	1508	
Db	601	TGTCAGATTTATGAGCTGCTTGGCTCTCTACAGATTGACAGACAGCCGTTTCTACATG	660	
QY	1509	GCTTTGATTAATGTTTGAAGGAGAGATGAGAAACAATGTGAAGTCTTCCCTGATTTGG	1567	
Db	661	GCTTTGATTAATGTTTGAAGGAGAGATGAGAAACAATGTGAAGTCTTCCCTGATTTGG	719	
RESULT 35				
LOCUS	BUI49760	921 bp	linear	EST 03-SEP-2002
DEFINITION	AGNCOURT_8074878 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6086248			
ACCESSION	BUI49760			
VERSION	BUI49760.1			
KEYWORDS	EST, mRNA sequence.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
TITLE	1 (bases 1 to 921)			
JOURNAL	NIH-MGC http://mgi.nci.nih.gov/			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished			
	Contact: Robert Strausberg, Ph.D.			
	Email: cga@bme-mail.nih.gov			
	Tissue Procurement: ATCC			

FEATURES	Source	Location/Qualifiers
CDNA Library Preparation: Rubin Laboratory		
CDNA Sequencing by: Agencourt Bioscience Corporation		
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:		
http://image.lnl.gov		
Plate: LICM2320 row: 0 column: 17		
High quality sequence stop: 647.		
1. 921		
/organism="Homo sapiens"		
/mol_type="mRNA"		
/db_xref="taxon:9606"		
/clone="IMAGE:6086248"		
/tissue_type="ductal carcinoma, cell line"		
/lab_host="DH10B (phage-resistant)"		
/clone_1b="NIH_MGC_110"		
/note="Organ: pancreas; Vector: pOT57; Site_1: XhoI; Site_2: SmaI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."		
BASE COUNT	183 a	231 c 278 g 229 t
ORIGIN		
Query Match	25.8%; Score 668; DB 13; Length 921;	
Best Local Similarity	99.9%; Pred. No. 0;	
Matches	716; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
849	CCCCCTGCCCGTGAAGGGCGAGCTTTTGCATGACCCCGCCACCGGCTTCTGAGCCTCATC	908
1	CCCCCTGCCCGTGAAGGGCGAGCTTTTGCATGACCCCGCCACCGGCTTCTGAGCCTCATC	60
909	ACCTGGGAGCTGAGCCTGATGAGAGCCTTGAGACCGATGACCCCTGTGCAAGGCGCTCTC	968
61	ACCTGGGAGCTGAGCCTGATGAGAGCCTTGAGACCGATGACCCCTGTGCAAGGCGCTCTC	120
969	TGCCAGCCCCACAGCCACAGCAGCTGTGTATGTGTGCAAGCGACCTTGTGGAGAGCCGT	1028
121	TGCCAGCCCCACAGCCACAGCAGCTGTGTATGTGTGCAAGCGACCTTGTGGAGAGCCGT	180
1029	GACCAAGATGGGAGAGATCTCTGCTCCCAAGAGAGTCCCCCATGATGATGAAGTTGGACG	1088
181	GACCAAGATGGGAGAGATCTCTGCTCCCAAGAGAGTCCCCCATGATGATGAAGTTGGACG	240
1089	TTTATGAGAGAGAGTGGCCACAGAGACTTGAGAGAGCTTGAGAGAGAGCTGACATGAGAGATG	1148
241	TTTATGAGAGAGAGTGGCCACAGAGACTTGAGAGAGAGCTTGAGAGAGAGCTGAGAGAGATG	300
1149	GCAGCTGGAGAGAGCTGCGGCTGCCCGCGCTGCACTGCTGGAGAGGAGAAATTTAGATC	1208
301	GCAGCTGGAGAGAGCTGCGGCTGCCCGCGCTGCACTGCTGGAGAGGAGAAATTTAGATC	360
1209	TGAGACAGAGCTGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1268
361	TGAGACAGAGCTGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	420
1269	CTTTAGAGGCTGGAGAGCTGAGAGAGCTTCTTCTTCAATCTTCTTCCAGTAAAGTTTCCCTCT	1328
421	CTTTAGAGGCTGGAGAGCTGAGAGAGCTTCTTCTTCAATCTTCTTCCAGTAAAGTTTCCCTCT	480
1329	GGCTTGAACAGATAGAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1388
481	GGCTTGAACAGATAGAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	540
1389	CACAGTCTGGAGCTTGGAGAGAGTGGAGAGAGGTTAACTGAGAGAGAGTGTGGACACCC	1448
541	CACAGTCTGGAGCTTGGAGAGAGTGGAGAGAGGTTAACTGAGAGAGAGTGTGGACACCC	600
1449	TGTCCAGATTATTTGGCTGCTTGGCTCTTCAACAGATTGGAGAGACACCGTTTGTCTTCAATG	1508

Db 601 TGTCCAGATTAATGCTGCTTTCCTCTACAGGTTGGAGACAGCCGTTGTTACATG 660  
QY 1509 GCTTTGATTAATGTTTGGAGGAGAGATGGAACAATGTGGAGTCTCCCTGTATGG 1567  
Db 661 GCTTTGATTAATGTTTGGAGGAGAGATGGAACAATGTGGAGTCTCCCTGTATGG 719

RESULT 36  
B0689566 996 bp mRNA linear EST 15-JUL-2002  
LOCUS B0689566  
DEFINITION AGENCOURT\_8341957 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6248912  
5' mRNA sequence.  
ACCESSION B0689566  
VERSION B0689566.1 GI:21814882  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
1 (bases 1 to 996)  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-rcmail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCM2389 row: 1 column: 09  
High quality sequence stop: 610.  
Location/Qualifiers  
1. 996  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6248912"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 110"  
/note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH MGC Library."

BASE COUNT 196 a 256 c 292 g 252 t  
ORIGIN

Query Match 25.8%; Score 668; DB 13; Length 996;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 849 CCCCTGCGGTGAGGAGGAGCTTGTGCGATGACCCGCGAGCGCTTGTGACCTCATC 908  
Db 1 CCCTGCGGTGAGGAGGAGCTTGTGCGATGACCCGCGAGCGCTTGTGACCTCATC 60

QY 909 ACCTGGAGCTAGAGCTGATGAGCTTGGACCGATGCTTGTGCGAGTGCCTCTTC 968  
Db 61 ACCTGGAGCTAGAGCTGATGAGCTTGGACCGATGCTTGTGCGAGTGCCTCTTC 120

QY 969 TGCCAGCCCAACAGCAAGCTGTATGTATGTGCAAGCGACCTTGTGAGGAGCCGT 1028  
Db 121 TGCCAGCCCAACAGCAAGCTGTATGTATGTGCAAGCGACCTTGTGAGGAGCCGT 180

QY 1029 GACCAAGATGGGAGATCTGCTGCGCAAGAGGTCCCGCATGATGAAGTTGGACG 1088

Db 181 GACCAAGATGGGAGATCTGCTGCGCAAGAGGTCCCGCATGATGAAGTTGGACG 240  
QY 1089 TTATGAGAGAGGTGCGCCAGAGCTGAGAGACCTGAGAGAGCCCTGACTGAAGATG 1148  
Db 241 TTATGAGAGAGGTGCGCCAGAGCTGAGAGACCTGAGAGAGCCCTGACTGAAGATG 300  
QY 1149 GCGCTGGGAGAGCTTGGCGGTGCGCCGCGCTGACCTGCTGGAGAGGAGATTGATC 1208  
Db 301 GCGCTGGGAGAGCTTGGCGGTGCGCCGCGCTGACCTGCTGGAGAGGAGATTGATC 360

QY 1209 TGACACAGCTGTGGGTGATGTGCAATAGATTAATTTATTTCCCAAGTGTG 1268  
Db 361 TGACACAGCTGTGGGTGATGTGCAATAGATTAATTTATTTCCCAAGTGTG 420

QY 1269 CTTTGGCGGTGAGTACCAAGCTTCTTCTTCAATCTTCTCCAGTAAGTTCCCTCT 1328  
Db 421 CTTTGGCGGTGAGTACCAAGCTTCTTCTTCAATCTTCTCCAGTAAGTTCCCTCT 480

QY 1329 GGCTTGACAGATGAGATGTTGTGCAATTTGTGAGCTCCCGCAGGCTGTCTCAGGCTT 1388  
Db 481 GGCTTGACAGATGAGATGTTGTGCAATTTGTGAGCTCCCGCAGGCTGTCTCAGGCTT 540

QY 1389 CACAGTGTGCTTGGAGAGTCAAGGAGGTTAACTGCAAGACGTTTGCACCCC 1448  
Db 541 CACAGTGTGCTTGGAGAGTCAAGGAGGTTAACTGCAAGACGTTTGCACCCC 600

QY 1449 TGTCCAGATTAATGCTGCTTCTTCTTCAATGTCAGTTGGCAGACGCTTGTCTACATG 1508  
Db 601 TGTCCAGATTAATGCTGCTTCTTCTTCAATGTCAGTTGGCAGACGCTTGTCTACATG 660

QY 1509 GCTTTGATTAATGTTTGGAGGAGAGATGGAACAATGTGGAGTCTCCCTGTATGG 1567  
Db 661 GCTTTGATTAATGTTTGGAGGAGAGATGGAACAATGTGGAGTCTCCCTGTATGG 719

RESULT 37  
B0689791 858 bp mRNA linear EST 15-JUL-2002  
LOCUS B0689791  
DEFINITION AGENCOURT\_8046319 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6209170  
5' mRNA sequence.  
ACCESSION B0689791  
VERSION B0689791.1 GI:21815107  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
1 (bases 1 to 858)  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-rcmail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCM2368 row: a column: 11  
High quality sequence stop: 584.  
Location/Qualifiers  
1. 858  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6209170"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 110"  
/note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming."

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library. "

BASE COUNT 170 a 212 c 263 g 212 t 1 others  
ORIGIN

Query Match 25.8%; Score 667; DB 13; Length 858;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 767; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 849 CCCCTGCCCTGGAGGGCGAGCTTGGCATGACCCCGGACCGGCTTGTGACCTCATC 908
Db 1 CCCCTGCCCTGGAGGGCGAGCTTGGCATGACCCCGGACCGGCTTGTGACCTCATC 60
QY 909 ACCGTGGAGCTAGAGCCTGTGATGAGACCTTGGACCGATGACCTTGTGACCTCTC 968
Db 61 ACCGTGGAGCTAGAGCCTGTGATGAGACCTTGGACCGATGACCTTGTGACCTCTC 120
QY 969 TGGCAGCCCCCAAGCCCAAGCCTGTGTATGTGTGCAAGCCGACTTCTGTGGGAGCCGT 1028
Db 121 TGGCAGCCCCCAAGCCCAAGCCTGTGTATGTGTGCAAGCCGACTTCTGTGGGAGCCGT 180
QY 1029 GACCAAGATGGGAGATCCTGTGCTGCCAGAGAGATCCCGATGATGATGAAGTTGGCAGC 1088
Db 181 GACCAAGATGGGAGATCCTGTGCTGCCAGAGAGATCCCGATGATGATGAAGTTGGCAGC 240
QY 1089 TTCATGAGAGAGGTGCCCGCAAGAGCTGTGAGAGCCTGTGAGAGAGAGCTGACTGAAGAAGATG 1148
Db 241 TTCATGAGAGAGGTGCCCGCAAGAGCTGTGAGAGCCTGTGAGAGAGAGCTGACTGAAGAAGATG 300
QY 1149 GCGGTGGGGAGCCTGTGCGTGCAGCGCGCTGTGCACTGTGGAGAGGAGAGATTGATC 1208
Db 301 GCGGTGGGGAGCCTGTGCGTGCAGCGCGCTGTGCACTGTGGAGAGGAGAGATTGATC 360
QY 1209 TGGACCAAGCTGTGGGTGATGTGCAATAGAAATAGCTAATTTATTTCCCAAGGTGTG 1268
Db 361 TGGACCAAGCTGTGGGTGATGTGCAATAGAAATAGCTAATTTATTTCCCAAGGTGTG 420
QY 1269 CTTTAGGCGTGGGTGAGCCAGGCTTCTCTACATCTTCTCCAGTAAGTTCCCTCT 1328
Db 421 CTTTAGGCGTGGGTGAGCCAGGCTTCTCTACATCTTCTCCAGTAAGTTCCCTCT 480
QY 1329 GAGCTTGACAGATGAGGTGTGTGCAATTTGTCAAGTCCCGAGGCTGTTCACAGCTT 1388
Db 481 GAGCTTGACAGATGAGGTGTGTGCAATTTGTGTCAAGTCCCGAGGCTGTTCACAGCTT 540
QY 1389 CACAGCTGTGCTGTGGAGAGTCAAGGAGGTTAAATGTGAGAGAGAGTTTGGCAGCC 1448
Db 541 CACAGCTGTGCTGTGGAGAGTCAAGGAGGTTAAATGTGAGAGAGAGTTTGGCAGCC 600
QY 1449 TGTCCAGATATTGGTGTGCTTGTGCTTACAGATTGGCAGAGAGCGTTTGTCTACATG 1508
Db 601 TGTCCAGATATTGGTGTGCTTGTGCTTACAGATTGGCAGAGAGCGTTTGTCTACATG 660
QY 1509 GCTTTGATTAATTGTTTGAAGGAGAGAGATGAAAATAATGTGAGTCTCCCTCTGATTTG 1568
Db 661 GCTTTGATTAATTGTTTGAAGGAGAGAGATGAAAATAATGTGAGTCTCCCTCTGATTTG 720
QY 1569 TTTGGGAGAAATGTGAGAGAGAGTCCCTGTTTGGCAAAACATCAACCTGG 1617
Db 721 TTTGGGAGAAATGTGAGAGAGAGTCCCTGTTTGGCAAAACATCAACCTGG 769
```

RESULT 38  
BO688783 940 bp mRNA linear EST 15-JUL-2002  
LOCUS AGENCOURT 8344454 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:5251276  
DEFINITION 5', mRNA sequence.  
ACCESSION BO688783  
VERSION BO688783.1 GI:21814099

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 940)  
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LNCM2395 row: k column: 21  
High quality sequence stop: 684.

FEATURES  
source location/Qualifiers  
1..940  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6251276"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="RDH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOT7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-CDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library. "

BASE COUNT 188 a 235 c 276 g 239 t 2 others  
ORIGIN

Query Match 25.8%; Score 667; DB 13; Length 940;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 767; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 849 CCCCTGCCCTGGAGGGCGAGCTTGGCATGACCCCGGACCGGCTTGTGACCTCATC 908
Db 1 CCCCTGCCCTGGAGGGCGAGCTTGGCATGACCCCGGACCGGCTTGTGACCTCATC 60
QY 909 ACCGTGGAGCTAGAGCCTGTGATGAGACCTTGGACCGATGACCTTGTGACCTCTC 968
Db 61 ACCGTGGAGCTAGAGCCTGTGATGAGACCTTGGACCGATGACCTTGTGACCTCTC 120
QY 969 TGGCAGCCCCCAAGCCCAAGCCTGTGTATGTGTGCAAGCCGACTTGTGGGAGCCGT 1028
Db 121 TGGCAGCCCCCAAGCCCAAGCCTGTGTATGTGTGCAAGCCGACTTGTGGGAGCCGT 180
QY 1029 GACCAAGATGGGAGATCCTGTGCTGCCAGAGAGATCCCGATGATGATGAAGTTGGCAGC 1088
Db 181 GACCAAGATGGGAGATCCTGTGCTGCCAGAGAGATCCCGATGATGAAGTTGGCAGC 240
QY 1089 TTCATGAGAGAGGTGCCCGCAAGAGCTGTGAGAGCCTGTGAGAGAGCCTGACTGAAGAAGT 1148
Db 241 TTCATGAGAGAGGTGCCCGCAAGAGCTGTGAGAGCCTGTGAGAGAGCCTGACTGAAGAAGT 300
QY 1149 GCGGTGGGGAGCCTGTGCGTGCAGCGCGCTGTGCACTGTGGAGAGGAGAAATTTAGATC 1208
Db 301 GCGGTGGGGAGCCTGTGCGTGCAGCGCGCTGTGCACTGTGGAGAGGAGAAATTTAGATC 360
QY 1209 TGGACCAAGCTGTGGGTGATGTGCAATAGAAATAGCTAATTTATTTCCCAAGGTGTG 1268
Db 361 TGGACCAAGCTGTGGGTGATGTGCAATAGAAATAGCTAATTTATTTCCCAAGGTGTG 420
QY 1269 CTTTAGGCGTGGGTGAGCCAGGCTTCTCTACATCTTCTCCAGTAAGTTCCCTCT 1328
```

Db 421 CTTAGAGCGTGGCTACACGAGCTTCTTCTCATCTTTCTCCAGTAAGTTTCCCTCT 480  
QY 1329 GGGTTGACAGCATGAGGTGTGTGATTTGTTCACTCCCAAGCTGTTCACAGCTT 1388  
Db 481 GGGTTGACAGCATGAGGTGTGTGATTTGTTCACTCCCAAGCTGTTCACAGCTT 540  
QY 1389 CACAGTCTGTGTGGAGAGTCAGGAGGTTAACTGACAGAGCACTTGGCAACCC 1448  
Db 541 CACAGTCTGTGTGGAGAGTCAGGAGGTTAACTGACAGAGCACTTGGCAACCC 600  
QY 1449 TGTCCAGATTATTTGCTGCTTCTCTTACAGATTGGACAGACCGTTTGTCTACATG 1508  
Db 601 TGTCCAGATTATTTGCTGCTTCTCTTACAGATTGGACAGACCGTTTGTCTACATG 660  
QY 1509 GCTTTGATTAATTTGTTGAGGGAGAGAGATGAAACAAATGGAGTCTCCCTGATTTGAT 1568  
Db 661 GCTTTGATTAATTTGTTGAGGGAGAGAGATGAAACAAATGGAGTCTCCCTGATTTGAT 720  
QY 1569 TTGGGGAATGTGAGAAAGTGCCTGCTTTCACAAATCAACCTG 1617  
Db 721 TTGGGGAATGTGAGAAAGTGCCTGCTTTCACAAATCAACCTG 769  
RESULT 39  
BU191108 871 bp mRNA linear EST 04-SEP-2002  
LOCUS AGENCOURT\_7975077 NIH\_MGC\_110 Homo sapiens CDNA clone IMAGE:6081790  
DEFINITION 5', mRNA sequence.  
ACCESSION BU191108  
VERSION BU191108.1 GI:22705092  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE NIH-MGC http://mgs.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCM2309 row: e column: 23  
High quality sequence stop: 502.  
Location/Qualifiers  
1..871  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6081790"  
/issue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_110"  
/notes="Organ: pancreas; Vector: pOTB7, Site\_1: XhoI;  
Site\_2: EcoRI; CDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-CDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC library."  
BASE COUNT 177 a 218 c 260 g 216 t  
Query Match 25.7%; Score 665; DB 13; Length 871;  
Best Local Similarity 99.9%; Pred. No. 0;

Matches 715; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 849 CCCCTGCCCTGGAGAGCGAGCTTTGTCATGACCCCGACCGGCTTCTGACCTGATC 908  
Db 1 CCCCTGCCCTGGAGAGCGAGCTTTGTCATGACCCCGACCGGCTTCTGACCTGATC 60  
QY 909 ACCTGGAGCTAGAGCTGTATGAGAGCTTGAACCGATGCCCTTGTGCAATGACCTCTC 968  
Db 61 ACCTGGAGCTAGAGCTGTATGAGAGCTTGAACCGATGCCCTTGTGCAATGACCTCTC 120  
QY 969 TGCCAGCCCCACACGACAGCTGTGTATGTGTGCAAGCCGACTTGTGGAGACCGT 1028  
Db 121 TGCCAGCCCCACACGACAGCTGTGTATGTGTGCAAGCCGACTTGTGGAGACCGT 180  
QY 1029 GACCAAGTGGAGAGATCTGTGCTGCCAGAGAGTCCCGATGATGAATGATGGCAGC 1088  
Db 181 GACCAAGTGGAGAGATCTGTGCTGCCAGAGAGTCCCGATGATGAATGATGGCAGC 240  
QY 1089 TTCAATGAGAGAGTGCAGAGCTGTGAGAGCTGTGAGAGAGCTGACTGAAGAGATG 1148  
Db 241 TTCAATGAGAGAGTGCAGAGCTGTGAGAGCTGTGAGAGAGCTGACTGAAGAGATG 300  
QY 1149 GCGCTGGGGAGACCTGTGCGCTGTGCGCCGCTGCACTGTGGAGAGGAGATTTGATC 1208  
Db 301 GCGCTGGGGAGACCTGTGCGCTGTGCGCCGCTGCACTGTGGAGAGGAGATTTGATC 360  
QY 1209 TGACACAGGCTGTGGGTAGATGTGCATATGAAATAGCTAATTTATTTCCACAGGTGTG 1268  
Db 361 TGACACAGGCTGTGGGTAGATGTGCATATGAAATAGCTAATTTATTTCCACAGGTGTG 420  
QY 1269 CTTTAAAGCGTGGGTGACACAGCTTCTTCTACATCTTCTCCAGTAATTTCCCTCT 1328  
Db 421 CTTTAAAGCGTGGGTGACACAGCTTCTTCTACATCTTCTCCAGTAATTTCCCTCT 480  
QY 1329 GCGTTGACAGATGAGGTGTGTGATTTGTCAGTCTCCCAAGCTGTCTCAGGCTT 1388  
Db 481 GCGTTGACAGATGAGGTGTGTGATTTGTCAGTCTCCCAAGCTGTCTCAGGCTT 540  
QY 1389 CACAGTCTGTGTGGAGAGTGCAGAGGTTAACTGACAGAGCACTTGGCAACCC 1448  
Db 541 CACAGTCTGTGTGGAGAGTGCAGAGGTTAACTGACAGAGCACTTGGCAACCC 600  
QY 1449 TGTCCAGATTATTTGCTGCTTCTCTTACAGATTGGACAGACCGTTTGTCTACATG 1508  
Db 601 TGTCCAGATTATTTGCTGCTTCTCTTACAGATTGGACAGACCGTTTGTCTACATG 660  
QY 1509 GCTTTGATTAATTTGTTGAGGGAGAGATGAAACAAATGGAGTCTCCCTGATTTGAT 1564  
Db 661 GCTTTGATTAATTTGTTGAGGGAGAGATGAAACAAATGGAGTCTCCCTGATTTGAT 716  
RESULT 40  
BO876718 923 bp mRNA linear EST 16-AUG-2002  
LOCUS AGENCOURT\_8415247 Lupski\_sympathetic\_trunk Homo sapiens CDNA clone  
DEFINITION IMAGE:6192192 5', mRNA sequence.  
ACCESSION BO876718  
VERSION BO876718.1 GI:22268726  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE NIH-MGC http://mgs.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Dr. James R. Lupski  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation











LOCUS BUI57606 908 bp mRNA linear EST 04-SEP-2002  
 DEFINITION AGENCOURT\_8042460 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6085176  
 5' mRNA sequence.  
 ACCESSION BUI57606  
 VERSION BUI57606.1 GI:22671138  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 908)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov  
 Plate: LNCM2318 row: c column: 01  
 High quality sequence stop: 574.  
 Location/Qualifiers  
 1..908  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6085176"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pOT7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."  
 BASE COUNT 179 a 226 c 275 g 225 t 3 others  
 ORIGIN  
 Query Match 25.1%; Score 648; DB 13; Length 908;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 698; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy CCCCTGCCCCGAGGAGGAGCTTGGCCATGAGCCCGCCAGCCGGCTTCTGACCTCATC 908  
 Db 1 CCCCTGCCCCGAGGAGGAGCTTGGCCATGAGCCCGCCAGCCGGCTTCTGACCTCATC 60  
 Oy 909 ACCTGGAGCTAGAGCTGATGAGCTTGAAGCTTGGCCAGTGGCTTCCTC 968  
 Db 61 ACCTGGAGCTAGAGCTGATGAGCTTGAAGCTTGGCCAGTGGCTTCCTC 120  
 Oy 969 TGGCAGCCCCCAGCCAGCAGCTGATGATGTCAGAGCCGACCTTGTGGGAGGCGT 1028  
 Db 121 TGGCAGCCCCCAGCCAGCAGCTGATGATGTCAGAGCCGACCTTGTGGGAGGCGT 180  
 Oy 1029 GACCAAGTGGGAGAGTCTCTGCTGCCAGAGAGTCCCGCATGATGATGAAGTTGGAGC 1088  
 Db 181 GACCAAGTGGGAGAGTCTCTGCTGCCAGAGAGTCCCGCATGATGATGAAGTTGGAGC 240  
 Oy 1089 TTCAATGAGAGAGTGCAGAGAGTGGAGAGCTTGAGAGAGAGCTGACTGAAGAGATG 1148  
 Db 241 TTCAATGAGAGAGTGCAGAGAGTGGAGAGCTTGAGAGAGAGCTGACTGAAGAGATG 300  
 Oy 1149 GCGCTGAGGAGAGCTTGGGCTGCGCGCTGCACTGCTGGAGGGGAGAGAGATTGAATC 1208  
 Db 301 GCGCTGAGGAGAGCTTGGGCTGCGCGCTGCACTGCTGGAGGGGAGAGAGATTGAATC 360

RESULT 47  
 B0686410 879 bp mRNA linear EST 15-JUL-2002  
 LOCUS AGENCOURT\_8046835 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6209080  
 DEFINITION 5' mRNA sequence.  
 ACCESSION B0686410  
 VERSION B0686410.1 GI:21811726  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 879)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov  
 Plate: LNCM2367 row: m column: 17  
 High quality sequence stop: 614.  
 Location/Qualifiers  
 1..879  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6209080"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pOT7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."  
 BASE COUNT 174 a 219 c 262 g 223 t 1 others  
 ORIGIN  
 Query Match 24.9%; Score 643; DB 13; Length 879;  
 Oy 1209 TGAACAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTTCCCCAGGTGTG 1268  
 Db 361 TGAACAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTTCCCCAGGTGTG 420  
 Oy 1269 CTTTAGGCGGTGGGCTGACAGAGGCTTCTCTACATCTTCTCCAGTAAGTTCCCTCT 1328  
 Db 421 CTTTAGGCGGTGGGCTGACAGAGGCTTCTCTACATCTTCTCCAGTAAGTTCCCTCT 480  
 Oy 1329 GGCCTGACAGCATAGGTGTGTGCAATTTGTCAGCTCCCCCAGGCTGTCTCAGGCTT 1388  
 Db 481 GGCCTGACAGCATAGGTGTGTGCAATTTGTCAGCTCCCCCAGGCTGTCTCAGGCTT 540  
 Oy 1389 CACAGCTGTGCTTGGAGAGATGACAGGCTTAACCTGACAGAGAGATTTGGACCCC 1448  
 Db 541 CACAGCTGTGCTTGGAGAGATGACAGGCTTAACCTGACAGAGAGATTTGGACCCC 600  
 Oy 1449 TGTCAGATTATTTGGCTGTGCTTGTGCTTACAGTTGGACAGACGCGTTTCTACATG 1508  
 Db 601 TGTCAGATTATTTGGCTGTGCTTGTGCTTACAGTTGGACAGACGCGTTTCTACATG 660  
 Oy 1509 GCTTTGATTAATTTTGGAGGAGAGAGATGGAACATG 1547  
 Db 661 GCTTTGATTAATTTTGGAGGAGAGAGATGGAACATG 699

Best Local Similarity 99.9%; Pred. No. 0;  
Matches 693; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 849 CCCCTGCGGCTGAGAGGCGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 908
Db 1 CCCCTGCGGCTGAGAGGCGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 60
QY 909 ACCCTGGAGGCTGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 968
Db 61 ACCCTGGAGGCTGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 120
QY 969 TCCAGAGGCTGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 1028
Db 121 TCCAGAGGCTGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 180
QY 1029 GACCAAGATGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 1088
Db 181 GACCAAGATGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 240
QY 1089 TTTATGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 1148
Db 241 TTTATGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 300
QY 1149 GCGCTGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 1208
Db 301 GCGCTGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 360
QY 1209 TGGACAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 1268
Db 361 TGGACAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 420
QY 1269 CTTTACAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 1328
Db 421 CTTTACAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 480
QY 1329 GCGCTGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 1388
Db 481 GCGCTGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 540
QY 1389 CACAGTCTGCTGCTTGGAGAGTCAAGGCTTTAACTGCAAGAGCACTTGGCAACCC 1448
Db 541 CACAGTCTGCTGCTTGGAGAGTCAAGGCTTTAACTGCAAGAGCACTTGGCAACCC 600
QY 1449 TGTCCAGATTTATGCTTGGAGAGTCAAGGCTTTAACTGCAAGAGCACTTGGCAACCC 1508
Db 601 TGTCCAGATTTATGCTTGGAGAGTCAAGGCTTTAACTGCAAGAGCACTTGGCAACCC 660
QY 1509 GCTTTGATTAATTTGTTGAGGAGAGATGGA 1542
Db 661 GCTTTGATTAATTTGTTGAGGAGAGATGGA 694

```

RESULT 48  
B0687171 883 bp mRNA linear EST 15-JUL-2002  
LOCUS AGENCOURT 8039967 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6210042  
DEFINITION 5', mRNA sequence.  
ACCESSION B0687171  
VERSION B0687171.1 GI:21812487  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 883)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
AUTHORS Unpublished  
TITLES Contact: Robert Strausberg, Ph.D.  
JOURNAL Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
COMMENT Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.jnl.gov>  
Plate: LNCM2370 row: e column: 19  
High quality sequence stop: 567.  
Location/Qualifiers

## FEATURES

source

1. 883  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6210042"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_note="PH10B (phage-resistant)"  
/clone\_1ib="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pORF7, Site: 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC library."

BASE COUNT 178 a 222 c 263 g 219 t 1 others  
ORIGIN

Query Match 24.9%; Score 643; DB 13; Length 883;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 693; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 849 CCCCTGCGGCTGAGAGGCGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 908
Db 1 CCCCTGCGGCTGAGAGGCGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 60
QY 909 ACCCTGGAGGCTGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 968
Db 61 ACCCTGGAGGCTGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 120
QY 969 TCCAGAGGCTGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 1028
Db 121 TCCAGAGGCTGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 180
QY 1029 GACCAAGATGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 1088
Db 181 GACCAAGATGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 240
QY 1089 TTTATGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 1148
Db 241 TTTATGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 300
QY 1149 GCGCTGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 1208
Db 301 GCGCTGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 360
QY 1209 TGGACAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 1268
Db 361 TGGACAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 420
QY 1269 CTTTACAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 1328
Db 421 CTTTACAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 480
QY 1329 GCGCTGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 1388
Db 481 GCGCTGAGAGGCTTTGCCATGACCCCGCAGCCGGCTTTGACCTCCTC 540
QY 1389 CACAGTCTGCTGCTTGGAGAGTCAAGGCTTTAACTGCAAGAGCACTTGGCAACCC 1448
Db 541 CACAGTCTGCTGCTTGGAGAGTCAAGGCTTTAACTGCAAGAGCACTTGGCAACCC 600
QY 1449 TGTCCAGATTTATGCTTGGAGAGTCAAGGCTTTAACTGCAAGAGCACTTGGCAACCC 1508
Db 601 TGTCCAGATTTATGCTTGGAGAGTCAAGGCTTTAACTGCAAGAGCACTTGGCAACCC 660

```

QY 1509 GCTTGTATATTGTTTGAGGGGAGAGATGGA 1542  
 DB 661 GCTTGTATATTGTTTGAGGGGAGAGATGGA 694  
 RESULT 49  
 LOCUS BQ878479  
 DEFINITION BQ878479 871 bp mRNA linear EST 16-ANG-2002  
 AGENCOURT 8064671 NIH\_MGC\_110 Homo sapiens CDNA clone IMAGE:6206301  
 5', mRNA sequence.  
 ACCESSION BQ878479  
 VERSION BQ878479.1 GI:22270487  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 871)  
 NIH-MGC http://mgs.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LNCM2360 row: 1 column: 22  
 High quality sequence stop: 686.  
 Location/Qualifiers  
 1..871  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6206301"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI;  
 Site\_2: EcoRI; CDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-CDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."  
 BASE COUNT 173 a 219 c 262 g 216 t 1 others  
 ORIGIN  
 Query Match 24.7%; Score 640; DB 13; Length 871;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 690; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 849 CCCCTGCCCTGGAGGGGAGAGCTTTGCCATACCCCGCAGCCGCTTGGACCTATC 908  
 DB 1 CCCCTGCCCTGGAGGGGAGAGCTTTGCCATACCCCGCAGCCGCTTGGACCTATC 60  
 QY 909 ACCGGGAGCTAGAGCTGTAGAGCTTTGGACGATGCTTGTGCGAGTGCCCTC 968  
 DB 61 ACCGGGAGCTAGAGCTGTAGAGCTTTGGACGATGCTTGTGCGAGTGCCCTC 120  
 QY 969 TGGCAGCCCAAGCCACAGCCTGTGTATGTGTGCAAGCCGACCTTGTGGGAGCCGT 1028  
 DB 121 TGGCAGCCCAAGCCACAGCCTGTGTATGTGTGCAAGCCGACCTTGTGGGAGCCGT 180  
 QY 1029 GACCAAGATGGGGAGATCTGTGCTGCCAGAGAGGTCGCCGATGATGAAGTTGGCAGC 1088  
 DB 181 GACCAAGATGGGGAGATCTGTGCTGCCAGAGAGGTCGCCGATGATGAAGTTGGCAGC 240

QY 1089 TTCTAGAGAGAGGTCGCCAGAGCTGTAGAGACCTGTGAGAGAGCTGATGAAGATG 1148  
 DB 241 TTCTAGAGAGAGGTCGCCAGAGCTGTAGAGACCTGTGAGAGAGCTGATGAAGATG 300  
 QY 1149 GCGCTGAGGAGAGCCTGCGGCTGCCGCGCTGACCTGTGGAGGGGAGAGATTAGATC 1208  
 DB 301 GCGCTGAGGAGAGCCTGCGGCTGCCGCGCTGACCTGTGGAGGGGAGAGATTAGATC 360  
 QY 1209 TGGACCGAGCTGTGGTGTAGATGTCAATAGAAATAGCTAATTTATTTCCAGGTGTGT 1268  
 DB 361 TGGACCGAGCTGTGGTGTAGATGTCAATAGAAATAGCTAATTTATTTCCAGGTGTGT 420  
 QY 1269 CTTTACGCGTGGGCTGACACAGGCTTCTTCCATACCTCTTCCAGTAACTTCCCTCT 1328  
 DB 421 CTTTACGCGTGGGCTGACACAGGCTTCTTCCATACCTCTTCCAGTAACTTCCCTCT 480  
 QY 1329 GCGTTGACAGATAGAGTGTGTGCTTGTGCTTACAGCTTCCAGGCTTCCAGGCTT 1388  
 DB 481 GCGTTGACAGATAGAGTGTGTGCTTGTGCTTACAGCTTCCAGGCTTCCAGGCTT 540  
 QY 1389 CACAGCTGTGTGCTTGGAGAGATGACGAGCGGTTAACTGACAGAGCAGTTGCCCCC 1448  
 DB 541 CACAGCTGTGTGCTTGGAGAGATGACGAGCGGTTAACTGACAGAGCAGTTGCCCCC 600  
 QY 1449 TGTCCAGATTATTTGGCTGCTTGTGCTTACAGCTTGGCAGACAGCCGTTGTCTACATG 1508  
 DB 601 TGTCCAGATTATTTGGCTGCTTGTGCTTACAGCTTGGCAGACAGCCGTTGTCTACATG 660  
 QY 1509 GCTTGTATATTGTTTGAGGGGAGAGATG 1539  
 DB 661 GCTTGTATATTGTTTGAGGGGAGAGATG 691  
 RESULT 50  
 BQ689559 926 bp mRNA linear EST 15-JUL-2002  
 LOCUS BQ689559  
 DEFINITION AGENCOURT 8345000 NIH\_MGC\_110 Homo sapiens CDNA clone IMAGE:6250179  
 5', mRNA sequence.  
 ACCESSION BQ689559  
 VERSION BQ689559.1 GI:21814875  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 926)  
 NIH-MGC http://mgs.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LNCM2392 row: n column: 04  
 High quality sequence stop: 584.  
 Location/Qualifiers  
 1..926  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6250179"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI;  
 Site\_2: EcoRI; CDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACAG(G). Library constructed by



Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH WGC Library."

BASE COUNT 181 a 232 c 272 g 237 t 4 others  
ORIGIN

Query Match 24.7%; Score 640; DB 13; Length 926;  
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;  
Matches 690; Conservative 0;

QY 849 CCCCTGCCCGTGGAGGCGAGCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATC 908  
DB 1 CCCCTGCCCGTGGAGGCGAGCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATC 60  
QY 909 ACCTGGAGACTAGAGCTGATGAGGCTTGGACCGATGCTTGTGCCAGTGGCCCTCTC 968  
DB 61 ACCTGGAGACTAGAGCTGATGAGGCTTGGACCGATGCTTGTGCCAGTGGCCCTCTC 120  
QY 969 TGGCAGCCCCACAGCAGCAGCTGTGTATGTGTGCAGCCGACTTGTGGGAGCCGT 1028  
DB 121 TGGCAGCCCCACAGCAGCAGCTGTGTATGTGTGCAGCCGACTTGTGGGAGCCGT 180  
QY 1029 GACCAAGATGGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGAAATTTGGCAGC 1088  
DB 181 GACCAAGATGGGGAGATCTCTGCTGCCAGAGAGTCCCGATGATGAAATTTGGCAGC 240  
QY 1089 TTGATGAGAGAGGTGGCCAGAGAGCTGAGAGACCTGAGAGAGAGCTGAGAGAGATG 1148  
DB 241 TTGATGAGAGAGGTGGCCAGAGAGCTGAGAGAGCTGAGAGAGAGCTGAGAGAGATG 300  
QY 1149 GCGCTGGGGAGAGCTTGGCGCTGCGCGCTGCACTGTGGAGGGAGAGAGATTTAGATC 1208  
DB 301 GCGCTGGGGAGAGCTTGGCGCTGCGCGCTGCACTGTGGAGGGAGAGAGATTTAGATC 360  
QY 1209 TGGACAGAGCTGGGTAGATGTGCAATGAAATAGCTAATTTATTTCCCGAGGTGTG 1268  
DB 361 TGGACAGAGCTGGGTAGATGTGCAATGAAATAGCTAATTTATTTCCCGAGGTGTG 420  
QY 1269 CTTTAGGCGTGGGCTGACAGAGCTTCTTCAATCTTCTCCAGTAAAGTTCCCTCT 1328  
DB 421 CTTTAGGCGTGGGCTGACAGAGCTTCTTCAATCTTCTCCAGTAAAGTTCCCTCT 480  
QY 1329 GCGTTGACAGCATGAGGTGTGTGCAATTTGTCAAGTCCCGCAGGCTTCTCCAGGCTT 1388  
DB 481 GCGTTGACAGCATGAGGTGTGTGCAATTTGTGTCAAGTCCCGCAGGCTTCTCCAGGCTT 540  
QY 1389 CACAGTCTGGTCTTGGAGAGTCAAGCAGGTTAACTGACAGAGCAGTTTGCACCCC 1448  
DB 541 CACAGTCTGGTCTTGGAGAGTCAAGCAGGTTAACTGACAGAGCAGTTTGCACCCC 600  
QY 1449 TGTCCAGATTAATGGGCTTGTGCTTACCACTTGGCAGACAGCGTTTGTCTACATG 1508  
DB 601 TGTCCAGATTAATGGGCTTGTGCTTACCACTTGGCAGACAGCGTTTGTCTACATG 660  
QY 1509 GCTTTGATAATTTGTTGAGGGAGAGATGG 1539  
DB 661 GCTTTGATAATTTGTTGAGGGAGAGATGG 691

Search completed: February 20, 2004, 05:50:44  
Job time : 5389 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 20, 2004, 19:18:30 ; Search time 74 Seconds  
(without alignments)  
750.734 Million cell updates/sec

Title: US-10-063-671-8

Perfect score: 350

Sequence: 1 MGRIGATLCLLAAVPTA.....EMALGEPAALAAALIGEEI 350

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 6

Total number of hits satisfying chosen parameters: 8391

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database : A\_Geneseq.19Jun03:\*  
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Query Match Length	ID	Description
1	350	100.0	350 19	AAAG2535 Homo sapiens cereb
2	350	100.0	350 21	AAAG2070 Human DKK-3. Homo
3	350	100.0	350 22	AAAG80271 Human DKK-3. Protei
4	350	100.0	350 22	AAAG62468 Human reduced expr
5	350	100.0	350 22	AAAB87528 Human PRO295. Hom
6	350	100.0	350 22	AAAB80252 Human PRO295. prote
7	350	100.0	350 23	ABG35854 Human secreted/tra
8	350	100.0	350 23	ABG35447 Human angiotensin
9	350	100.0	350 23	ABB90735 Human Tumour Endot

10	350	100.0	350 23	ABB84841 Human PRO295 prote
11	350	100.0	350 24	ABU69662 Novel human secret
12	350	100.0	350 24	ABU71485 Human PRO polypept
13	350	100.0	350 24	ABU71509 Human secreted pol
14	350	100.0	350 24	ABU71931 Human secreted/tra
15	350	100.0	350 24	ABU71955 Novel human secret
16	350	100.0	350 24	ABU72112 Human PRO polypept
17	350	100.0	350 24	ABU67385 Human secreted pro
18	350	100.0	350 24	ABU64539 Human secreted/tra
19	350	100.0	350 24	AAE34069 DKK 3 protein. Un
20	350	100.0	350 24	ABU55915 Human protein DKK3
21	350	100.0	350 24	ABU54387 Human secreted/tra
22	350	100.0	350 24	ABU54442 Human tumour endot
23	279	79.7	350 20	AAU13384 Amino acid sequenc
24	233	66.6	350 19	AAAB73016 Human cysteine-ric
25	233	66.6	350 19	AAAB08874 Amino acid sequenc
26	41	11.7	349 19	AAW73021 Mouse cysteine-ric
27	41	11.7	349 19	AAW73021 A murine Dickkopf
28	41	11.7	349 21	AAU92069 Murine DKK-3. Mus
29	30	4.0	14 22	AAU24777 Schizophrenia-asso
30	14	4.0	14 22	AAU15121 Schizophrenia-asso
31	12	3.4	12 22	ABBS6096 Vascular dementia-
32	12	3.4	12 22	ABBS6097 Vascular dementia-
33	12	3.4	12 22	ABBS2342 Human APL-121 tryp
34	10	2.9	10 22	ABBS6098 Vascular dementia-
35	10	2.9	10 22	AAAG80272 Human DKK-3 protei
36	10	2.9	10 22	ABBS2202 Human APL-153 tryp
37	10	2.9	10 22	ABBS2341 Human APL-121 tryp
38	10	2.9	10 22	ABBS2343 Human APL-121 tryp
39	10	2.9	10 22	ABBS2343 Human APL-121 tryp
40	10	2.9	10 22	AAU28428 DPI tryptic digest
41	10	2.9	10 22	AAU28553 DPI tryptic digest
42	10	2.9	10 22	AAU28566 DPI tryptic digest
43	10	2.9	10 22	AAU25210 Schizophrenia-asso
44	10	2.9	10 22	AAU25377 Schizophrenia-asso
45	10	2.9	10 22	AAU26074 Schizophrenia-asso
46	10	2.9	10 22	AAU26200 Depression-Asso
47	10	2.9	10 22	AAU26213 Depression-Asso
48	10	2.9	10 22	AAU26213 Schizophrenia-asso
49	10	2.9	10 22	AAU25554 Schizophrenia-asso
50	10	2.9	10 22	AAU15721 Multiple sclerosis
51	10	2.9	10 22	ABG78843 Cysteine protease
52	10	2.6	109 22	AAAB65761 Human OREX ORF1732
53	9	2.6	434 21	AAAB41968 Human DEC2a protei
54	9	2.6	482 23	ABG96308 Human DEC2b protei
55	9	2.6	482 23	ABG96308 Protein of NOVX 5
56	9	2.6	484 22	ABU06444 DPI tryptic digest
57	9	2.6	767 22	AAU28429 DPI tryptic digest
58	8	2.3	8 22	AAU28567 Schizophrenia-asso
59	8	2.3	8 22	AAU28567 Schizophrenia-asso
60	8	2.3	8 22	AAU25211 Depression-Asso
61	8	2.3	8 22	AAU25211 Depression-Asso
62	8	2.3	8 22	AAU26075 Schizophrenia-asso
63	8	2.3	8 22	AAU26212 Schizophrenia-asso
64	8	2.3	8 22	AAU15122 Schizophrenia-asso
65	8	2.3	8 22	AAU15555 KIA class I molecu
66	8	2.3	9 24	ABP96458 KIA class I molecu
67	8	2.3	9 24	ABP96458 Human cytomagalovi
68	8	2.3	20 22	AAU05756 Amino acid sequenc
69	8	2.3	20 22	AAAB68491 Peptide derived fr
70	8	2.3	21 14	AAW42513 Human cytomagalovi
71	8	2.3	31 14	AAAR3086 Human cytomagalovi
72	8	2.3	31 14	AAAR3087 Human cytomagalovi
73	8	2.3	32 14	AAAR3087 Peptide derived fr
74	8	2.3	32 14	AAAR3087 Peptide derived fr
75	8	2.3	42 21	AAAY72126 Protein fragment #
76	8	2.3	42 21	AAAB49551 Protein fragment #
77	8	2.3	51 14	AAAR3091 Human cytomagalovi
78	8	2.3	78 22	AAAP80077 Cyomagalovirus (C
79	8	2.3	78 22	AAAP80077 Amino transferase d
80	8	2.3	92 23	ABB89050 Murine MCP3 fragme
81	8	2.3	97 16	AAAR70803 Growth factor-acti
82	8	2.3	119 22	AAAG4079 Human reproductive

83	2.3	120	21	ABG23292	Arabidopsis thaliana	156	8	2.3	823	23	AAE13608	Human EGF-like mol
84	2.3	132	22	ABG15204	Novel human diageno	157	8	2.3	823	24	ABP81730	Human EGF-like mol
85	2.3	143	21	AAV72129	Protein fragment #	158	8	2.3	850	22	ABE65164	Drosophila melanog
86	2.3	143	21	AAE49554	Protein fragment	159	8	2.3	1028	22	ABE62708	Drosophila melanog
87	2.3	146	22	AAE25508	Human protein sequ	160	8	2.3	1040	18	AAE24559	Presenilin-interac
88	2.3	149	22	AAE90721	C glutathion prote	161	8	2.3	1048	13	AAE20637	Human Cytochrome
89	2.3	156	20	AAE29907	Murine MCP-3 and h	162	8	2.3	1048	18	AAE27277	Human Cytochrome
90	2.3	171	20	AAE29909	Murine MCP-3 and h	163	8	2.3	1061	20	AAE87504	Human N-methyl-D-a
91	2.3	208	21	AAE77571	Human cytochrome	164	8	2.3	1081	21	AAE26240	Human N-methyl-D-a
92	2.3	222	23	ABP41497	Human cytochrome	165	8	2.3	1081	23	ABE56523	Human NMDA recepto
93	2.3	267	22	AAU29566	Novel human secret	166	8	2.3	1084	24	ABE61440	Human N-methyl-D-a
94	2.3	284	22	AAE78512	Human protein SEQ	167	8	2.3	1084	24	AAE23500	Human resensilin bi
95	2.3	300	17	AAE89201	Recombinant synerg	168	8	2.3	1130	22	ABG22733	Novel human diageno
96	2.3	300	20	AAE05754	Human cytochrome	169	8	2.3	1175	23	AAU98501	Mouse nebulin-rela
97	2.3	302	17	AAE89202	Recombinant synerg	170	8	2.3	1212	20	AAE87503	Human N-methyl-D-a
98	2.3	302	20	AAE05755	Human cytochrome	171	8	2.3	1225	21	AAE07973	A human neural pla
99	2.3	305	22	ABG02081	Novel human diageno	172	8	2.3	1232	21	AAE26239	Human N-methyl-D-a
100	2.3	330	11	AAE05528	High density lipop	173	8	2.3	1232	23	AAE47961	Human NMDA recepto
101	2.3	332	21	AAE95898	Human myristoylate	174	8	2.3	1232	24	ABE61439	Human N-methyl-D-a
102	2.3	332	21	AAE95899	Human myristoylate	175	8	2.3	1233	22	ABG04996	Novel human diageno
103	2.3	372	22	AAE80229	Human PRO287 prote	176	8	2.3	1367	22	ABE63769	Drosophila melanog
104	2.3	381	22	ABG15205	Human human diageno	177	8	2.3	1540	22	ABE61913	Drosophila melanog
105	2.3	415	20	AAE31743	Human protease HPR	178	8	2.3	2421	22	ABE65643	Drosophila melanog
106	2.3	415	20	AAE13361	Katuno acid sequenc	179	8	2.3	2768	22	ABE68397	Novel human diageno
107	2.3	415	21	AAE24404	Human PRO287 prote	180	8	2.3	3338	22	ABG09919	Novel human diageno
108	2.3	415	22	AAE88559	Human membrane or	181	8	2.0	9	18	AAE04637	Null peptide that
109	2.3	415	22	AAE88559	Human membrane or	182	8	2.0	9	22	AAE62424	Immunogenic peptid
110	2.3	415	24	ABE69639	Human PRO287 prote	183	8	2.0	9	24	ABE696452	HLA class I molecu
111	2.3	415	24	ABU71462	Human secreted pro	184	8	2.0	9	24	ABE696454	HLA class I molecu
112	2.3	415	24	ABU71462	Human secreted pro	185	8	2.0	9	24	ABE696461	HLA class I molecu
113	2.3	415	24	ABU67362	Human secreted pro	186	8	2.0	9	24	ABE696462	HLA class I molecu
114	2.3	415	24	ABU64564	Human secreted/tra	187	8	2.0	9	24	ABE696464	HLA class I molecu
115	2.3	415	24	ABU64564	Human secreted/tra	188	8	2.0	9	24	ABE696465	HLA class I molecu
116	2.3	417	21	AAE94319	Murine Mnt-10A pro	189	8	2.0	9	24	ABE696466	HLA class I molecu
117	2.3	419	22	ABG22064	Novel human diageno	190	8	2.0	9	24	ABE696467	HLA class I molecu
118	2.3	427	22	ABE65442	Drosophila melanog	191	8	2.0	9	24	ABE696469	HLA class I molecu
119	2.3	449	22	AAE68879	Human RBCAP polype	192	8	2.0	9	24	ABE696470	HLA class I molecu
120	2.3	453	21	AAE94340	Human cell surface	193	8	2.0	9	24	ABE696473	HLA class I molecu
121	2.3	503	15	AAE55370	Human Activin rece	194	8	2.0	9	24	ABE696475	HLA class I molecu
122	2.3	503	19	AAE49909	Signal regulatory	195	8	2.0	9	24	ABE696479	HLA class I molecu
123	2.3	503	19	AAE40481	Human SH2 binding	196	8	2.0	10	19	AAE61561	HLA class I molecu
124	2.3	503	20	AAE33303	Human hAUK-5 clone	197	8	2.0	10	19	AAE61561	HLA class I molecu
125	2.3	503	21	AAE59452	Human Transforming	198	8	2.0	12	23	ABE68392	HLA class I molecu
126	2.3	503	23	AAU79935	Human SHPS-1 (not	199	8	2.0	13	24	ABU57821	Peptide based on t
127	2.3	521	20	AAE30638	Partial human 7-tr	200	8	2.0	14	17	AAE02569	AKAP79 A37-50 muta
128	2.3	537	22	ABE60713	Drosophila melanog	201	8	2.0	14	21	AAE14809	Mutant peptide AKA
129	2.3	540	15	AAE48667	Chitinase 1, Rhiz	202	8	2.0	17	24	ABE38873	MGRLA putative si
130	2.3	551	21	AAE42049	Human ORFX ORF1813	203	8	2.0	20	22	ABE68494	Amino acid sequenc
131	2.3	576	21	AAE24234	Human vesicle asso	204	8	2.0	20	22	ABE68496	Amino acid sequenc
132	2.3	576	22	AAE95100	Human protein sequ	205	8	2.0	21	22	AAE67602	Human RIZ alternat
133	2.3	577	23	ABG70269	Human Epsin-like p	206	8	2.0	22	17	AAE92102	5' terminus of hum
134	2.3	593	23	AAE020499	Protein of App rel	207	8	2.0	22	23	AAE12111	Peptide sequence #
135	2.3	593	24	AAE26245	Aspergillus fumiga	208	8	2.0	22	23	AAU10792	Human Rb-interacti
136	2.3	611	23	AAE18647	Human G-protein co	209	8	2.0	23	23	ABE05790	HIV tat related am
137	2.3	638	22	ABE71320	Drosophila melanog	210	8	2.0	26	14	AAE41301	Peptide fragment F
138	2.3	645	23	AAE020500	Protein of App rel	211	8	2.0	30	14	AAE33088	Human cytochrome
139	2.3	646	23	AAE020501	Protein of App rel	212	8	2.0	30	22	ABE59489	Human liver peptid
140	2.3	647	11	AAE06001	Insect receptor po	213	8	2.0	30	22	ABE44107	Peptide #11613 enc
141	2.3	651	24	ABG74687	Human CGSD protein	214	8	2.0	30	22	ABE26997	Protein #8996 enco
142	2.3	652	20	AAE30637	Human 7-epsilon	215	8	2.0	30	22	AAE65129	Human bone marrow
143	2.3	652	21	AAE59300	Human EGF-like	216	8	2.0	30	22	AAE77835	Peptide #8173 enco
144	2.3	652	24	ABE75634	Human EGF-like	217	8	2.0	30	22	AAE21739	Peptide #12091 enc
145	2.3	652	24	ABE81739	Human EGF-like	218	8	2.0	30	22	AAE38054	Human peptide enco
146	2.3	661	22	ABE03062	Human expressed po	219	8	2.0	30	22	ABE46867	Human cytochrome
147	2.3	661	22	ABE10371	Human CDNA SEQ ID	220	8	2.0	32	17	AAE05632	l. actinophilus S 1
148	2.3	661	22	AAE18138	Novel human uterin	221	8	2.0	32	17	AAE06912	Arctic fish antifer
149	2.3	661	22	AAE18139	Human endocrine po	222	8	2.0	33	18	AAE27490	Human cytochrome
150	2.3	661	22	AAE18138	Human novel secret	223	8	2.0	35	14	AAE33083	Human liver peptid
151	2.3	661	23	ABE68558	Human polypeptide	224	8	2.0	35	14	ABE56523	Human cytochrome
152	2.3	661	23	ABE05765	Novel human protei	225	8	2.0	35	22	ABE41080	Peptide #8586 enco
153	2.3	696	22	ABE04995	Novel human diageno	226	8	2.0	35	22	ABE25142	Protein #1141 enco
154	2.3	757	22	ABE5017	Shrimp white spot	227	8	2.0	35	22	ABE25142	Human brain expres
155	2.3	800	23	AAE13609	Human mature EGF-1	228	8	2.0	35	22	AAE61938	

229	7	2.0	35	22	AAW74740	Human bone marrow	302	7	2.0	87	22	AAW5996	Peptide #10033 enc
230	7	2.0	35	22	AAW20398	Peptide #6832 enco	303	7	2.0	87	23	ABG55672	Oest 3 protein
231	7	2.0	35	22	AAW44856	Peptide #8893 enco	304	7	2.0	87	23	ABG45328	Human peptide enco
232	7	2.0	35	23	ABG44539	Human peptide enco	305	7	2.0	93	22	AAW06419	Human foetal prote
233	7	2.0	37	13	AAW26105	Antifreeze protein	306	7	2.0	95	22	ABW03487	Human musculoskele
234	7	2.0	37	20	AAW23879	Protein derived fr	307	7	2.0	95	24	ABW12781	Novel human muscul
235	7	2.0	37	20	AAW23880	Protein derived fr	308	7	2.0	96	22	AAU49577	Propionibacterium
236	7	2.0	37	20	AAW61557	P. americanus anti	309	7	2.0	97	20	AAW61560	P. americanus anti
237	7	2.0	37	20	AAW61558	P. americanus anti	310	7	2.0	97	20	AAW61560	Human reproductive
238	7	2.0	37	20	AAW61558	P. americanus anti	311	7	2.0	102	21	AAW61560	Zea mays protein f
239	7	2.0	37	21	AAW44713	Wntler floclunder 11	312	7	2.0	102	22	AAW10668	Human polypeptide
240	7	2.0	38	12	AAW14375	Wntler p. depress	313	7	2.0	104	19	AAW56088	Murine monocyste ch
241	7	2.0	38	20	AAW25447	P. americanus anti	314	7	2.0	104	19	AAW57322	Mouse monocyste che
242	7	2.0	39	18	AAW22874	P. americanus skin	315	7	2.0	105	21	AAW19719	Arabidopsis thalia
243	7	2.0	40	11	AAW20807	Synthetic antifree	316	7	2.0	105	21	AAW19719	Arabidopsis thalia
244	7	2.0	40	21	AAW20091	Arabidopsis thalia	317	7	2.0	106	22	ABG03609	Novel human diagno
245	7	2.0	41	11	AAW08080	Synthetic antifree	318	7	2.0	107	22	AAW08084	Propionibacterium
246	7	2.0	41	11	AAW08082	Synthetic antifree	319	7	2.0	110	22	ABG23072	Novel human diagno
247	7	2.0	41	11	AAW08086	Synthetic antifree	320	7	2.0	111	22	ABG54420	Human liver peptid
248	7	2.0	41	11	AAW08097	Synthetic antifree	321	7	2.0	111	22	ABW39430	Peptide #6936 enco
249	7	2.0	41	14	AAW33090	Human cytomagalovi	322	7	2.0	111	22	ABW24202	Protein #6201 enco
250	7	2.0	41	14	AAW33092	Human cytomagalovi	323	7	2.0	111	22	AAW60110	Human brain expres
251	7	2.0	43	20	AAW24058	Synthetic antifree	324	7	2.0	111	22	AAW72722	Human bone marrow
252	7	2.0	46	11	AAW08088	Synthetic antifree	325	7	2.0	111	22	AAW19703	Peptide #6137 enco
253	7	2.0	50	22	AAW63812	Propionibacterium	326	7	2.0	111	22	AAW22953	Peptide #6990 enco
254	7	2.0	51	11	AAW08088	Synthetic antifree	327	7	2.0	111	22	ABG42546	Human peptide enco
255	7	2.0	51	11	AAW08081	Synthetic antifree	328	7	2.0	112	23	ABW60402	Drosophila melanog
256	7	2.0	52	11	AAW08083	Synthetic antifree	329	7	2.0	112	23	ABG80431	Moraxella catarrha
257	7	2.0	52	22	ABG56552	Human liver peptid	330	7	2.0	112	23	ABW25291	Mouse BACE-interac
258	7	2.0	52	22	ABW41079	Peptide #8585 enco	331	7	2.0	114	20	AAW12363	Human 5' EST seque
259	7	2.0	52	22	ABW25141	Protein #7140 enco	332	7	2.0	114	20	AAW11765	Human polypeptide
260	7	2.0	52	22	ABW61537	Human brain expres	333	7	2.0	114	23	ABW88127	Human polypeptide
261	7	2.0	52	22	AAW74739	Human bone marrow	334	7	2.0	114	24	ABW76179	Human GENSER prote
262	7	2.0	52	22	AAW20397	Peptide #6831 enco	335	7	2.0	114	24	ABW76179	Human GENSER prote
263	7	2.0	52	22	AAW44855	Peptide #8892 enco	336	7	2.0	116	22	AAW67380	Propionibacterium
264	7	2.0	52	23	ABG44538	Human peptide enco	337	7	2.0	117	22	ABW78211	N. gonorrhoeae amf
265	7	2.0	54	18	AAW22875	P. americanus skin	338	7	2.0	119	22	AAW88653	Human immune/haem
266	7	2.0	54	21	AAW00150	Human secreted pro	339	7	2.0	120	22	ABW59393	Drosophila melanog
267	7	2.0	55	22	ABW14770	Human nervous syst	340	7	2.0	121	23	AAW98749	Chicken anemia vir
268	7	2.0	57	21	AAW19770	Arabidopsis thalia	341	7	2.0	122	21	AAW41997	Arabidopsis thalia
269	7	2.0	57	21	AAW61016	Propionibacterium	342	7	2.0	125	21	AAW57848	Zea mays protein f
270	7	2.0	57	22	AAW44856	Synthetic antifree	343	7	2.0	126	21	AAW35185	Zea mays protein f
271	7	2.0	62	11	AAW08079	Synthetic antifree	344	7	2.0	127	20	AAW12339	Human 5' EST seque
272	7	2.0	63	21	AAW08090	Arabidopsis thalia	345	7	2.0	131	20	AAW23876	Hypothetical hybr
273	7	2.0	66	11	AAW08087	Synthetic antifree	346	7	2.0	131	20	AAW95195	Arabidopsis thalia
274	7	2.0	68	22	ABW58436	Human liver peptid	347	7	2.0	131	21	AAW08967	Arabidopsis thalia
275	7	2.0	68	22	ABW43028	Peptide #10534 enc	348	7	2.0	131	21	AAW26759	Zea mays protein f
276	7	2.0	68	22	ABW26216	Protein #8215 enco	349	7	2.0	131	21	AAW46356	Arabidopsis thalia
277	7	2.0	68	22	AAW63933	Human bone marrow	350	7	2.0	132	21	AAW34164	Zea mays protein f
278	7	2.0	68	22	AAW67551	Human bone marrow	351	7	2.0	132	21	AAW92498	TMV AL3 mutant, m
279	7	2.0	68	22	AAW20992	Peptide #7425 enco	352	7	2.0	133	23	ABW43013	Human ovarian anti
280	7	2.0	68	22	AAW68858	Peptide #10895 enc	353	7	2.0	135	22	ABW67507	Drosophila melanog
281	7	2.0	68	23	ABW45929	Human peptide enco	354	7	2.0	135	22	ABW02058	Novel human diagno
282	7	2.0	69	19	AAW20990	Human glial fibril	355	7	2.0	135	22	ABW25332	Novel human diagno
283	7	2.0	70	23	ABW09457	L. helveticus exp	356	7	2.0	136	22	AAW88593	Secreted protein e
284	7	2.0	73	11	AAW08068	Synthetic antifree	357	7	2.0	136	22	ABW50517	Human secreted pro
285	7	2.0	73	16	AAW81407	Hepatitis GB virus	358	7	2.0	137	22	ABW49580	Human liver peptid
286	7	2.0	73	21	AAW42000	Hepatitis GB virus	359	7	2.0	137	22	ABW29575	Peptide #2226 enco
287	7	2.0	73	21	AAW08990	Arabidopsis thalia	360	7	2.0	137	22	ABW34752	Peptide #2258 enco
288	7	2.0	73	22	ABW18265	Novel human diagno	361	7	2.0	137	22	ABW50360	Human secreted pro
289	7	2.0	75	22	ABW64202	Drosophila melanog	362	7	2.0	137	22	ABW20167	Protein #2166 enco
290	7	2.0	76	13	AAW22354	Antigen tc-10a. E	363	7	2.0	137	22	AAW55554	Human brain expres
291	7	2.0	82	20	AAW3877	Wntler floclunder an	364	7	2.0	137	22	AAW67938	Human bone marrow
292	7	2.0	82	23	AAW79431	Human transcritp	365	7	2.0	137	22	AAW15755	Peptide #2189 enco
293	7	2.0	86	21	AAW08968	Arabidopsis thalia	366	7	2.0	137	22	AAW28264	Peptide #2301 enco
294	7	2.0	86	21	AAW46357	Human transcritp	367	7	2.0	137	22	AAW03489	Peptide #2171 enco
295	7	2.0	86	23	ABW22535	Human liver peptid	368	7	2.0	137	23	ABW37472	Human peptide enco
296	7	2.0	87	22	ABW37619	Peptide #9695 enco	369	7	2.0	139	13	AAW22382	Antigen tc-11e. E
297	7	2.0	87	22	ABW42189	Protein #7738 enco	370	7	2.0	139	20	AAW12341	Human 5' EST seque
298	7	2.0	87	22	ABW25739	Human brain expres	371	7	2.0	139	22	ABW22196	Novel human diagno
299	7	2.0	87	22	AAW63074	Human bone marrow	372	7	2.0	140	22	ABW10534	Human cDNA SEQ ID
300	7	2.0	87	22	AAW75885	Peptide #7162 enco	373	7	2.0	140	22	AAW18150	Novel human uterin
301	7	2.0	87	22	AAW20728	Peptide #7162 enco	374	7	2.0	140	22	AAW18488	Human endocrine po

375	7	2.0	140	22	AAU17050	Human novel secret
376	7	2.0	140	23	ABP67121	Human polypeptide
377	7	2.0	140	23	ABJ05777	Novel human protei
378	7	2.0	143	22	AAH95440	Human reproductive
379	7	2.0	143	22	AAH63868	Human prostate can
380	7	2.0	143	22	AAH63870	Human prostate can
381	7	2.0	147	20	AAV01304	Human tropoelastin
382	7	2.0	148	21	AAH41960	Arabidopsis thalia
383	7	2.0	149	21	AAH41959	Arabidopsis thalia
384	7	2.0	149	21	AAH43074	Arabidopsis thalia
385	7	2.0	150	21	AAH43073	Arabidopsis thalia
386	7	2.0	152	21	AAH32737	Eucalyptus grandis
387	7	2.0	152	21	AAH26931	Zea mays protein f
388	7	2.0	153	21	AAH19083	Zea mays protein f
389	7	2.0	154	21	AAH16176	Arabidopsis thalia
390	7	2.0	154	21	AAH45351	Arabidopsis thalia
391	7	2.0	155	21	AAH17704	Arabidopsis thalia
392	7	2.0	156	21	AAH32713	Zea mays protein f
393	7	2.0	158	21	AAH18977	Zea mays protein f
394	7	2.0	158	22	ABG09060	Novel human diagno
395	7	2.0	158	22	ABG22477	Novel human diagno
396	7	2.0	159	22	AAH31604	Novel human secret
397	7	2.0	161	22	ABG59561	Human liver peptid
398	7	2.0	161	22	ABH44188	Peptide #11694 enc
399	7	2.0	161	22	ABH27066	Protein #905 enc
400	7	2.0	161	22	AAH65529	Human brain expres
401	7	2.0	161	22	AAH77922	Human bone marrow
402	7	2.0	161	22	AAH21817	Peptide #8251 enc
403	7	2.0	161	22	AAH38141	Peptide #12178 enc
404	7	2.0	161	23	ABG46944	Human peptide enc
405	7	2.0	162	23	ABH89143	Human polypeptide
406	7	2.0	162	24	ABP75980	Human GENSER prote
407	7	2.0	162	24	ABP76145	Human GENSER prote
408	7	2.0	163	20	AAH59861	Human normal uteru
409	7	2.0	163	21	AAH95953	Porcine adenovirus
410	7	2.0	164	21	AAH40880	Zea mays protein f
411	7	2.0	164	22	ABH41418	Peptide #8924 enc
412	7	2.0	164	22	AAH62288	Human brain expres
413	7	2.0	164	22	AAH75092	Human bone marrow
414	7	2.0	165	21	AAH61075	Arabidopsis thalia
415	7	2.0	165	21	AAH45350	Arabidopsis thalia
416	7	2.0	166	18	AAH14568	Streptococcus pneu
417	7	2.0	166	18	AAH26757	Zea mays protein f
418	7	2.0	167	18	AAH14575	Streptococcus pneu
419	7	2.0	167	21	AAH57847	Zea mays protein f
420	7	2.0	167	22	ABH69302	Drosophila melanog
421	7	2.0	167	22	ABH69302	Drosophila melanog
422	7	2.0	171	21	AAH41453	Zea mays protein f
423	7	2.0	171	21	AAH69157	Amino acid sequenc
424	7	2.0	172	21	AAH32668	Eucalyptus grandis
425	7	2.0	172	21	AAH55069	M. catarrhalis BAS
426	7	2.0	172	21	AAH55069	M. catarrhalis BAS
427	7	2.0	172	21	AAH55091	M. catarrhalis BAS
428	7	2.0	172	21	AAH55092	M. catarrhalis BAS
429	7	2.0	174	22	AAH67551	Propionibacterium
430	7	2.0	176	23	ABH94004	Herpically activ
431	7	2.0	178	22	AAH00756	Human polypeptide
432	7	2.0	180	13	AAH22392	Antigen tc-7a. E1
433	7	2.0	180	21	AAH44933	Arabidopsis thalia
434	7	2.0	180	22	ABH18272	Novel human diagno
435	7	2.0	182	22	ABH52916	Human metabolism-a
436	7	2.0	182	23	ABH05526	M. tuberculosis an
437	7	2.0	183	18	AAH14570	Streptococcus pneu
438	7	2.0	183	20	AAH01311	Human tropoelastin
439	7	2.0	183	21	AAH69158	Amino acid sequenc
440	7	2.0	186	22	AAH86530	P. panotrophus GB
441	7	2.0	187	23	ABH90185	Human polypeptide
442	7	2.0	188	23	ABH62953	Human polypeptide
443	7	2.0	190	21	AAH26252	Corn cyclin-dependent
444	7	2.0	190	24	ABH8758	Maize CKI C. Zea
445	7	2.0	191	22	ABH18218	Novel human diagno
446	7	2.0	194	22	AAH2383	Antigen tc-259. E
447	7	2.0	194	23	AAH21254	Human gene 10 enc

448	7	2.0	195	22	ABH70905	Drosophila melanog
449	7	2.0	197	20	AAH8467	Rice ferritin OsFe
450	7	2.0	198	22	ABH67664	Drosophila melanog
451	7	2.0	198	22	ABH16672	Novel human diagno
452	7	2.0	200	20	AAH01305	Human tropoelastin
453	7	2.0	201	21	AAH24057	Arabidopsis thalia
454	7	2.0	202	22	ABH61097	Human tropoelastin
455	7	2.0	202	22	ABH10487	Drosophila melanog
456	7	2.0	204	22	AAH89007	Human CPNA SEQ ID
457	7	2.0	204	22	AAH18050	Human immune/haem
458	7	2.0	204	22	AAH67074	Human polypeptide
459	7	2.0	206	18	AAH14574	Streptococcus pneu
460	7	2.0	206	22	AAH40578	Human polypeptide
461	7	2.0	207	21	AAH30074	Arabidopsis thalia
462	7	2.0	208	20	AAH60316	Human endometrium
463	7	2.0	209	21	AAH3767	Zea mays protein f
464	7	2.0	210	22	ABH15461	Novel human diagno
465	7	2.0	212	21	AAH05693	Arabidopsis thalia
466	7	2.0	214	21	AAH30073	Arabidopsis thalia
467	7	2.0	214	21	AAH7579	Neisseria meningit
468	7	2.0	214	22	ABH02238	Novel human diagno
469	7	2.0	214	22	AAH60079	Human breast cance
470	7	2.0	215	22	AAH99926	Human eHAND protei
471	7	2.0	215	22	AAH64325	Human eHAND protei
472	7	2.0	215	22	AAH64855	Heart muscle cell
473	7	2.0	216	20	AAH01310	Human tropoelastin
474	7	2.0	219	21	AAH44272	Arabidopsis thalia
475	7	2.0	219	21	AAH51177	Arabidopsis thalia
476	7	2.0	221	22	ABH17903	Novel human diagno
477	7	2.0	223	22	ABH47474	Human liver peptid
478	7	2.0	223	22	ABH27470	Human peptide #121
479	7	2.0	223	22	ABH2621	Peptide #127 enc
480	7	2.0	223	22	ABH18119	Protein #118 enc
481	7	2.0	223	22	AAH53451	Human brain expres
482	7	2.0	223	22	AAH58828	Human bone marrow
483	7	2.0	223	22	AAH13690	Peptide #124 enc
484	7	2.0	223	22	AAH26090	Peptide #127 enc
485	7	2.0	223	22	AAH01440	Peptide #122 enc
486	7	2.0	223	23	ABH35462	Human peptide enc
487	7	2.0	223	23	ABH42145	Human ovarian anti
488	7	2.0	224	22	ABH63816	Drosophila melanog
489	7	2.0	227	20	AAH07083	Renal cancer assoc
490	7	2.0	228	21	AAH24056	Arabidopsis thalia
491	7	2.0	230	21	AAH56799	Human prostate can
492	7	2.0	230	21	AAH24055	Arabidopsis thalia
493	7	2.0	230	24	ABH70826	Human adipocyte Se
494	7	2.0	233	23	ABH64796	Human protein SEO
495	7	2.0	234	22	ABH18269	Novel human diagno
496	7	2.0	234	23	ABH11341	Human ovarian anti
497	7	2.0	237	20	AAH6187	Human bladder tumo
498	7	2.0	237	22	AAH40093	Human polypeptide
499	7	2.0	241	22	AAH70963	S. spinosa protein
500	7	2.0	241	23	ABH65245	Human albumin fusi

## ALIGNMENTS

RESULT 1  
ID AAH62595 standard; Protein; 350 AA.  
AAH62595;  
AC  
XX  
XX 09-NOV-1998 (first entry)  
XX  
XX Homo sapiens cerebellum and embryo specific protein.  
DE  
XX Homo sapiens cerebellum and embryo specific protein; restenosis;  
XX CESP; cerebellum and embryo specific protein; restenosis;  
XX Myocardial infarction; arrhythmia; heart disease;  
XX atherosclerosis.  
XX  
OS Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..21  
 FT /note= "signal peptide"  
 XX  
 XX MO9827932-A2.  
 XX  
 XX 02-JUL-1998.  
 XX  
 XX 18-DEC-1997; 97WO-US23518.  
 XX  
 XX 20-DEC-1996; 96US-0033870.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Ruben SM, Soppet DR;  
 XX  
 XX WPI: 1998-377366/32.  
 XX  
 XX N-PSDB; AAV38798.  
 XX  
 XX New isolated cerebellum and embryo specific polypeptide - used to  
 PT develop products for treating e.g. coronary restenosis, myocardial  
 PT infarction, heart disease and artery or venous thrombosis  
 XX  
 XX Claim 17; Fig 1; 77pp; English.  
 XX  
 CC The sequence is that of cerebellum and embryo specific protein  
 CC (CESP). CESP is involved in: (i) the regulation of collateral  
 CC circulation (particularly in the heart), coronary artery restenosis  
 CC following a revascularisation procedure, apoptosis in myocytes; (ii) the  
 CC regulation of myocyte development in the developing heart; (iii) the  
 CC regulation of circulating blood volume, vascular tone, blood pressure and  
 CC cardiac output, diuresis, natriuresis; (iv) facilitation of transudation  
 CC of plasma water to the interstitium, and (iv) inhibition of the release  
 CC or action of hormones such as aldosterone, angiotensin II, endothelins,  
 CC renin and vasopressin. The products can be used in the diagnosis and  
 CC treatment of CESP related disorders, e.g. coronary restenosis following  
 CC coronary revascularisation, coronary artery thrombus or occlusion,  
 CC myocardial infarction, atrial and/or ventricular arrhythmias, heart  
 CC block, hereditary medial necrosis of small coronary arteries,  
 CC cardiomyopathy, arrhythmogenic right ventricular dysplasia, athero-  
 CC sclerotic heart disease, venous thrombosis or Reynaud's syndrome.  
 XX  
 XX Sequence 350 AA:  
 XX  
 XX Query Match 100.0%; Score 350; DB 19; Length 350;  
 XX Best Local Similarity 100.0%; Pred. No. 0;  
 XX Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 MORLGATLLCLLAAAVPTAPAPATATSAVPKGPALSTPOEATLNEMFRVEELMED 60  
 Db 1 MORLGATLLCLLAAAVPTAPAPATATSAVPKGPALSTPOEATLNEMFRVEELMED 60  
 QY 61 TORHLSAYEEMAEBAEAAASSEVNLANLPSTYNETNTDTYVGNNTIHVREIKITN 120  
 Db 61 TORHLSAYEEMAEBAEAAASSEVNLANLPSTYNETNTDTYVGNNTIHVREIKITN 120  
 QY 121 NOTGQWVFSEFTVTSYGDERSHSHCIIDEDCGPSMYCOFASFOYTQCPGQRMCTR 180  
 Db 121 NOTGQWVFSEFTVTSYGDERSHSHCIIDEDCGPSMYCOFASFOYTQCPGQRMCTR 180  
 QY 121 NOTGQWVFSEFTVTSYGDERSHSHCIIDEDCGPSMYCOFASFOYTQCPGQRMCTR 180  
 Db 121 NOTGQWVFSEFTVTSYGDERSHSHCIIDEDCGPSMYCOFASFOYTQCPGQRMCTR 180  
 QY 181 DSFCCGDQLCVWGHCITKMATRGSGNTICDNQDQPGQLCCAFQRLGLFPVCTPLPYEGEL 240  
 Db 181 DSFCCGDQLCVWGHCITKMATRGSGNTICDNQDQPGQLCCAFQRLGLFPVCTPLPYEGEL 240  
 QY 241 CHDPASRLDPLTWELPDGALDRCPCASGLTQPSHSLVYVCKPTFGSSRDQDEILL 300  
 Db 241 CHDPASRLDPLTWELPDGALDRCPCASGLTQPSHSLVYVCKPTFGSSRDQDEILL 300  
 QY 301 PREVPDEYEVGSMEEVROELDLERSLTEVVALGSPAAAAALLGGEET 350  
 Db 301 PREVPDEYEVGSMEEVROELDLERSLTEVVALGSPAAAAALLGGEET 350

RESULT 2  
 AAY92070  
 ID AAY92070 standard; Protein, 350 AA.  
 XX  
 XX AAY92070;  
 XX  
 XX 01-AUG-2000 (first entry)  
 XX  
 XX Human DKR-3.  
 XX  
 XX DKR-3; human rig-like 7-1 mRNA; chicken lens fiber protein; cleft 4;  
 KW dkx-1; dickkopf-1; antagonist; wnt-8 signaling; morphogenesis;  
 KW growth factor; cyostatic; sonic hedgehog; tissue differentiation.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FH Peptide 1..20  
 FT /label= "signal\_peptide"  
 FT /note= "putative"  
 FT  
 FT Peptide 1..21  
 FT /label= "signal peptide"  
 FT /note= "putative"  
 FT  
 FT Cleavage-site 16..17  
 FT /note= "putative endogenous processing site"  
 FT  
 FT Region 21..145  
 FT /note= "alpha helical region and region of N-linked glycosylation"  
 FT  
 FT Cleavage-site 22..23  
 FT /note= "putative endogenous processing site"  
 FT  
 FT Cleavage-site 32..33  
 FT /note= "putative endogenous processing site"  
 FT  
 FT Cleavage-site 41..42  
 FT /note= "putative endogenous processing site"  
 FT  
 FT Modified-site 96  
 FT /note= "N-glycosylated"  
 FT  
 FT Modified-site 106  
 FT /note= "N-glycosylated"  
 FT  
 FT Modified-site 121  
 FT /note= "N-glycosylated"  
 FT  
 FT Modified-site 204  
 FT /note= "N-glycosylated"  
 FT  
 FT Region 300..350  
 FT /note= "alpha helical region"  
 FT  
 XX MO200018914-A2.  
 XX  
 XX 06-APR-2000.  
 XX  
 XX 17-SEP-1999; 99WO-US21647.  
 XX  
 XX 25-SEP-1998; 98US-0161241.  
 XX  
 XX (AMGE-) AMGEN INC.  
 XX  
 XX Base MB, Sullivan JK, Theill IE, Wang D;  
 XX  
 XX WPI: 2000-293153/25.  
 XX  
 XX N-PSDB; AAA08839.  
 XX  
 XX New nucleic acid molecule encoding a biologically active DKR  
 PT polypeptide, useful in treatment of cancer, e.g. mammary tumors and  
 PT stem cell tumors  
 XX  
 XX Claim 18; Page 126-127; 143pp; English.  
 XX  
 CC AAY92069-75 are novel mouse and human DKR polypeptides.  
 CC The human DKR-3 open reading frame has homology to human rig-like 7-1  
 CC mRNA and to chicken lens fiber protein cleft 4 gene. Human DKR-3  
 CC appears to be secreted, with a signal peptide cleavage site after either  
 CC amino acid 20 or 21.  
 CC DKR-1 is a human ortholog of dkx-1 (dickkopf-1), a novel gene identified



CC in Xenopus and mouse, purportedly an antagonist of wnt-8 signaling.  
 CC DKK-2, -3 and -4 are each related to DKK-1 by their cysteine pattern.  
 CC DKK-1 is also involved in morphogenesis in the developing embryo, and  
 CC therefore a growth factor, by inference DKK polypeptides are also  
 CC growth factors. The DKK polypeptides are useful for treating cancer,  
 CC e.g. mammary tumors, stem cell tumors, or other cancers in which the wnt  
 CC and/or sonic hedgehog (shh) signal transduction pathways are activated.  
 CC They can also be used to enhance tissue differentiation, such as bone  
 CC formation and hematopoietic cell formation.

XX Sequence 350 AA;

Query Match 100.0%; Score 350; DB 21; Length 350;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORLGATILLCILAAVPTAPAPATSAVVKPGPALSYPOEATLNEMFREVEELMED 60  
 DB 1 MORLGATILLCILAAVPTAPAPATSAVVKPGPALSYPOEATLNEMFREVEELMED 60  
 QY 61 TQKLRSAVEEMEAEEAAKASSEVNLANLPSYHNETHNTDTKVGNNTHVREIHKITN 120  
 DB 61 TQKLRSAVEEMEAEEAAKASSEVNLANLPSYHNETHNTDTKVGNNTHVREIHKITN 120  
 QY 121 NOTGQWVFSEVTITVSDDEGRSHSCIIDEDCGPSMYCQFASFOYTCQPCRGQRLCTR 180  
 DB 121 NOTGQWVFSEVTITVSDDEGRSHSCIIDEDCGPSMYCQFASFOYTCQPCRGQRLCTR 180  
 QY 181 DSECCGQQLCWGHCTKMATRSGNGTICDNORCCQPGCLCAFGRLGILFPVCTPLPVEGEL 240  
 DB 181 DSECCGQQLCWGHCTKMATRSGNGTICDNORCCQPGCLCAFGRLGILFPVCTPLPVEGEL 240  
 QY 241 CHDPASRLDLITWLEPDPDALRCPASGLICQPHSHSLVYCKPTFVGSRDQDEIIL 300  
 DB 241 CHDPASRLDLITWLEPDPDALRCPASGLICQPHSHSLVYCKPTFVGSRDQDEIIL 300  
 QY 301 PREVPDEYEVGSFMEVROLEDLERSLTFEVALGEPAAAAALLGGEEL 350  
 DB 301 PREVPDEYEVGSFMEVROLEDLERSLTFEVALGEPAAAAALLGGEEL 350

RESULT 3

AAG80271 AAG80271 standard; Protein; 350 AA.

XX AAG80271;

XX 11-FEB-2002 (first entry)

XX Human DKK-3 protein.

XX DKK-3; detection; schizophrenia; neuroleptic; vaccine; gene therapy;  
 KW neuralgic defect; neuropsychiatric disorder; human.

XX Homo sapiens.

XX WO200163295-A2.

XX 30-AUG-2001.

XX 26-FEB-2001; 2001WO-1B00259.

XX 24-FEB-2000; 2000GB-0004412.

XX 24-FEB-2000; 2000GB-0004415.

XX 15-MAR-2000; 2000GB-0006285.

XX 24-NOV-2000; 2000GB-0028734.

XX 28-NOV-2000; 2000US-0724391.

XX 08-DEC-2000; 2000GB-0030050.

XX 12-DEC-2000; 2000US-0254830.

XX 28-DEC-2000; 2000US-0750395.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herach HWAC, Parekh RB, Ronliff C, Patel TP;

XX WPI; 2001-570652/64.

DR N-PSDB; AAI69309.

XX Diagnosing and monitoring Schizophrenia by detecting the presence of  
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein  
 PT Isoforms in samples of cerebrospinal fluid -

XX Claim 1a; Fig 1; 91pp; English.

CC This invention describes a novel method for detecting the presence of  
 CC schizophrenia associated features (SfFs) and schizophrenia associated  
 CC protein isoforms (SPIs) in samples, e.g. by electrophoresis, immunoassay  
 CC or hybridisation assay, for diagnosing and monitoring schizophrenia,  
 CC studying the effectiveness of treatments and for identifying potential  
 CC therapeutic agents. The products of the invention have neuroleptic  
 CC activity and can be used in vaccines or for gene therapy. The method (I)  
 CC is used: (i) for screening or diagnosis of schizophrenia and the relative  
 CC abundance of at least 1 chosen feature correlates with the presence or  
 CC absence of schizophrenia and for monitoring the effect of therapy  
 CC administered to a subject with schizophrenia and the relative abundance  
 CC of at least 1 chosen feature which correlates with the severity of  
 CC schizophrenia. The expression and activity of the SfFs, SPIs and related  
 CC molecules (e.g. secondary messengers) are studied to diagnose  
 CC schizophrenia, monitor the progress of the disorder and the effectiveness  
 CC of treatment and as targets to identify and produce potential therapeutic  
 CC agents for the treatment of schizophrenia. The paucity of detectable  
 CC neurologic defects distinguishes neuropsychiatric disorders such as  
 CC schizophrenia from neurological disorders, where manifestations of  
 CC anatomical and biochemical changes have been identified in many cases.  
 CC Consequently the identification and characterisation of cellular and/or  
 CC molecular causative defects and neuropathies are necessary for improved  
 CC treatment of neuropsychiatric disorders. This sequence represents the  
 CC human DKK-3 protein described in the method of the invention.

XX Sequence 350 AA;

Query Match 100.0%; Score 350; DB 22; Length 350;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORLGATILLCILAAVPTAPAPATSAVVKPGPALSYPOEATLNEMFREVEELMED 60  
 DB 1 MORLGATILLCILAAVPTAPAPATSAVVKPGPALSYPOEATLNEMFREVEELMED 60  
 QY 61 TQKLRSAVEEMEAEEAAKASSEVNLANLPSYHNETHNTDTKVGNNTHVREIHKITN 120  
 DB 61 TQKLRSAVEEMEAEEAAKASSEVNLANLPSYHNETHNTDTKVGNNTHVREIHKITN 120  
 QY 121 NOTGQWVFSEVTITVSDDEGRSHSCIIDEDCGPSMYCQFASFOYTCQPCRGQRLCTR 180  
 DB 121 NOTGQWVFSEVTITVSDDEGRSHSCIIDEDCGPSMYCQFASFOYTCQPCRGQRLCTR 180  
 QY 181 DSECCGQQLCWGHCTKMATRSGNGTICDNORCCQPGCLCAFGRLGILFPVCTPLPVEGEL 240  
 DB 181 DSECCGQQLCWGHCTKMATRSGNGTICDNORCCQPGCLCAFGRLGILFPVCTPLPVEGEL 240  
 QY 241 CHDPASRLDLITWLEPDPDALRCPASGLICQPHSHSLVYCKPTFVGSRDQDEIIL 300  
 DB 241 CHDPASRLDLITWLEPDPDALRCPASGLICQPHSHSLVYCKPTFVGSRDQDEIIL 300  
 QY 301 PREVPDEYEVGSFMEVROLEDLERSLTFEVALGEPAAAAALLGGEEL 350  
 DB 301 PREVPDEYEVGSFMEVROLEDLERSLTFEVALGEPAAAAALLGGEEL 350

RESULT 4

AAG62468 AAG62468 standard; Protein; 350 AA.

XX AAG62468;

```

DT 10-SEP-2001 (first entry)
XX Human reduced expression in immortalised cells protein.
DE REIC; reduced expression in immortalised cells; cancer; tumour;
XX proliferation inhibitor; viral infection; human.
OS Homo sapiens.
XX MO200138528-A1.
XX 31-MAY-2001.
XX 30-AUG-2000; 2000WO-JP05879.
XX 19-NOV-1999; 99JP-0330604.
XX (HISM) HISAMITSU PHARM CO LTD.
XX Namba M, Tsuji T;
PI WPI; 2001-367688/38.
XX N-PSDB; AAH45489, AAH45490, AAH45491.
XX Cell proliferation inhibiting protein REIC and polynucleotide encoding
PT it for diagnosis and therapy of cancer and as an antiviral agent
XX Claim 2; Page 56-57; 66pp; Japanese.
XX This invention relates to a protein designated REIC (reduced expression
CC in immortalised cells) which inhibits proliferation. REIC shows reduced
CC or suppressed expression in immortalised cells such as cancer cells. The
CC invention includes DNA and protein sequences for REIC. The protein is
CC useful for the treatment and diagnosis of a wide range of benign and
CC malignant tumours and of viral infections (including HIV, influenza,
CC hepatitis and Epstein-Barr virus). The present sequence represents REIC.
XX
SQ Sequence 350 AA;
Query Match 100.0%; Score 350; DB 22; Length 350;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MORIGATILLCILAAAVPTAPAPATATSAVVKGPALSYPOEATLNEMFREVEELMED 60
DB 1 MORIGATILLCILAAAVPTAPAPATATSAVVKGPALSYPOEATLNEMFREVEELMED 60
QY 61 TOHKLRAVEMEEMEAARAKASSEVNLANLPSSYHNETNTDTKVGNNTHVHREIHKITN 120
DB 61 TOHKLRAVEMEEMEAARAKASSEVNLANLPSSYHNETNTDTKVGNNTHVHREIHKITN 120
QY 121 NOTGOMVSEFVITVSGDEGRSHCEIIDDCGSPMYCOPASFOYTCOPCRGRLCTR 180
DB 121 NOTGOMVSEFVITVSGDEGRSHCEIIDDCGSPMYCOPASFOYTCOPCRGRLCTR 180
QY 181 DSECCGQDLCVWGCHCTKMATRGSGNGTICDNQDCCPGLCAFORGLLPVCTPLPVEGEL 240
DB 181 DSECCGQDLCVWGCHCTKMATRGSGNGTICDNQDCCPGLCAFORGLLPVCTPLPVEGEL 240
QY 241 CHDPASLILDLITWELPPDGLDRCPCASGLICOPSHSLVYVCKTLPVGSRRQDEIILL 300
DB 241 CHDPASLILDLITWELPPDGLDRCPCASGLICOPSHSLVYVCKTLPVGSRRQDEIILL 300
QY 301 PREVPDEYEVGSFMEEVROELIEDLERSLTERVALGEPAAAAALLGGEET 350
DB 301 PREVPDEYEVGSFMEEVROELIEDLERSLTERVALGEPAAAAALLGGEET 350

```

```

XX 15-MAY-2001 (first entry)
DT Human PRO295.
XX Human; PRO protein; mapping.
XX Homo sapiens.
XX MO200116318-A2.
XX 08-MAR-2001.
XX 24-AUG-2000; 2000WO-US23328.
XX 01-SEP-1999; 99WO-US20111.
XX 15-SEP-1999; 99WO-US21090.
XX 07-DEC-1999; 99US-0169495.
XX 09-DEC-1999; 99US-0170262.
XX 11-JUN-2000; 2000US-0175481.
XX 18-FEB-2000; 2000WO-US04341.
XX 22-FEB-2000; 2000WO-US04342.
XX 01-MAR-2000; 2000WO-US05601.
XX 03-MAR-2000; 2000US-0187202.
XX 25-APR-2000; 2000US-0199397.
XX 22-MAY-2000; 2000WO-US14042.
XX 05-JUN-2000; 2000US-0209832.
XX (GETH) GENENTECH INC.
XX Eaton DL, Flivarov E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WJ;
XX WPI; 2001-183260/18.
XX N-PSDB; AAF92061.
XX Eighty four nucleic acids encoding PRO polypeptides, useful in
PT molecular biology, including use as hybridization probes, and in
PT chromosome and gene mapping.
XX Claim 12; Fig 8; 276pp; English.
XX The present sequence is a human PRO polypeptide (secreted and
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
CC hybridisation probes, and in chromosome and gene mapping.
XX
SQ Sequence 350 AA;
Query Match 100.0%; Score 350; DB 22; Length 350;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MORIGATILLCILAAAVPTAPAPATATSAVVKGPALSYPOEATLNEMFREVEELMED 60
DB 1 MORIGATILLCILAAAVPTAPAPATATSAVVKGPALSYPOEATLNEMFREVEELMED 60
QY 61 TOHKLRAVEMEEMEAARAKASSEVNLANLPSSYHNETNTDTKVGNNTHVHREIHKITN 120
DB 61 TOHKLRAVEMEEMEAARAKASSEVNLANLPSSYHNETNTDTKVGNNTHVHREIHKITN 120
QY 121 NOTGOMVSEFVITVSGDEGRSHCEIIDDCGSPMYCOPASFOYTCOPCRGRLCTR 180
DB 121 NOTGOMVSEFVITVSGDEGRSHCEIIDDCGSPMYCOPASFOYTCOPCRGRLCTR 180
QY 181 DSECCGQDLCVWGCHCTKMATRGSGNGTICDNQDCCPGLCAFORGLLPVCTPLPVEGEL 240
DB 181 DSECCGQDLCVWGCHCTKMATRGSGNGTICDNQDCCPGLCAFORGLLPVCTPLPVEGEL 240

```

QY 241 CHDPASRLDLITWLEPDGALDRCPGASGLLQPHSHSLVYVCKPTFGSRDQDGEILL 300  
 DB 241 CHDPASRLDLITWLEPDGALDRCPGASGLLQPHSHSLVYVCKPTFGSRDQDGEILL 300  
 QY 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEET 350  
 DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEET 350

## RESULT 6

AA880252  
 ID AAB80252 standard; Protein: 350 AA.

XX AAB80252;  
 XX

DT 24-APR-2001 (first entry)  
 XX

DE Human PRO295 protein.  
 XX

KW Human; PRO; dermatological; antipruritic; cytostatic; antiinflammatory;  
 KW antiParkinsonian neurotropic; neuroprotective; vulnerary; cardiant;  
 KW antiangiogenic; vasotropic; antiaesthetic; antineumatic; cancer;  
 KW antidiabetic; antihypertensive; antidiabetic; antiviral; diabetes;  
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;  
 KW ischaemia; inflammation.  
 XX

OS Homo sapiens.  
 XX

PN W0200104311-A1.  
 XX

PD 18-JAN-2001.  
 XX

PF 22-FEB-2000; 2000WC-US04414.  
 XX

XX 07-JUL-1999; 99US-0143048.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 08-SEP-1999; 99WC-US20594.  
 PR 13-SEP-1999; 99WC-US20944.  
 PR 15-SEP-1999; 99WC-US21090.  
 PR 15-SEP-1999; 99WC-US21547.  
 PR 05-OCT-1999; 99WC-US23089.  
 PR 29-NOV-1999; 99WC-US28214.  
 PR 30-NOV-1999; 99WC-US28313.  
 PR 16-DEC-1999; 99WC-US30095.  
 PR 20-DEC-1999; 99WC-US30911.  
 PR 20-DEC-1999; 99WC-US30999.  
 PR 05-JAN-2000; 99WC-US00219.  
 XX

PA (GETH ) GENENTECH INC.  
 XX

PI Ashkenazi AJ, Botstein D, Desnoyers J, Eaton DL, Ferrara N;  
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin JT;  
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WI;  
 XX

DR WPI; 2001-081051/09.  
 DR N-PSDB; AAF72413.  
 XX

PT Sixty one nucleic acids encoding PRO polypeptides which are useful in  
 PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung  
 PT squamous cell carcinoma) and neurodegenerative diseases (e.g.  
 PT Alzheimer's disease) -  
 XX

XX Claim 1; Fig 84; 393BP; English.  
 XX

CC The present sequence is one of sixty one novel secreted and  
 CC transmembrane PRO polypeptides. The PRO polypeptides are  
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung  
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.  
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,  
 CC

CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.  
 CC endometrial bleeding angiogenesis, ischaemias such as coronary  
 CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,  
 CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and  
 CC diabetes and retinal disorders such as retinitis pigmentosa.  
 CC The PRO nucleic acids have applications in molecular biology, including  
 CC use as hybridization probes, and in chromosome and gene mapping.  
 XX

XX Sequence 350 AA;

Query Match 100.0%; Score 350; DB 22; Length 350;  
 Best local similarity 100.0%; Pred. No. 0;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORGATLLCLLLAAVPTAPAPATSAVKKPAPALSYPOEBATINMEFREVEELMED 60  
 DB 1 MORGATLLCLLLAAVPTAPAPATSAVKKPAPALSYPOEBATINMEFREVEELMED 60  
 QY 61 TOHKLRSAVEMEAEEAAKASSEVNLANLPSPYHNETNTDTKGNNTIHHREIHKITN 120  
 DB 61 TOHKLRSAVEMEAEEAAKASSEVNLANLPSPYHNETNTDTKGNNTIHHREIHKITN 120  
 QY 121 NOTGQWVSEFVITVSGDEGRSHCEIIDECCGSPMYCQFASFOYTCOPCRGRLCTR 180  
 DB 121 NOTGQWVSEFVITVSGDEGRSHCEIIDECCGSPMYCQFASFOYTCOPCRGRLCTR 180  
 QY 121 NOTGQWVSEFVITVSGDEGRSHCEIIDECCGSPMYCQFASFOYTCOPCRGRLCTR 180  
 DB 181 DSECCGQLCWGHCTKMATPGSNCTICDNORDCQPGLCAPFCQGLFPVCTPLPVGEEL 240  
 DB 181 DSECCGQLCWGHCTKMATPGSNCTICDNORDCQPGLCAPFCQGLFPVCTPLPVGEEL 240  
 QY 241 CHDPASRLDLITWLEPDGALDRCPGASGLLQPHSHSLVYVCKPTFGSRDQDGEILL 300  
 DB 241 CHDPASRLDLITWLEPDGALDRCPGASGLLQPHSHSLVYVCKPTFGSRDQDGEILL 300  
 QY 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEET 350  
 DB 301 PREVPDEYVGSFMEVROELEDLERSLTERMALGEPAAAAALLGGEET 350

## RESULT 7

ABG95854  
 ID ABG95854 standard; Protein: 350 AA.

XX ABG95854;  
 XX

DT 10-DEC-2002 (first entry)  
 XX

DE Human secreted/transmembrane protein PRO295.  
 XX

KW Human; secreted protein; transmembrane protein; antineumatic;  
 KW antiarthritic; osteopathic; sports-related joint problem;  
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.  
 XX

OS Homo sapiens.  
 XX

PN US2002119130-A1.  
 XX

PD 29-AUG-2002.  
 XX

PF 06-DEC-2001; 2001US-0006867.  
 XX

XX 29-OCT-1997; 97US-063435P.  
 PR 29-OCT-1997; 97US-064215P.  
 PR 22-APR-1998; 98US-082797P.  
 PR 22-APR-1998; 98US-083495P.  
 PR 15-MAY-1998; 98US-085579P.  
 PR 10-JUN-1998; 98US-088811P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 10-JUN-1998; 98US-088825P.  
 PR 11-JUN-1998; 98US-088863P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 16-SEP-1998; 98WC-US19330.  
 XX



PR 08-NOV-2000; 2000MO-US30952.  
 PR 10-NOV-2000; 2000MO-US30873.  
 PR 01-DEC-2000; 2000MO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000MO-US34956.  
 PR 22-JAN-2001; 2001US-0767699.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001MO-US06520.  
 PR 01-MAR-2001; 2001MO-US06666.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828356.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001MO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001MO-US17443.  
 PR 01-JUN-2001; 2001MO-US17800.  
 PR 20-JUN-2001; 2001MO-US19692.  
 PR 28-JUN-2001; 2001MO-US00000.

XX (GETH ) GENENTECH INC.  
 PA (BAKE/) BAKER K P.  
 PA (FERR/) FERRARA N.  
 PA (GERB/) GERBER H.  
 PA (GERB/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODD/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (MARS/) MARSTERS S A.  
 PA (PANU/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (STEP/) STEPHAN J F.  
 PA (WATA/) WATANABE C K.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.

PI Baker KP, Ferreira N, Gerber H, Gerritsen ME, Goddard A, Godowski P, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W, WPI; 2002-171999/22.  
 DR N-PSDB; ABL95585.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -  
 PT  
 PS  
 XX Claim 11; Fig 50; 567pp; English.

XX The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumor  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a PRO protein of the invention.

XX Sequence 350 AA;

Query Match 100.0%; Score 350; DB 23; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MORIGATLCLLLAAAVPTAPAPATSAVVKGPALSYPOEATLNMFEVLEWMD 60  
 Db 1 MORIGATLCLLLAAAVPTAPAPATSAVVKGPALSYPOEATLNMFEVLEWMD 60

OY 61 TQHKLSAVEEMEAFAAKASSEVNLANLPSSYHNETNDTKVGNNTIHYREIHKITN 120  
 Db 61 TQHKLSAVEEMEAFAAKASSEVNLANLPSSYHNETNDTKVGNNTIHYREIHKITN 120  
 OY 121 NOTGMVSEETVITVSVDGEGRSHCECTIDDCGPPSYCOPASFOYTCOPRCGRMCTR 180  
 Db 121 NOTGMVSEETVITVSVDGEGRSHCECTIDDCGPPSYCOPASFOYTCOPRCGRMCTR 180  
 OY 181 DSECCGDLCTWGHCTKATGNSGTICDNORDCPGCAFGGLFPVCTPAPVEGEL 240  
 Db 181 DSECCGDLCTWGHCTKATGNSGTICDNORDCPGCAFGGLFPVCTPAPVEGEL 240  
 OY 241 CHDPASRLDILITWLEPFDGALDRCPASGLLCPHSHSLVYCKPTFVGSRDDGELL 300  
 Db 241 CHDPASRLDILITWLEPFDGALDRCPASGLLCPHSHSLVYCKPTFVGSRDDGELL 300  
 OY 301 PREVPDEYEVGSFMEYVQGEJEDLERSITTEPMALGEPAAAAALLGGEI 350  
 Db 301 PREVPDEYEVGSFMEYVQGEJEDLERSITTEPMALGEPAAAAALLGGEI 350

RESULT 9  
 ABB90735  
 ID ABB90735 standard; Protein; 350 AA.

XX ABB90735;

DT 30-MAY-2002 (first entry)

DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 202.

XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;  
 KW antiangiogenic; tumour; neovascularisation; vascularised tumour;  
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
 KW psoriasis.

OS Homo sapiens.

PN MO200210217-A2.

XX 07-FEB-2002.

PF 01-AUG-2001; 2001MO-US24031.

PR 02-AUG-2000; 2000US-222599P.

PR 11-AUG-2000; 2000US-224360P.

PR 11-APR-2001; 2001US-282850P.

XX (UTIO ) UNIV JOHNS HOPKINS.

PI St Croix B, Kinzler KW, Vogelstein B;

XX WPI; 2002-291656/33.

DR N-PSDB; ABL92089.

XX An isolated molecule comprising an antibody variable region which

PT specifically binds to an extracellular domain of a tumor endothelial

PT marker (TEM) protein, useful for inhibiting tumor growth -

XX Claim 54; Page 156-157; 331pp; English.

XX The invention relates to an isolated molecule comprising an antibody  
 CC variable region which specifically binds to an extracellular domain of a  
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.  
 CC They are useful for inhibiting tumour growth, neovascularisation in  
 CC subjects bearing a vascularised tumour, polycystic kidney disease,  
 CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse  
 CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and  
 CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide  
 CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and

CC ABL92143-ABL92191, normal endothelial markers (NEM) ABL92042-ABL92074;  
 CC and pan-endothelial markers (PEM) ABL91903-ABL91995.  
 XX Sequence 350 AA;  
 Query Match 100.0%; Score 350; DB 23; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MORLGATLLCLLLAAVPTAPAPATSAVPKPGALSYPOEATLNMFEVEELMED 60  
 Db 1 MORLGATLLCLLLAAVPTAPAPATSAVPKPGALSYPOEATLNMFEVEELMED 60  
 QY 61 TQHLKRSVEMEAEEAAKASSEVNLANLPSYHNETNTDTKVGNNITHVHREIHKITN 120  
 Db 61 TQHLKRSVEMEAEEAAKASSEVNLANLPSYHNETNTDTKVGNNITHVHREIHKITN 120  
 QY 121 NOTGQWVFSEVITVSVDDEGRSHHECIIDEDGSPMYCQFASFOYTCQPCRGRLCTR 180  
 Db 121 NOTGQWVFSEVITVSVDDEGRSHHECIIDEDGSPMYCQFASFOYTCQPCRGRLCTR 180  
 QY 181 DSECCGQDLCTWGHCTKMATRGSGNGTICDNQDCQPGLCARFQGLLPVCTPLPVEGEL 240  
 Db 181 DSECCGQDLCTWGHCTKMATRGSGNGTICDNQDCQPGLCARFQGLLPVCTPLPVEGEL 240  
 QY 241 CHDPAARLDLITWELPQDALDRCPASGLLCQPHSHSLVVCXKPTFVGSRDQDEITL 300  
 Db 241 CHDPAARLDLITWELPQDALDRCPASGLLCQPHSHSLVVCXKPTFVGSRDQDEITL 300  
 QY 301 PREVPDEYGVGSFMEVRQELDLERSLTENALGPAAAAALLGGEI 350  
 Db 301 PREVPDEYGVGSFMEVRQELDLERSLTENALGPAAAAALLGGEI 350  
 RESULT 10  
 ID ABB84841 standard; Protein; 350 AA.  
 XX ABB84841;  
 AC ABB84841;  
 DT 16-MAY-2002 (first entry)  
 XX Human PRO295 protein sequence SEQ ID NO:50.  
 KW Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;  
 KW vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophilicities;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; gene mapping.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX WO200200690-A2.  
 PN 03-JAN-2002.  
 PD 20-JUN-2001; 2001WO-US19692.  
 PF 23-JUN-2000; 2000US-213637P.  
 PR 26-JUL-2000; 2000US-21956P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220664P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 02-AUG-2000; 2000US-222695P.  
 PR 17-AUG-2000; 2000US-0643657.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 18-SEP-2000; 2000US-0665350.

PR 24-OCT-2000; 2000US-242922P.  
 PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-FEB-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796493.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 09-MAR-2001; 2001WO-US06666.  
 PR 14-MAR-2001; 2001US-0802706.  
 PR 22-MAR-2001; 2001US-0808689.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PA (GETH ) GENENTECH INC.  
 PI Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A,  
 PI Godowski PJ, Gurney AL, Hillan KJ, Masters SA, Pan D, Paoni NF,  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,  
 DR WPI; 2002-090516/12.  
 DR N-PSDB; ABL88096.  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX "PS  
 XX Claim 11; Fig 50; 565pp; English.  
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytosolic,  
 CC antiangiogenic, hypotensive, vulnerability, antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophilicities,  
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
 CC carcinoma) and wound healing. The PRO polynucleotides have applications  
 CC in molecular biology, including use as hybridisation probes, and in  
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
 CC probes used in the exemplification of the present invention.  
 XX Sequence 350 AA;  
 QY 1 MORLGATLLCLLLAAVPTAPAPATSAVPKPGALSYPOEATLNMFEVEELMED 60  
 Db 1 MORLGATLLCLLLAAVPTAPAPATSAVPKPGALSYPOEATLNMFEVEELMED 60  
 QY 61 TQHLKRSVEMEAEEAAKASSEVNLANLPSYHNETNTDTKVGNNITHVHREIHKITN 120  
 Db 61 TQHLKRSVEMEAEEAAKASSEVNLANLPSYHNETNTDTKVGNNITHVHREIHKITN 120  
 QY 121 NOTGQWVFSEVITVSVDDEGRSHHECIIDEDGSPMYCQFASFOYTCQPCRGRLCTR 180  
 Db 121 NOTGQWVFSEVITVSVDDEGRSHHECIIDEDGSPMYCQFASFOYTCQPCRGRLCTR 180  
 QY 181 DSECCGQDLCTWGHCTKMATRGSGNGTICDNQDCQPGLCARFQGLLPVCTPLPVEGEL 240



```

DB      181 DECCGDCQVGHGCHTQATRSNGTICNQRDCPGCCAFQGLPVCPTPLVEGEL 240
QY      241 CHDPASRLDLITWELPEPGALDRCPGASGLLCOPHSILVYVCKPTFGSDQDGEILL 300
DB      241 CHDPASRLDLITWELPEPGALDRCPGASGLLCOPHSILVYVCKPTFGSDQDGEILL 300
QY      301 PREVPDEYVGSFMEVRQELDLERSLTEMALGEPAAAAALLIGBEI 350
DB      301 PREVPDEYVGSFMEVRQELDLERSLTEMALGEPAAAAALLIGBEI 350

RESULT 11
ABU69662
ID      ABU69662 standard; Protein; 350 AA.
XX
XX      ABU69662;
AC
XX
XX      05-JUN-2003 (first entry)
DT
XX
XX      Novel human secreted and transmembrane protein PRO295.
DE
XX
XX      Human; secreted and transmembrane protein; gene therapy; psoriasis;
XX      enterocolitis; gastrointestinal ulceration; skin disease;
XX      keratinocyte differentiation; epithelial cancer; Alzheimer's disease;
XX      squamous cell carcinoma; Parkinson's disease; inflammatory disease;
XX      amyotrophic lateral sclerosis; rheumatoid arthritis; asthma;
XX      multiple sclerosis; organ failure; atherosclerosis; cardiac injury;
XX      infertility; birth defect; premature aging; AIDS; cancer;
XX      diabetic complication; wound repair; tissue re-growth.
OS      Homo sapiens.
XX
XX      US2003017463-A1.
PN
XX
XX      23-JAN-2003.
PD
XX
XX      11-JUL-2001; 2001US-0903640.
PF
XX
XX      10-SEP-1998; 98WO-US18624.
PR      14-SEP-1998; 98WO-US19177.
PR      16-SEP-1998; 98WO-US19330.
PR      17-SEP-1998; 98WO-US19437.
PR      01-DEC-1998; 98WO-US25108.
PR      08-SEP-1999; 99WO-US20594.
PR      13-SEP-1999; 99WO-US20944.
PR      15-SEP-1999; 99WO-US21090.
PR      15-SEP-1999; 99WO-US21547.
PR      05-OCT-1999; 99WO-US23089.
PR      29-NOV-1999; 99WO-US28214.
PR      30-NOV-1999; 99WO-US28313.
PR      01-DEC-1999; 99WO-US28301.
PR      02-DEC-1999; 99WO-US28564.
PR      02-DEC-1999; 99WO-US28565.
PR      16-DEC-1999; 99WO-US30095.
PR      20-DEC-1999; 99WO-US30811.
PR      20-DEC-1999; 99WO-US30811.
PR      05-JAN-1999; 99WO-US30811.
PR      05-JAN-2000; 2000WO-US00219.
PR      11-FEB-2000; 2000WO-US03565.
PR      22-FEB-2000; 2000WO-US04414.
PR      24-FEB-2000; 2000WO-US05004.
PR      02-MAR-2000; 2000WO-US05841.
PR      20-MAR-2000; 2000WO-US07377.
PR      30-MAR-2000; 2000WO-US08439.
PR      22-MAY-2000; 2000WO-US14042.
PR      02-JUN-2000; 2000WO-US15264.
PR      28-JUL-2000; 2000WO-US20710.
PR      24-AUG-2000; 2000WO-US23328.
PR      17-SEP-1997; 97US-059113P.
PR      17-SEP-1997; 97US-059115P.
PR      17-SEP-1997; 97US-059117P.
PR      17-SEP-1997; 97US-059119P.
PR      17-SEP-1997; 97US-059121P.

```

```

PR      17-SEP-1997; 97US-059122P.
PR      17-SEP-1997; 97US-059184P.
PR      18-SEP-1997; 97US-059263P.
PR      18-SEP-1997; 97US-059266P.
PR      15-OCT-1997; 97US-062125P.
PR      17-OCT-1997; 97US-062285P.
PR      17-OCT-1997; 97US-062287P.
PR      21-OCT-1997; 97US-063486P.
PR      24-OCT-1997; 97US-062814P.
PR      24-OCT-1997; 97US-062816P.
PR      24-OCT-1997; 97US-063045P.
PR      24-OCT-1997; 97US-063120P.
PR      24-OCT-1997; 97US-063121P.
PR      24-OCT-1997; 97US-063127P.
PR      24-OCT-1997; 97US-063128P.
PR      27-OCT-1997; 97US-063327P.
PR      27-OCT-1997; 97US-063329P.
PR      28-OCT-1997; 97US-063541P.
PR      28-OCT-1997; 97US-063542P.
PR      28-OCT-1997; 97US-063544P.
PR      28-OCT-1997; 97US-063549P.
PR      28-OCT-1997; 97US-063550P.
PR      28-OCT-1997; 97US-063564P.
PR      29-OCT-1997; 97US-063435P.
PR      29-OCT-1997; 97US-063704P.
PR      29-OCT-1997; 97US-063732P.
PR      29-OCT-1997; 97US-063734P.
PR      29-OCT-1997; 97US-063735P.
PR      29-OCT-1997; 97US-063738P.
PR      29-OCT-1997; 97US-064215P.
PR      31-OCT-1997; 97US-063870P.
PR      31-OCT-1997; 97US-064103P.
PR      03-NOV-1997; 97US-064248P.
PR      07-NOV-1997; 97US-064809P.
PR      12-NOV-1997; 97US-065186P.
PR      17-NOV-1997; 97US-065846P.
PR      18-NOV-1997; 97US-065693P.
PR      21-NOV-1997; 97US-066120P.
PR      24-NOV-1997; 97US-066453P.
PR      24-NOV-1997; 97US-066456P.
PR      24-NOV-1997; 97US-066511P.
PR      24-NOV-1997; 97US-066770P.
PR      24-NOV-1997; 97US-066772P.
PR      25-NOV-1997; 97US-066840P.
PR      12-DEC-1997; 97US-069425P.
PR      04-JUN-1998; 98US-088026P.
PR      10-SEP-1998; 98US-089803P.
PR      14-SEP-1998; 98US-100262P.
PR      17-SEP-1998; 98US-100858P.
PR      13-OCT-1998; 98US-104808P.
PR      20-NOV-1998; 98US-109304P.
PR      22-DEC-1998; 98US-113296P.
PR      07-JUL-1999; 99US-143048P.
PR      26-JUL-1999; 99US-145698P.
PR      28-JUL-1999; 99US-146222P.
PR      18-SEP-2000; 2000US-0665350.

(GETH ) GENENTECH INC.
XX
XX      Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
PI      Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI      Godowski PJ, Grimaldi JC, Gurney AL, Hillen KJ, Kljavin IJ;
PI      Mather UP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI      Williams FM, Wood WI;
XX
XX      WPI; 2003-341586/32.
DR      N-PSDB; ACAS5002.
XX
XX      New PRO polypeptides and nucleic acid molecules, useful in diagnosing
PT      or treating inflammatory diseases, organ failure, atherosclerosis,
PT      cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or
PT      Parkinson's disease -

```

XX PS Claim 12; Fig 84; 473bp; English.  
 CC The invention describes sixty one nucleic acids encoding PRO polypeptides  
 CC (secreted and transmembrane). The PRO polypeptides and nucleic acids are  
 CC useful in diagnosing or treating enterocolitis, gastrointestinal  
 CC ulceration, skin diseases associated with abnormal Keratinocyte  
 CC differentiation, e.g. psoriasis or epithelial cancers such as squamous  
 CC cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic  
 CC lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis,  
 CC asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac  
 CC injury, infertility, birth defects, premature aging, AIDS, cancer, are  
 CC diabetic complications, or mutations in general. The polypeptides are  
 CC also useful for wound repair and associated therapies concerned with  
 CC re-growth of tissue. The PRO polypeptides and nucleic acid molecules  
 CC are also useful in gene therapy, and as molecular weight markers for  
 CC protein electrophoresis purposes. The anti-PRO antibodies may be used  
 CC in diagnostic assays for PRO, or for the affinity purification of PRO  
 CC from recombinant cell culture or natural sources. This is the amino  
 CC acid sequence of a novel human PRO polypeptide.

XX SQ Sequence 350 AA;

Query Match 100.0%; Score 350; DB 24; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORIGATLLCLLAAVPTAPAPATSAVPKPGALSTYPOEATLNEMFREVEELMED 60  
 DB 1 MORIGATLLCLLAAVPTAPAPATSAVPKPGALSTYPOEATLNEMFREVEELMED 60  
 QY 61 TORHLSAVEMEAEAAKASSEVNLANLPSTHNETINDTVGNNTIHVHEIKITN 120  
 DB 61 TORHLSAVEMEAEAAKASSEVNLANLPSTHNETINDTVGNNTIHVHEIKITN 120  
 QY 121 NOTGQWVSEFTVTSVDEEGRSRSHCEIIDECGFSMYCQFASFOYTCOPCRGRLCTR 180  
 DB 121 NOTGQWVSEFTVTSVDEEGRSRSHCEIIDECGFSMYCQFASFOYTCOPCRGRLCTR 180  
 QY 181 DSBCCGDOLCVMGHCTMATRSGNGTICDNRDCCQGLCCAFGRGLTFPCTPLPVEGEL 240  
 DB 181 DSBCCGDOLCVMGHCTMATRSGNGTICDNRDCCQGLCCAFGRGLTFPCTPLPVEGEL 240  
 QY 241 CHDPASRLDLITWELPDGALDRCPASGILCQPHSHSLVYVCKPTFVGSRDQGEILL 300  
 DB 241 CHDPASRLDLITWELPDGALDRCPASGILCQPHSHSLVYVCKPTFVGSRDQGEILL 300  
 QY 301 PREVPDEYEVGSMEEVRQELDLERSLTREMLGEPAAAAALLGGEET 350  
 DB 301 PREVPDEYEVGSMEEVRQELDLERSLTREMLGEPAAAAALLGGEET 350

RESULT 12  
 ABUT1485  
 ID ABUT1485 standard; Protein: 350 AA.  
 XX AC ABUT1485;  
 XX DT 10-JUN-2003 (first entry)  
 XX DE Human PRO polypeptide #41.  
 XX KW Human; secreted and transmembrane protein; PRO polypeptide; cancer;  
 XX KW Alzheimer's disease; ischaemia; cytosolic; nootropic; vasotropic;  
 XX KW neuroprotective.  
 XX OS Homo sapiens.  
 XX PN US2002192659-A1.  
 XX PD 19-DEC-2002.  
 XX PF 10-JUL-2001; 2001US-0902853.

XX PR 10-SEP-1998; 98WO-US18824.  
 PR 14-SEP-1998; 98WO-US19177.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 08-SEP-1999; 98WO-US20594.  
 PR 13-SEP-1999; 95WO-US20944.  
 PR 15-SEP-1999; 95WO-US21090.  
 PR 15-SEP-1999; 95WO-US21547.  
 PR 05-OCT-1999; 95WO-US23089.  
 PR 01-DEC-1999; 95WO-US28301.  
 PR 02-DEC-1999; 95WO-US28564.  
 PR 02-DEC-1999; 98WO-US28565.  
 PR 16-DEC-1999; 95WO-US30095.  
 PR 20-DEC-1999; 95WO-US30911.  
 PR 05-JAN-2000; 95WO-US30999.  
 PR 11-FEB-2000; 2000WO-US00219.  
 PR 22-FEB-2000; 2000WO-US04565.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 17-SEP-1997; 97US-059113P.  
 PR 17-SEP-1997; 97US-059115P.  
 PR 18-SEP-1997; 97US-059117P.  
 PR 15-OCT-1997; 97US-062125P.  
 PR 17-OCT-1997; 97US-062285P.  
 PR 17-OCT-1997; 97US-062287P.  
 PR 21-OCT-1997; 97US-063486P.  
 PR 24-OCT-1997; 97US-062814P.  
 PR 24-OCT-1997; 97US-062816P.

XX PA (GETH ) GENENTECH INC.

XX PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N,  
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,  
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ,  
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TM, Tunnas D,  
 PI Williams PM, Wood WI,  
 XX DR WPI: 2003-361832/34.  
 DR N-PSDB; AOA58487.

XX PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or  
 PT PRO1868, useful in molecular biology, chromosome and gene mapping, in  
 PT generating antisense RNA and DNA, and in gene therapy

XX PS Claim 12; Fig 84; 474bp; English.

XX CC The present invention relates to the isolation of novel human secreted  
 CC and transmembrane proteins (PRO polypeptides), and the polynucleotide  
 CC sequences encoding them. The polynucleotide sequences are useful in  
 CC molecular biology, as hybridisation probes, in chromosome and gene  
 CC mapping, in generating antisense RNA and DNA, and in gene therapy. The  
 CC polynucleotide sequences may also be used in preparing PRO polypeptides  
 CC by recombinant techniques, and in generating either transgenic animals  
 CC or knock-out animals which, in turn, are useful in the development and  
 CC screening of therapeutically useful reagents. The PRO polypeptides or  
 CC their antibodies are useful in preparing a medicament for treating a  
 CC condition responsive to the polypeptide or antibody, such as cancer,  
 CC Alzheimer's disease or ischaemia, and in various diagnostic assays.  
 CC ABUT1445-ABUT1505 represent human PRO polypeptides of the invention.

XX SQ Sequence 350 AA;

Query Match 100.0%; Score 350; DB 24; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORIGATLLCLLAAVPTAPAPATSAVPKPGALSTYPOEATLNEMFREVEELMED 60  
 DB 1 MORIGATLLCLLAAVPTAPAPATSAVPKPGALSTYPOEATLNEMFREVEELMED 60



ID ABU71931 standard; Protein; 350 AA.  
 XX AC ABU71931;  
 XX DT 12-JUN-2003 (first entry)  
 XX Human secreted/transmembrane protein PRO295.  
 XX Human; secreted protein; transmembrane protein; PRO;  
 KM gene therapy; chromosome identification; chromosome marker.  
 XX Homo sapiens.  
 XX US2003003530-A1.  
 PD 02-JAN-2003.  
 XX 11-JUL-2001; 2001US-0904011.  
 XX 10-SEP-1998; 98MO-US18824.  
 PR 14-SEP-1998; 98MO-US19177.  
 PR 16-SEP-1998; 98MO-US19330.  
 PR 17-SEP-1998; 98MO-US19337.  
 PR 01-DEC-1998; 98MO-US25108.  
 PR 08-SEP-1999; 99MO-US20594.  
 PR 13-SEP-1999; 99MO-US20944.  
 PR 15-SEP-1999; 99MO-US21090.  
 PR 05-OCT-1999; 99MO-US21547.  
 PR 29-NOV-1999; 99MO-US28214.  
 PR 30-NOV-1999; 99MO-US28313.  
 PR 01-DEC-1999; 99MO-US28301.  
 PR 02-DEC-1999; 99MO-US28564.  
 PR 02-DEC-1999; 99MO-US28565.  
 PR 16-DEC-1999; 99MO-US30095.  
 PR 20-DEC-1999; 99MO-US30911.  
 PR 20-DEC-1999; 99MO-US30999.  
 PR 05-JAN-2000; 2000MO-US02119.  
 PR 11-FEB-2000; 2000MO-US03565.  
 PR 22-FEB-2000; 2000MO-US04414.  
 PR 24-FEB-2000; 2000MO-US05004.  
 PR 02-MAR-2000; 2000MO-US05841.  
 PR 20-MAR-2000; 2000MO-US07377.  
 PR 30-MAR-2000; 2000MO-US08439.  
 PR 22-MAY-2000; 2000MO-US14042.  
 PR 28-JUL-2000; 2000MO-US15264.  
 PR 28-AUG-2000; 2000MO-US23328.  
 PR 17-SEP-1997; 97US-059113P.  
 PR 17-SEP-1997; 97US-059115P.  
 PR 17-SEP-1997; 97US-059117P.  
 PR 17-SEP-1997; 97US-059119P.  
 PR 17-SEP-1997; 97US-059121P.  
 PR 17-SEP-1997; 97US-059122P.  
 PR 17-SEP-1997; 97US-059184P.  
 PR 18-SEP-1997; 97US-059263P.  
 PR 18-SEP-1997; 97US-059266P.  
 PR 15-OCT-1997; 97US-062125P.  
 PR 17-OCT-1997; 97US-062285P.  
 PR 17-OCT-1997; 97US-062287P.  
 PR 21-OCT-1997; 97US-063486P.  
 PR 24-OCT-1997; 97US-062814P.  
 PR 24-OCT-1997; 97US-062816P.  
 PR 24-OCT-1997; 97US-063045P.  
 PR 24-OCT-1997; 97US-063120P.  
 PR 24-OCT-1997; 97US-063121P.  
 PR 24-OCT-1997; 97US-063127P.  
 PR 24-OCT-1997; 97US-063128P.  
 PR 27-OCT-1997; 97US-063327P.  
 PR 27-OCT-1997; 97US-063329P.  
 PR 28-OCT-1997; 97US-063541P.  
 PR 28-OCT-1997; 97US-063542P.  
 PR 28-OCT-1997; 97US-063544P.

PR 28-OCT-1997; 97US-063549P.  
 PR 28-OCT-1997; 97US-063550P.  
 PR 28-OCT-1997; 97US-063564P.  
 PR 29-OCT-1997; 97US-063435P.  
 PR 29-OCT-1997; 97US-063704P.  
 PR 29-OCT-1997; 97US-063732P.  
 PR 29-OCT-1997; 97US-063733P.  
 PR 29-OCT-1997; 97US-063734P.  
 PR 29-OCT-1997; 97US-063735P.  
 PR 29-OCT-1997; 97US-063738P.  
 PR 29-OCT-1997; 97US-064215P.  
 PR 31-OCT-1997; 97US-063870P.  
 PR 31-OCT-1997; 97US-064103P.  
 PR 03-NOV-1997; 97US-064240P.  
 PR 07-NOV-1997; 97US-064809P.  
 PR 12-NOV-1997; 97US-065186P.  
 PR 17-NOV-1997; 97US-065846P.  
 PR 18-NOV-1997; 97US-065693P.  
 PR 21-NOV-1997; 97US-066120P.  
 PR 21-NOV-1997; 97US-066364P.  
 PR 24-NOV-1997; 97US-066453P.  
 PR 24-NOV-1997; 97US-066466P.  
 PR 24-NOV-1997; 97US-066511P.  
 PR 24-NOV-1997; 97US-066770P.  
 PR 24-NOV-1997; 97US-066772P.  
 PR 18-SEP-2000; 2000US-0665350.  
 XX (GETH ) GENENTECH INC.  
 XX Ashkenazi A, Botstein D, Desnovers L, Eaton DU, Ferrara N;  
 PI Pilyavoff E, Fong S, Gerber H, Gertlsen ME, Goddard A;  
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;  
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WI;  
 XX WPI; 2003-329602/31.  
 DR N-PSDB; ACA60194.  
 PT New transmembrane polypeptides and nucleic acids encoding the  
 PT polypeptides, useful in gene therapy, in chromosome identification, as  
 PT chromosome markers, in generating probes and in tissue typing  
 XX  
 XX Claim 12; Fig 84; 484p; English.  
 CC The invention relates to an isolated nucleic acid with at least 80%  
 CC nucleic acid sequence identity to a nucleic acid sequence encoding one of  
 CC 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a  
 CC PRO protein extracellular domain. Also included are a vector comprising a  
 CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO  
 CC polypeptide (by culturing the host cell for the expression of the PRO  
 CC polypeptide, and recovering the PRO polypeptide from the cell culture),  
 CC an isolated PRO polypeptide (having at least 80% sequence identity  
 CC to: (a) an amino acid sequence selected from the 61 PRO proteins;  
 CC (b) an amino acid sequence encoded by a nucleic acid molecule deposited  
 CC with an ATCC number (detailed in the specification); or (c) an  
 CC extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking  
 CC its associated signal peptide), a chimeric molecule comprising a PRO  
 CC polypeptide of fused to a heterologous amino acid sequence, an anti-PRO  
 CC antibody, detecting a PRO245 or PRO186 in a sample suspected of  
 CC containing the polypeptide, linking a bioactive molecule to a cell  
 CC expressing a PRO245 or PRO186 and modulating at least one biological  
 CC activity of a cell expressing a PRO245 or PRO186. Nucleic acids which  
 CC encode PRO can be used to generate either transgenic animals or knock-out  
 CC animals which may be used in the development and screening of  
 CC therapeutically useful reagents. The nucleic acids may also be used in  
 CC gene therapy, in chromosome identification, as chromosome markers, or in  
 CC generating probes. The PRO polypeptides are useful as molecular markers  
 CC for protein electrophoresis, and the isolated nucleic acids may be used  
 CC for recombinantly expressing those markers. The PRO polypeptides and  
 CC nucleic acids may also be used in tissue typing. Anti-PRO antibodies  
 CC are useful in diagnostic assays for PRO, and in affinity purification  
 CC of PRO from recombinant cell culture or natural sources. The  
 CC present sequence represents a PRO protein.  
 XX



XX DR MFI: 2003-331484/31.  
XX N-PSDB; ACA63376.  
PT Novel monoclonal antibody that binds to secreted and transmembrane  
PT polypeptide, useful for detecting and purifying the polypeptide and  
PT also for treating conditions responsive to the antibody -  
XX  
XX Disclosure; Fig 8; 408bp; English.  
CC The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The  
CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides and polynucleotides are useful for preparing a  
CC medicament useful in the treatment of a condition responsive to  
CC anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic  
CC assays for PRO, by detecting its expression in specific cells,  
CC tissues or serum, and for affinity purification of PRO from  
CC recombinant cell culture or natural sources. AB072109-AB072192  
CC represent the human PRO polypeptides of the invention.  
XX  
XX Sequence 350 AA;  
SQ  
Query Match 100.0%; Score 350; DB 24; Length 350;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQLSGATLILLLAAVPTAPAPATAPAPVAVKPGPALSTYQGEATINEMFREVEELMED 60  
1 MQLSGATLILLLAAVPTAPAPATAPAPVAVKPGPALSTYQGEATINEMFREVEELMED 60  
Db 61 TQKLRSAVEMEAEEAAKASSEVNLANPSPYHNETNDTVGNNTLHVHEIKITN 120  
61 TQKLRSAVEMEAEEAAKASSEVNLANPSPYHNETNDTVGNNTLHVHEIKITN 120  
QY 121 NOTGOWFSEVTITVSGDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRMCTCR 180  
121 NOTGOWFSEVTITVSGDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRMCTCR 180  
Db 121 NOTGOWFSEVTITVSGDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRMCTCR 180  
121 NOTGOWFSEVTITVSGDEGRSHCEIIDDCGSPMYCQFASFOYTCQPCRCQRMCTCR 180  
QY 181 DSECCGQQLCVWGHCTMTARGSNCTICDNRQCCQGLCAFRGLLFPCTPLPVEGSL 240  
181 DSECCGQQLCVWGHCTMTARGSNCTICDNRQCCQGLCAFRGLLFPCTPLPVEGSL 240  
Db 181 DSECCGQQLCVWGHCTMTARGSNCTICDNRQCCQGLCAFRGLLFPCTPLPVEGSL 240  
181 DSECCGQQLCVWGHCTMTARGSNCTICDNRQCCQGLCAFRGLLFPCTPLPVEGSL 240  
QY 241 CHDPASRLDLITWELPDGALDRCPGASGLICQPHSHSLVYVCXKPTFGSSRDQDEILL 300  
241 CHDPASRLDLITWELPDGALDRCPGASGLICQPHSHSLVYVCXKPTFGSSRDQDEILL 300  
Db 241 CHDPASRLDLITWELPDGALDRCPGASGLICQPHSHSLVYVCXKPTFGSSRDQDEILL 300  
241 CHDPASRLDLITWELPDGALDRCPGASGLICQPHSHSLVYVCXKPTFGSSRDQDEILL 300  
QY 301 PREVPDEYEVGSMEEYRQLELIERSLTEVALGEPAAAAALLGGEET 350  
301 PREVPDEYEVGSMEEYRQLELIERSLTEVALGEPAAAAALLGGEET 350  
Db 301 PREVPDEYEVGSMEEYRQLELIERSLTEVALGEPAAAAALLGGEET 350  
301 PREVPDEYEVGSMEEYRQLELIERSLTEVALGEPAAAAALLGGEET 350  
RESULT 17  
AB067385  
ID AB067385 standard; Protein; 350 AA.  
XX AB067385;  
XX AC  
XX 29-MAY-2003 (first entry)  
XX  
XX Human secreted protein PRO295.  
XX  
XX Human; gene therapy; mucosal lesion; ulcer; enterocolitis; skin disease;  
XX psoriasis; cancer; lung cancer; colon cancer; nerve cell disease;  
XX Alzheimer's disease; Parkinson's disease; Usher syndrome; angiogenesis;  
XX atrophila areata; inflammatory disease; asthma; rheumatoid arthritis;  
XX ischaemia.  
XX  
XX Homo sapiens.  
XX  
XX US2003023054-A1.  
XX  
XX 30-JAN-2003.

XX  
XX 16-JUL-2001; 2001US-0906742.  
XX  
XX 10-SEP-1998; 98WO-US18824.  
XX 14-SEP-1998; 98WO-US19177.  
XX 16-SEP-1998; 98WO-US19330.  
XX 17-SEP-1998; 98WO-US19437.  
XX 01-DEC-1998; 98WO-US25108.  
XX 08-SEP-1999; 98WO-US20594.  
XX 13-SEP-1999; 98WO-US21090.  
XX 15-SEP-1999; 98WO-US21090.  
XX 15-SEP-1999; 98WO-US21547.  
XX 05-OCT-1999; 98WO-US22089.  
XX 29-NOV-1999; 98WO-US28214.  
XX 30-NOV-1999; 98WO-US28313.  
XX 01-DEC-1999; 98WO-US28301.  
XX 02-DEC-1999; 98WO-US28564.  
XX 02-DEC-1999; 98WO-US28565.  
XX 16-DEC-1999; 98WO-US30099.  
XX 20-DEC-1999; 98WO-US30911.  
XX 20-DEC-1999; 98WO-US30999.  
XX 05-JAN-2000; 2000WO-US00219.  
XX 11-FEB-2000; 2000WO-US03565.  
XX 22-FEB-2000; 2000WO-US04414.  
XX 24-FEB-2000; 2000WO-US05004.  
XX 02-MAR-2000; 2000WO-US05841.  
XX 20-MAR-2000; 2000WO-US07377.  
XX 30-MAR-2000; 2000WO-US08439.  
XX 22-MAY-2000; 2000WO-US14042.  
XX 02-JUN-2000; 2000WO-US15264.  
XX 28-JUL-2000; 2000WO-US20710.  
XX 24-AUG-2000; 2000WO-US23328.  
XX 17-SEP-1997; 97US-059112P.  
XX 17-SEP-1997; 97US-059115P.  
XX 17-SEP-1997; 97US-059117P.  
XX 17-SEP-1997; 97US-059119P.  
XX 17-SEP-1997; 97US-059121P.  
XX 17-SEP-1997; 97US-059122P.  
XX 17-SEP-1997; 97US-059184P.  
XX 18-SEP-1997; 97US-059263P.  
XX 18-SEP-1997; 97US-059266P.  
XX 15-OCT-1997; 97US-062125P.  
XX 17-OCT-1997; 97US-062285P.  
XX 17-OCT-1997; 97US-062287P.  
XX 21-OCT-1997; 97US-063486P.  
XX 24-OCT-1997; 97US-063814P.  
XX 24-OCT-1997; 97US-063816P.  
XX 24-OCT-1997; 97US-063045P.  
XX 24-OCT-1997; 97US-063120P.  
XX 24-OCT-1997; 97US-063121P.  
XX 24-OCT-1997; 97US-063127P.  
XX 24-OCT-1997; 97US-063128P.  
XX 27-OCT-1997; 97US-063327P.  
XX 27-OCT-1997; 97US-063329P.  
XX 28-OCT-1997; 97US-063541P.  
XX 28-OCT-1997; 97US-063542P.  
XX 28-OCT-1997; 97US-063544P.  
XX 28-OCT-1997; 97US-063549P.  
XX 28-OCT-1997; 97US-063550P.  
XX 28-OCT-1997; 97US-063564P.  
XX 29-OCT-1997; 97US-063435P.  
XX 29-OCT-1997; 97US-063704P.  
XX 29-OCT-1997; 97US-063732P.  
XX 29-OCT-1997; 97US-063734P.  
XX 29-OCT-1997; 97US-063735P.  
XX 29-OCT-1997; 97US-063738P.  
XX 29-OCT-1997; 97US-064215P.  
XX 31-OCT-1997; 97US-063870P.  
XX 31-OCT-1997; 97US-064102P.  
XX 03-NOV-1997; 97US-064248P.  
XX 07-NOV-1997; 97US-064809P.  
XX 12-NOV-1997; 97US-065186P.  
XX 17-NOV-1997; 97US-065846P.



PR 18-NOV-1997; 97US-065633P.  
PR 21-NOV-1997; 97US-066120P.  
PR 21-NOV-1997; 97US-066343P.  
PR 24-NOV-1997; 97US-066453P.  
PR 24-NOV-1997; 97US-066466P.  
PR 24-NOV-1997; 97US-066511P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-NOV-1997; 97US-066772P.  
PR 12-DEC-1997; 97US-066840P.  
PR 04-JUN-1998; 98US-069425P.  
PR 10-SEP-1998; 98US-098026P.  
PR 14-SEP-1998; 98US-100262P.  
PR 17-SEP-1998; 98US-100858P.  
PR 13-OCT-1998; 98US-104080P.  
PR 20-NOV-1998; 98US-109304P.  
PR 22-DEC-1998; 98US-113296P.  
PR 07-JUL-1999; 99US-143048P.  
PR 26-JUL-1999; 99US-145698P.  
PR 28-JUL-1999; 99US-146222P.  
PR 18-SEP-2000; 2000US-066530P.

(GETH ) GENENTECH INC.

XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
PI Filvaroff E, Fong S, Gao W, Garber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavitt I;  
PI Mather JP, Pan U, Reoni NF, Roy MA, Stewart TA, Thomas D;  
PI Williams PM, Wood WI;  
XX MPI; 2003-331485/31.  
DR N-PSDB; ACA05532.

PT Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g.  
PT PRO245 or PRO1868, useful in chromosome and gene mapping, in generating  
PT antisense RNA and DNA, and in treating cancer and Alzheimer's disease -  
XX Example 38; Fig 84; 481p; English.

XX The invention relates to sixty one nucleic acids encoding PRO  
CC polypeptides (secreted and transmembrane). The polynucleotide is useful  
CC in molecular biology, including uses as hybridization probes, in  
CC chromosome and gene mapping, in generating antisense RNA and DNA, and in  
CC gene therapy. The polynucleotide may also be used in preparing PRO  
CC polypeptides by recombinant techniques, and in generating either  
CC transgenic animals or knock-out animals which, in turn, are useful in the  
CC development and screening of therapeutically useful reagents. The PRO  
CC polypeptide or the antibody is used in preparing a medicament for  
CC treating a condition responsive to the polypeptide or antibody, such as  
CC mucosal lesions e.g. ulcers and enterocolitis, skin disease e.g.  
CC psoriasis, cancer e.g. lung cancer and colon cancer, nerve cell disease  
CC e.g. Alzheimer's disease and Parkinson's disease, Usher syndrome,  
CC atrophie areata, angiogenesis, inflammatory disease e.g asthma and  
CC rheumatoid arthritis, ischaemia, and in various diagnostic assays. The  
CC present sequence represents the amino acid sequence of a PRO polypeptide.

SQ Sequence 350 AA;

Query Match 100.0%; Score 350; DB 24; Length 350;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRIGTILCLIAAAPTAPAPATGAPKPGALSYPOEATLNMFEVEELMED 60  
DB 1 MQRIGTILCLIAAAPTAPAPATGAPKPGALSYPOEATLNMFEVEELMED 60  
QY 61 TQHKLSAVEEMEAERAAKASEVNLAMPPSYNHEITLTDKVGNNTHVREIHKITN 120  
DB 61 TQHKLSAVEEMEAERAAKASEVNLAMPPSYNHEITLTDKVGNNTHVREIHKITN 120  
QY 121 NOTGQWVFSEYITYSVGDEGRRSHECIIIDEDCGPMYQFASFOYTCQPCRGQMLCTR 180  
DB 121 NOTGQWVFSEYITYSVGDEGRRSHECIIIDEDCGPMYQFASFOYTCQPCRGQMLCTR 180

QY 181 DSECCGDLQVWGHCTMTATGSGNGTICDNQDCQPGICAFQRGILLFVCTPLPYEGEL 240  
DB 181 DSECCGDLQVWGHCTMTATGSGNGTICDNQDCQPGICAFQRGILLFVCTPLPYEGEL 240  
QY 241 CHDPASRLDLITWELPPDALRCPASGLLQPSHSLVYCKPTFVGSRODGEILL 300  
DB 241 CHDPASRLDLITWELPPDALRCPASGLLQPSHSLVYCKPTFVGSRODGEILL 300  
QY 301 PREVPDEYEVGSFMEYVQLELERSLTREMAIGEPAAAAALLGGEI 350  
DB 301 PREVPDEYEVGSFMEYVQLELERSLTREMAIGEPAAAAALLGGEI 350

RESULT 18  
ABU64539  
ID ABU64539 standard; Protein; 350 AA.  
XX  
AC ABU64539;  
XX  
DT 13-MAY-2003 (first entry)

DE Human secreted/transmembrane protein, #43.

XX Human; PRO; secreted; transmembrane; pharmaceutical;  
XX diagnostic; biosensor; bioreactor; therapeutic; hyperplasia;  
XX endometriosis; cancer; tumour; ischaemia; coronary arterial disease;  
XX polycystic kidney disease; renal failure; inflammatory response; asthma;  
XX rheumatoid arthritis; psoriasis; multiple sclerosis; gene therapy;  
XX cycostatic; gynecological; cardiac; nephrotropic; hepatotropic;  
XX antiinflammatory.

OS Homo sapiens.

EN US2002160374-A1.

XX 31-OCT-2002.

PF 12-JUL-2001; 2001US-0905291.

XX 10-SEP-1998; 98WO-US18824.  
PR 14-SEP-1998; 98WO-US19177.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 01-DEC-1998; 98WO-US2108.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28313.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30999.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 17-SEP-1997; 97US-059113P.  
PR 17-SEP-1997; 97US-059115P.  
PR 17-SEP-1997; 97US-059117P.  
PR 17-SEP-1997; 97US-059119P.

PR 17-SEP-1997; 97US-059121P.  
 PR 17-SEP-1997; 97US-059122P.  
 PR 17-SEP-1997; 97US-059148P.  
 PR 18-SEP-1997; 97US-059263P.  
 PR 18-SEP-1997; 97US-059266P.  
 PR 15-OCT-1997; 97US-062125P.  
 PR 17-OCT-1997; 97US-062285P.  
 PR 17-OCT-1997; 97US-062287P.  
 PR 21-OCT-1997; 97US-063486P.  
 PR 24-OCT-1997; 97US-062814P.  
 PR 24-OCT-1997; 97US-063045P.  
 PR 24-OCT-1997; 97US-063120P.  
 PR 24-OCT-1997; 97US-063121P.  
 PR 24-OCT-1997; 97US-063127P.  
 PR 24-OCT-1997; 97US-063128P.  
 PR 27-OCT-1997; 97US-063329P.  
 PR 27-OCT-1997; 97US-063329P.  
 PR 28-OCT-1997; 97US-063541P.  
 PR 28-OCT-1997; 97US-063542P.  
 PR 28-OCT-1997; 97US-063544P.  
 PR 28-OCT-1997; 97US-063549P.  
 PR 28-OCT-1997; 97US-063550P.  
 PR 28-OCT-1997; 97US-063564P.  
 PR 29-OCT-1997; 97US-063435P.  
 PR 29-OCT-1997; 97US-063704P.  
 PR 29-OCT-1997; 97US-063732P.  
 PR 29-OCT-1997; 97US-063734P.  
 PR 29-OCT-1997; 97US-063735P.  
 PR 29-OCT-1997; 97US-063738P.  
 PR 29-OCT-1997; 97US-064215P.  
 PR 31-OCT-1997; 97US-063870P.  
 PR 31-OCT-1997; 97US-064103P.  
 PR 03-NOV-1997; 97US-064248P.  
 PR 07-NOV-1997; 97US-064809P.  
 PR 12-NOV-1997; 97US-065186P.  
 PR 17-NOV-1997; 97US-065846P.  
 PR 18-NOV-1997; 97US-065693P.  
 PR 21-NOV-1997; 97US-066120P.  
 PR 21-NOV-1997; 97US-066364P.  
 PR 24-NOV-1997; 97US-066453P.  
 PR 24-NOV-1997; 97US-066466P.  
 PR 24-NOV-1997; 97US-066511P.  
 PR 24-NOV-1997; 97US-066770P.  
 PR 24-NOV-1997; 97US-066772P.  
 PR 18-SEP-2000; 2000US-0665350.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
 PI Filvaroff E, Fong S, Gao W, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;  
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WI;  
 XX  
 XX WPI, 2003-288105/28.  
 XX N-PSDB; ABX96211.  
 XX  
 PT New secreted and transmembrane PRO polypeptides (e.g. PRO533 or PRO245)  
 PT and genes encoding them, useful for detecting or treating e.g.  
 PT hyperplasia, endometriosis, cancers, ischemia, coronary arterial  
 PT disease or inflammations -  
 XX  
 XX Claim 12; Fig 84; 477PP; English.  
 XX  
 CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC and the nucleic acid encoding them. The polypeptides can be used to  
 CC raise antibodies that specifically bind to the PRO polypeptide, for  
 CC linking a bioactive molecule to a cell expressing a PRO protein and for  
 CC modulating at least one biological activity of a cell. The PRO  
 CC polypeptides or polynucleotides are also useful as pharmaceuticals,  
 CC diagnostics, biosensors or bioreactors, for detecting or treating e.g.  
 CC hyperplasia, endometriosis, cancers (e.g. those involving solid tumours),

CC ischaemia, coronary arterial disease, polycystic kidney disease, chronic  
 CC or acute renal failure, or inflammatory responses (e.g. asthma,  
 CC rheumatoid arthritis, psoriasis or multiple sclerosis) in mammals. The  
 CC PRO genes may also be used in gene therapy, particularly for replacing a  
 CC defective gene. The sequences presented in AB064499-AB064559 are the  
 CC PRO polynucleotides of the invention.  
 XX  
 XX Sequence 350 AA;  
 SQ  
 Query Match 100.0%; Score 350; DB 24; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MORGATLLCLLAAVPTAPAPATSAVPKPGALSTPOEERATINEMFREVEELMED 60  
 DB 1 MORGATLLCLLAAVPTAPAPATSAVPKPGALSTPOEERATINEMFREVEELMED 60  
 QY 61 TOHLRSAVEEMEAEBAAXASSEVNLANLPPSYHNETNTDTKGNNTIHYHREIHKITN 120  
 DB 61 TOHLRSAVEEMEAEBAAXASSEVNLANLPPSYHNETNTDTKGNNTIHYHREIHKITN 120  
 QY 121 NOTGQWVFSEITVITSVGDEBGRSHCEIIDECGSPMYCOFASFOYTQCPORGRMLCTR 180  
 DB 121 NOTGQWVFSEITVITSVGDEBGRSHCEIIDECGSPMYCOFASFOYTQCPORGRMLCTR 180  
 QY 181 DSECCGQOLCWGHCTKATRGSGTICDNORDCPQLCCAFQRGILLFPVCTPLPVGEL 240  
 DB 181 DSECCGQOLCWGHCTKATRGSGTICDNORDCPQLCCAFQRGILLFPVCTPLPVGEL 240  
 QY 241 CHDPASRLDLITWELEPDLDRPCASGLICOPHSHSLVYVCKPTFVSGRSDGELL 300  
 DB 241 CHDPASRLDLITWELEPDLDRPCASGLICOPHSHSLVYVCKPTFVSGRSDGELL 300  
 QY 301 PREVPDEYEVGSFMEYVROSLIEDLERSLTBEMALGEPAAAAALLGSEBI 350  
 DB 301 PREVPDEYEVGSFMEYVROSLIEDLERSLTBEMALGEPAAAAALLGSEBI 350  
 RESULT 19  
 ID AAE34069 standard; Protein: 350 AA.  
 XX AAE34069;  
 AC AAE34069;  
 XX  
 DT 02-MAY-2003 (first entry)  
 XX  
 DE DK 3 protein.  
 XX  
 KM Drug screening; toxicology assay; signalling pathway; DK 3.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 PT Misc-difference 1..94 /note= "Encoded by TAT"  
 FI  
 XX  
 FN WO200290992-A2.  
 XX  
 PD 14-NOV-2002.  
 XX  
 PD 29-APR-2002; 2002WO-GB01946.  
 XX  
 PR 04-MAY-2001; 2001GB-0011004.  
 XX  
 PA (AXOR-) AXORDIA LTD.  
 XX  
 PI Andrews P, Draper J, Walsh J;  
 XX  
 XX WPI, 2003-120579/11.  
 DR N-PSDB; AAD52567.  
 XX  
 PT Identifying biologically active agents comprises cloning transfected  
 PT cells into a cell array, exposing the array to an agent to be tested,

PT and detecting signals generated by a reporter molecule as a result of  
 PT exposure to the agent -  
 PS Claim 16; Fig 90; 90pp; English.

CC The present invention relates to a novel screening method which enables  
 CC the identification of biologically active agents which mediate their  
 CC effect through the activation of genes. The method involves providing a  
 CC population of cells stably transfected with a nucleic acid encoding a  
 CC reporter molecule, cloning the transfected cells into a cell array,  
 CC exposing the array to at least one agent to be tested and detecting a  
 CC signal generated by the reporter molecule as a result of exposure to  
 CC the agent. The method is useful in identifying biologically active agents  
 CC and the genes through which the agents act, in screening potential drugs  
 CC for their ability to activate certain drug targets in a high-throughput  
 CC assay, in identifying relationships between signalling pathways and  
 CC specific signals that could be useful in eventually directing the  
 CC differentiation of embryonic stem cells and in toxicology assays by  
 CC testing for unwanted activation or inhibition of specific signalling  
 CC pathways. The present sequence is DKF 3 protein used to illustrate the  
 CC method of the invention.

XX Sequence 350 AA;

Query Match 100.0%; Score 350; DB 24; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORGATLTCLLIAAAPTAPAPATATAPVKGPGALSTPOEATLNEMFEVEELMED 60  
 DB 1 MORGATLTCLLIAAAPTAPAPATATAPVKGPGALSTPOEATLNEMFEVEELMED 60  
 QY 61 TQHKRSAYEEMEAERAAKASSEVNLATLPPSYHNETMDPKVGNTHHRETHKTN 120  
 DB 61 TQHKRSAYEEMEAERAAKASSEVNLATLPPSYHNETMDPKVGNTHHRETHKTN 120  
 QY 121 NOTGQWVFSEVTVTSVGDSEGRSHSCIIDDCGSPMYCOPASFOYTCQPCGQMLCTR 180  
 DB 121 NOTGQWVFSEVTVTSVGDSEGRSHSCIIDDCGSPMYCOPASFOYTCQPCGQMLCTR 180  
 QY 121 NOTGQWVFSEVTVTSVGDSEGRSHSCIIDDCGSPMYCOPASFOYTCQPCGQMLCTR 180  
 DB 121 NOTGQWVFSEVTVTSVGDSEGRSHSCIIDDCGSPMYCOPASFOYTCQPCGQMLCTR 180  
 QY 181 DSCCGDGLCWGHCHCTKMAITRGNCTTCNNORDCQGLCCARQGLHPVCTPLFVEGEL 240  
 DB 181 DSCCGDGLCWGHCHCTKMAITRGNCTTCNNORDCQGLCCARQGLHPVCTPLFVEGEL 240  
 QY 241 CHDPASRLDLITWELPEPGALDRCPGASGLLCOPHSHSLVYVCKPTFVGSRDQGEILL 300  
 DB 241 CHDPASRLDLITWELPEPGALDRCPGASGLLCOPHSHSLVYVCKPTFVGSRDQGEILL 300  
 QY 301 PRVVPDEYEVGSPMEVROLEBLESITBEMALGEPAAAAALLGGERI 350  
 DB 301 PRVVPDEYEVGSPMEVROLEBLESITBEMALGEPAAAAALLGGERI 350

RESULT 20

ABU55915

ID ABU55915 standard; Protein; 350 AA.

XX AC ABU55915;

DT 25-MAR-2003 (first entry)

DE Human protein DKF3.

XX Notch; Wnt; embryonic stem cell; embryogenesis; human;

XX differentiation; ligand; Parkinson's disease; Huntington's disease;

XX motor neuron disease; heart disease; diabetes; liver disease;

XX cirrhosis; renal disease; AIDS; acquired immunodeficiency syndrome.

OS Homo sapiens.

XX MO200277204-A2.

XX 03-OCT-2002.

XX 25-MAR-2002; 2002MO-GS01195.

XX 23-MAR-2001; 2001GB-0007296.

XX 23-MAR-2001; 2001GB-0007296.

XX 17-APR-2001; 2001GB-0009346.

XX (AXOR-) AXORDIA LTD.

XX Andrews P, Walsh J, Gokhale P;

XX WPI: 2003-092852/08.

XX N-PSDS; ABX75342.

XX Modulating the differentiation of embryonic stem cells by providing

XX ligands which bind receptors in the Notch and Wnt pathways; useful for

XX treating diseases such as Parkinson's, Huntington's, heart disease,

XX diabetes and AIDS

XX Disclosure; Fig 96; 121pp; English.

XX The invention relates to modulating the differentiation of an embryonic

XX stem cell, comprising: (a) providing a culture of embryonic stem cells;

XX (b) providing at least one ligand or its active binding fragment,

XX capable of binding its cognate receptor polypeptide expressed by the

XX embryonic stem cell; (c) forming a culture comprising embryonic stem

XX cells and the ligand; and (d) growing the cell culture. Also included

XX are: (1) Modulating the differentiation of embryonic stem cells,

XX comprising: (a) providing a cell transfected with a nucleic acid molecule

XX selected from: (i) any of 9 fully defined Wnt nucleic acid sequences;

XX (ii) a nucleic acid molecule that hybridises to the nucleic acid in

XX (i), and which encodes a ligand capable of modulating embryonic stem

XX cell differentiation; or capable of binding a Wnt receptor; or

XX (iii) nucleic acid molecules which are degenerate as a result of the

XX genetic code to the sequences of (i) or (ii); (b) forming a culture

XX comprising the cell identified in (a) with an embryonic stem cell; and

XX (c) growing the culture for the maintenance and/or differentiation of

XX the embryonic stem cell; (2) Inhibiting the differentiation of embryonic

XX stem cells, comprising: (a) providing at least one polypeptide or its

XX active fragment, that are inhibitors of the Wnt signalling pathway;

XX (b) forming a culture comprising the cell identified in (a) with an

XX embryonic stem cell; and (c) growing the culture for the maintenance of

XX the differentiation of embryonic stem cells, comprising: (a) providing a cell

XX transfected with a nucleic acid molecule selected from: (i) a molecule

XX encoding a Wnt inhibitory polypeptide; (ii) a molecule which hybridises

XX to the molecule of (i) and encodes a polypeptide capable of inhibiting

XX Wnt signalling; and (iii) nucleic acid molecules which are degenerate as

XX a result of the genetic code to the sequences of (i) or (ii); (b) forming

XX a culture comprising the cell identified in (a) with an embryonic stem

XX cell; and (c) growing the culture for the maintenance of embryonic stem

XX cells in an undifferentiated state; and (4) A cell, therapeutic cell or

XX cell culture obtainable by any of the methods cited above.

XX The therapeutic cell of the present invention is useful in the

XX treatment of an animal, preferably a human, comprising administering a

XX cell composition comprising embryonic stem cells which have been

XX induced to differentiate into at least one cell-type. The cell is also

XX useful for the manufacture of a composition for use in treatment of

XX diseases such as Parkinson's disease, Huntington's disease, motor

XX neuron disease, heart disease, diabetes, liver disease (e.g.

XX cirrhosis), renal disease and AIDS (acquired immunodeficiency syndrome).

XX The present sequence is represents a Wnt or Notch pathway protein

XX (i.e. a ligand for the method of the invention).

XX Sequence 350 AA;

QY Query Match 100.0%; Score 350; DB 24; Length 350;

DB Best Local Similarity 100.0%; Pred. No. 0;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORGATLTCLLIAAAPTAPAPATATAPVKGPGALSTPOEATLNEMFEVEELMED 60

DB 1 MORGATLTCLLIAAAPTAPAPATATAPVKGPGALSTPOEATLNEMFEVEELMED 60

```

QY 61 TOHLRSAYEMEAFAAAKASSEVNLANLPSEYHNETNTDTKGNNTIHVREIHKTN 120
Db 61 TOHLRSAYEMEAFAAAKASSEVNLANLPSEYHNETNTDTKGNNTIHVREIHKTN 120
QY 121 NOTGQVVFSESTVTTVSQDEEGRSRSHCEIIDDCGSPMYCOFASFQYTCQPCRGQRLCTR 180
Db 121 NOTGQVVFSESTVTTVSQDEEGRSRSHCEIIDDCGSPMYCOFASFQYTCQPCRGQRLCTR 180
QY 181 DSECCGQDLCVWGCHCTKMAFRGNGTICDNQRCQCGLCAPFRGLLPVCTPLPVESGL 240
Db 181 DSECCGQDLCVWGCHCTKMAFRGNGTICDNQRCQCGLCAPFRGLLPVCTPLPVESGL 240
QY 241 CHDPASRLDLITWLEPDPGLDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDEILL 300
Db 241 CHDPASRLDLITWLEPDPGLDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDEILL 300
QY 301 PREVPDEYVGSFMEVROLETLESLTEFVALGSPAAAAALLGGEET 350
Db 301 PREVPDEYVGSFMEVROLETLESLTEFVALGSPAAAAALLGGEET 350
RESULT 21
ID ABUS4387 standard; Protein; 350 AA.
AC ABUS4387;
DT 10-MAR-2003 (first entry)
DE Human secreted/transmembrane protein PRO295.
XX
XX Human; PRO; secreted protein; transmembrane protein; enterocolitis;
XX gastrointestinal ulceration; skin disease;
XX abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
XX squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
XX amyotrophic lateral sclerosis; inflammatory disease;
XX rheumatoid arthritis; asthma; multiple sclerosis; organ failure;
XX atherosclerosis; cardiac injury; infertility; birth defect; cancer;
XX premature aging; AIDS; acquired immunodeficiency syndrome;
XX diabetic complication; wound repair.
XX Homo sapiens.
XX
XX US2002132240-A1.
PN
PD 19-SEP-2002.
XX
XX 18-JUL-2001; 2001US-0909320.
XX
XX 10-SEP-1998; 98MO-US18824.
XX 14-SEP-1998; 98MO-US19177.
XX 16-SEP-1998; 98MO-US19330.
XX 17-SEP-1998; 98MO-US19437.
XX 01-DEC-1998; 98MO-US20594.
XX 08-SEP-1999; 99MO-US20594.
XX 13-SEP-1999; 99MO-US20944.
XX 15-SEP-1999; 99MO-US21090.
XX 15-SEP-1999; 99MO-US21547.
XX 05-OCT-1999; 99MO-US23069.
XX 01-DEC-1999; 99MO-US28301.
XX 02-DEC-1999; 99MO-US28564.
XX 02-DEC-1999; 99MO-US28565.
XX 16-DEC-1999; 99MO-US30095.
XX 20-DEC-1999; 99MO-US30911.
XX 20-DEC-1999; 99MO-US30999.
XX 06-JAN-2000; 2000MO-US00219.
XX 11-FEB-2000; 2000MO-US03565.
XX 22-FEB-2000; 2000MO-US04414.
XX 28-JUL-2000; 2000MO-US20710.
XX 24-AUG-2000; 2000MO-US23328.
XX 17-SEP-1997; 97US-059113P.
XX 17-SEP-1997; 97US-059115P.

```

```

PR 17-SEP-1997; 97US-059117P.
PR 15-OCT-1997; 97US-062125P.
PR 17-OCT-1997; 97US-062285P.
PR 17-OCT-1997; 97US-062287P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-062814P.
PR 24-OCT-1997; 97US-062816P.
PA (GENTH ) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Deenoyers L, Eaton DL, Ferrara N,
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ,
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D,
PI Williams PM, Wood WI,
XX
XX MPI, 2003-147434/14.
XX N-PEDB; ABX71642.
XX
XX New PRO polypeptides and nucleic acid molecules, useful in diagnosing
PT or treating inflammatory diseases, organ failure, atherosclerosis,
PT cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or
PT Parkinson's disease -
XX
XX Claim 12; Fig 84; 473pp; English.
XX
XX The invention relates to an isolated PRO polypeptide having at least 80%
XX amino acid sequence identity to: (a) any one of 61 fully defined amino
XX acid sequences given in the specification (appearing as ABUS4387-
XX ABUS4407); (b) an amino acid sequence encoded by the nucleotide sequence
XX deposited under American Type Culture Collection (accession numbers
XX listed in the specification); (c) any one of the PRO sequences which
XX lacks its associated signal peptide; (d) an extracellular domain of the
XX PRO polypeptide with its associated signal peptide; or (e) an
XX extracellular domain of the PRO polypeptide which lacks its associated
XX signal peptide. Also include are the nucleic acids encoding the PRO
XX polypeptides, vectors, host cells and anti-PRO antibodies.
XX
XX The PRO polypeptides and nucleic acids are useful in diagnosing
XX or treating enterocolitis, gastrointestinal ulceration, skin diseases
XX associated with abnormal keratinocyte differentiation, e.g. psoriasis
XX or epithelial cancers such as squamous cell carcinoma, Alzheimer's
XX disease, Parkinson's disease, amyotrophic lateral sclerosis,
XX inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple
XX sclerosis, organ failure, atherosclerosis, cardiac injury, infertility,
XX birth defects, premature aging, AIDS, cancer, diabetic complications,
XX or mutations in general. The polypeptides are also useful for wound
XX repair and associated therapies concerned with re-growth of tissue. The
XX nucleotide sequences may be used as hybridisation probes in chromosome
XX and gene mapping, or in generating antisense RNA and DNA. PRO nucleic
XX acids are also useful in preparing PRO polypeptides, in assays to
XX identify other proteins or molecules involved in binding reaction, to
XX generate transgenic animals or knockout animals, which in turn are
XX useful in the development and screening of therapeutically useful
XX reagents, for chromosome identification, and tissue typing. The PRO
XX polypeptides and nucleic acid molecules are also useful in gene
XX therapy, and as molecular weight markers for protein electrophoresis
XX purposes. The anti-PRO antibodies may be used in diagnostic assays for
XX PRO, or for the affinity purification of PRO from recombinant cell
XX culture or natural sources. The present sequence represents a PRO
XX polypeptide.
XX
XX Sequence 350 AA;
SQ
XX
XX Query Match 100.0%; Score 350; DB 24; Length 350;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MORGATLILCLILAAAPPTAPAPPTATSPVVRGPAALSPQERATINEMFRVREELMED 60
Db 1 MORGATLILCLILAAAPPTAPAPPTATSPVVRGPAALSPQERATINEMFRVREELMED 60
QY 61 TOHLRSAYEMEAFAAAKASSEVNLANLPSEYHNETNTDTKGNNTIHVREIHKTN 120

```

D6	61	TOHKJSAVEEWEAEAAAAKASSEVUWLANLPSSYHNENTNTDTKQVGNNTIHYHRSIHKITN	120
QY	121	NOTGQWVEBETVYTSVGDEGGRSHECIIIDECGSMYCOFASFYTCQPRGRMCTR	160
D6	121	NOTGQWVFSYVTSYVGDEGGRSHECIIIDECGSMYCOFASFYTCQPRGRMCTR	180
QY	181	DSECCDOLCVMGHCTKKAATRGSGNGTICDQRCOPGICCAFORGLLPVCTPLPVEGEL	240
D6	181	DSECCGDOLCVMGHCTKKAATRGSGNGTICDQRCOPGICCAFORGLLPVCTPLPVEGEL	240
QY	241	CHDPASRLDLITWELEBDGALDRCPKASGLICQSHSLVYVCKPTFVSGRDDGELL	300
D6	241	CHDPASRLDLITWELEBDGALDRCPKASGLICQSHSLVYVCKPTFVSGRDDGELL	300
QY	301	PREVPPEYEVGSMFEVROELDLERSLTEEMALDEPAAAAAALLGGEI	350
D6	301	PREVPPEYEVGSMFEVROELDLERSLTEEMALDEPAAAAAALLGGEI	350

PR 24-OCT-1997; 97US-0062814.  
 PR 24-OCT-1997; 97US-0062816.  
 PR 24-OCT-1997; 97US-0063045.  
 PR 24-OCT-1997; 97US-0063121.  
 PR 24-OCT-1997; 97US-0063127.  
 PR 24-OCT-1997; 97US-0063128.  
 PR 24-OCT-1997; 97US-0063129.  
 PR 27-OCT-1997; 97US-0063327.  
 PR 27-OCT-1997; 97US-0063421.  
 PR 28-OCT-1997; 97US-0063542.  
 PR 28-OCT-1997; 97US-0063544.  
 PR 28-OCT-1997; 97US-0063549.  
 PR 28-OCT-1997; 97US-0063550.  
 PR 28-OCT-1997; 97US-0063564.  
 PR 29-OCT-1997; 97US-0063435.  
 PR 29-OCT-1997; 97US-0063704.  
 PR 29-OCT-1997; 97US-0063732.  
 PR 29-OCT-1997; 97US-0063738.  
 PR 29-OCT-1997; 97US-0063734.  
 PR 29-OCT-1997; 97US-0064215.  
 PR 31-OCT-1997; 97US-0063735.  
 PR 31-OCT-1997; 97US-0063870.  
 PR 31-OCT-1997; 97US-0064103.  
 PR 03-NOV-1997; 97US-0064248.  
 PR 07-NOV-1997; 97US-0064809.  
 PR 12-NOV-1997; 97US-0065186.  
 PR 17-NOV-1997; 97US-0065846.  
 PR 18-NOV-1997; 97US-0065693.  
 PR 21-NOV-1997; 97US-0066120.  
 PR 21-NOV-1997; 97US-0066364.  
 PR 24-NOV-1997; 97US-0066772.  
 PR 24-NOV-1997; 97US-0066466.  
 PR 24-NOV-1997; 97US-0066770.  
 PR 24-NOV-1997; 97US-0066511.  
 PR 24-NOV-1997; 97US-0066453.  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX  
 XX Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;  
 DR WPI; 1999-229533/19.  
 DR N-PSDB; AAX52255.  
 XX  
 PT New isolated human genes and polypeptides used in, e.g. treatment of  
 PT gastrointestinal ulceration  
 XX  
 XX Claim 12; Fig 84; 320pp; English.  
 XX  
 CC AAY13344-403 represent secreted and transmembrane human proteins.  
 CC The cDNA sequences are obtained from cDNA libraries, prepared from  
 CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.  
 CC The encoded polypeptides have specific uses based on their homology to  
 CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders  
 CC associated with the preservation and maintenance of gastrointestinal  
 CC mucosa and the repair of acute and chronic mucosal lesions  
 CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal  
 CC ulceration and congenital microvillus atrophy), skin diseases associated  
 CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial  
 CC cancers such as lung, squamous cell carcinoma of the vulva and gliomas),  
 CC potent effects on cell growth and development, diseases related to  
 CC growth or survival of nerve cells including Parkinson's disease,  
 CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as  
 CC for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used  
 CC as a target for anti-tumor drugs. PRO533 may be used in the treatment  
 CC of Usher Syndrome or Atrophia areata; PRO269 can be used as an  
 CC anti-thrombotic agent; PRO287 polypeptides and portions may have  
 CC therapeutic applications in wound healing and tissue repair; PRO317 can  
 CC be used for treating problems of the kidney, uterus, endometrium, blood  
 CC vessels, or related tissue, e.g. in the heart of genital tract.  
 CC  
 XX Sequence 350 AA;

Query Match 79.7%; Score 279; DB 20; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-263;  
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORGATLLCLLLAAVPTAPAPATPATSAPVPGPALSYPQEEATLNMFRVEELMED 60  
 DB 1 MORGATLLCLLLAAVPTAPAPATPATSAPVPGPALSYPQEEATLNMFRVEELMED 60  
 QY 61 TOKLRSAVEEMAEFAAASSEVNLAMPSPYHNETNTDTVGNTTIHVRHEIKITN 120  
 DB 61 TOKLRSAVEEMAEFAAASSEVNLAMPSPYHNETNTDTVGNTTIHVRHEIKITN 120  
 QY 121 NOTGQWVFSEVTIVSGDEGRSHCEIIDEDGFSNYCQFASFOYTQCPRCQRMCTR 180  
 DB 121 NOTGQWVFSEVTIVSGDEGRSHCEIIDEDGFSNYCQFASFOYTQCPRCQRMCTR 180  
 QY 181 DSECCGQLCVWGHCCTMARSGNGTICDNQRCQGLCCAPRGILFPCTPLPVEGEL 240  
 DB 181 DSECCGQLCVWGHCCTMARSGNGTICDNQRCQGLCCAPRGILFPCTPLPVEGEL 240  
 QY 241 CHDPASRLDLITWLEPDPDALDRCPCASGLLCQPSHS 279  
 DB 241 CHDPASRLDLITWLEPDPDALDRCPCASGLLCQPSHS 279

RESULT 24  
 AAW73016  
 ID AAW73016 standard; Protein; 350 AA.  
 XX  
 AC AAW73016;  
 XX  
 DT 18-JAN-1999 (first entry)  
 DE  
 DE Human cysteine-rich secreted protein CRSP-1.  
 XX  
 KW CRSP-1; cysteine-rich secreted protein 1; tumour; cancer; leukaemia;  
 KW tissue repair; wound healing; infection; Parkinson's disease;  
 KW Alzheimer's disease; Huntington's chorea; multiple sclerosis;  
 KW amyotrophic lateral sclerosis; pontine myelinolysis;  
 KW human immunodeficiency associated myelopathy; bulbar palsy;  
 KW spinal muscular atrophy; primary lateral sclerosis; poliomyelitis;  
 KW Fazio-Londe syndrome; Charcot-Marie-Tooth disease; therapy;  
 KW diagnosis; drug screening; human; CRISPY-1; TANGO 59;  
 KW signal transduction; cell differentiation; cell proliferation.  
 KW  
 OS Homo sapiens.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 XX PH 1..23  
 XX FT Peptide  
 XX FT /label= "Sig peptide  
 XX FT /note= "putative signal peptide spans amino acids  
 XX FT 1-19, 1-21 or 1-23"  
 XX  
 XX Protein  
 XX FT 24..350  
 XX FT /label= "Mat. protein  
 XX FT /note= "putative mature protein spans amino acids  
 XX FT 20-350, 22-350 or 24-350"  
 XX  
 XX Domain  
 XX FT 147..195  
 XX FT /note= "cysteine-rich domain"  
 XX FT 196..200  
 XX FT Peptide  
 XX FT /note= "spacer"  
 XX FT 201..284  
 XX FT /note= "cysteine-rich domain"  
 XX  
 PD W08846755-A1.  
 XX 22-OCT-1998.  
 XX  
 PF 16-APR-1998; 98WC-US07894.  
 XX  
 XX 20-JAN-1998; 98US-0009802.  
 PR 16-APR-1997; 97US-0843704.  
 PR 17-APR-1997; 97US-0842898.  
 PR 15-JAN-1998; 98US-0071589.





CC epilepsy, amnesia), inflammation, skeletal muscle disorders, pulmonary  
 CC disorders (Goodpasture's syndrome), cardiovascular disorders, and  
 CC hyperproliferative disorders (cancer). The Dk proteins and nucleic  
 CC acids may also be for research purposes, such as for chromosome  
 CC mapping, tissue typing and in screening assays to identify modulators.

XX Sequence 350 AA;

Query Match 66.6%; Score 233; DB 21; Length 350;  
 Best Local Similarity 99.7%; Pred. No. 2,9e-218;  
 Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MORLGATLLCLLAAAVPTAPAPATSAVPKPPALSYPOEATLNEMFREVELMED 60  
 1 MQLRGATLLCLLAAAVPTAPAPATSAVPKPPALSYPOEATLNEMFREVELMED 60  
 61 TQHKLRSAVEMEAEEAAVAASEVNIANLPSPYHNETNTDTVGNNTIHHREIHKITN 120  
 61 TQHKLRSAVEMEAEEAAVAASEVNIANLPSPYHNETNTDTVGNNTIHHREIHKITN 120  
 121 NOTGQWVFSEVTVTSVDEGRSRSHCEITDPCGPMYCOFASFOYTCCPCRGQMLCTR 180  
 121 NOTGQWVFSEVTVTSVDEGRSRSHCEITDPCGPMYCOFASFOYTCCPCRGQMLCTR 180  
 181 DSECCGDPQLCWMGHCTMATRGSGNTICDNQDCQDGLCCAFQGLLPVCTPLPVZGEL 240  
 181 DSECCGDPQLCWMGHCTMATRGSGNTICDNQDCQDGLCCAFQGLLPVCTPLPVZGEL 240  
 241 CHNPASATLLLLIWELEPPDGLRCPASGLLCQPSHSHLYVYCKPTFGSRDDEILL 300  
 241 CHNPASATLLLLIWELEPPDGLRCPASGLLCQPSHSHLYVYCKPTFGSRDDEILL 300  
 301 PREVPDEYEVGSFMEEVROLEDLERSLTREMA 334  
 301 PREVPDEYEVGSFMEEVROLEDLERSLTREMA 334

RESULT 26  
 AAW73021  
 ID AAW73021 standard; Protein, 349 AA.

AAW73021;  
 18-JAN-1999 (first entry)  
 DE Mouse cysteine-rich secreted protein-1.  
 KW CRSP-1; cysteine-rich secreted protein 1; tumour; cancer;  
 KW signal transduction; cell differentiation; cell proliferation;  
 KW mouse.  
 OS Mus sp.  
 XX Key Location/Qualifiers  
 XX Domain 147..195  
 XX Region /note= "cysteine-rich domain"  
 XX Domain /note= "spacer"  
 XX Domain 208..284  
 XX /note= "cysteine-rich domain"

MO9846755-A1.  
 22-OCT-1998.  
 16-APR-1998; 98MO-US07894.  
 20-JAN-1998; 98US-0009802.  
 16-APR-1997; 97US-0843704.  
 17-APR-1997; 97US-0842898.  
 15-JAN-1998; 98US-0071589.  
 (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX McCarthy SA;  
 XX WPI, 1998-568730/48.  
 DR N-PSDB; AAV07911.

XX New isolated cysteine-rich secreted proteins - used to develop  
 PT products for treating, e.g. hyperproliferative disorders, cancers,  
 PT wounds, infectious lesions, degenerative lesions or demyelating  
 PT diseases

PS Disclosure, Page 114-115; 142pp; English.

CC This is the amino acid sequence of novel mouse cysteine-rich  
 CC secreted protein 1 (CRSP-1), as deduced from an isolated cDNA clone  
 CC (see AAV07911). The invention relates to novel human CRSP-1, -2, -3  
 CC and -4 nucleic acid sequences (see AAV07905-09) and polypeptides (see  
 CC AAW73016-19) that are suggested to be involved in signal transduction  
 CC and cellular differentiation. These can be used in diagnostic,  
 CC screening and therapeutic methods of the invention e.g. for treating  
 CC hyperproliferative disorders, cancers, wounds, infectious or  
 CC degenerative lesions and demyelating diseases, and in drug  
 CC screening.

SQ Sequence 349 AA;

Query Match 11.7%; Score 41; DB 19; Length 349;  
 Best Local Similarity 100.0%; Pred. No. 3e-31;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

40 YPOEATLNEMFREVELMEDTQHKLRSAVEMEAEEAAK 80  
 40 YPOEATLNEMFREVELMEDTQHKLRSAVEMEAEEAAK 80

RESULT 27  
 AAB08879  
 ID AAB08879 standard; Protein, 349 AA.

AAB08879;  
 15-JAN-2001 (first entry)  
 DE A murine Dickkopf (Dkk)-3 protein.

XX Human; Dickkopf-3 protein; Dkk-3 protein; Soggy protein; optic disorder;  
 KW cysteine-rich secreted protein; glaucoma; conjunctivitis; brain disorder;  
 KW Alzheimer's disease; epilepsy; amnesia; inflammation; pulmonary disorder;  
 KW skeletal muscle disorder; Goodpasture's syndrome;  
 KW cardiovascular disorder; hyperproliferative disorder; cancer.

OS Mus sp.

XX WO200052047-A2.

XX 08-SEP-2000.

XX 03-MAR-2000; 2000MO-US05452.

XX 05-MAR-1999; 99US-0263022.

XX (MILL-) MILLENNIUM PHARM INC.

XX McCarthy S;

XX WPI, 2000-579276/54.

XX N-PSDB; AAV75137.

XX Human Dickkopf (hDkk) and soggy nucleic acids and proteins, useful as  
 PT modulating agents in regulating cellular processes and particularly for  
 PT treating disorders characterized by aberrant expression or activity of  
 PT Dkk, e.g. Alzheimer's,

PS Example 2; Fig 5A-B; 208bp; English.  
XX  
CC The present sequence represents a murine Dickkopf (Dkk)-3 protein. The  
CC specification also describes Soggy (Dkk-related) sequences. Dkk is a  
CC cysteine-rich secreted protein. The Dkk nucleic acids and proteins are  
CC useful as modulating agents in regulating cellular processes. They are  
CC particularly useful in treating subjects having a disorder characterized  
CC by aberrant expression or activity of Dkk such as optic disorders  
CC (glaucoma, constrictive), brain disorders (Alzheimer's disease,  
CC epilepsy, amnesia), inflammation, skeletal muscle disorders, pulmonary  
CC disorders (Goodpasture's syndrome), cardiovascular disorders, and  
CC hyperproliferative disorders (cancer). The Dkk proteins and nucleic  
CC acids may also be used for research purposes, such as for chromosome  
CC mapping, tissue typing and in screening assays to identify modulators.  
XX  
SQ Sequence 349 AA;  
Query Match 11.7%; Score 41; DB 21; Length 349;  
Best Local Similarity 100.0%; Pred. No. 3e-31;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 40 YPOEATLNEMFREVEIMEDTQHKLSAVEEMEAEEAAK 80  
DB 40 YPOEATLNEMFREVEIMEDTQHKLSAVEEMEAEEAAK 80  
RESULT 28  
AAV92069  
ID AAV92069 standard; Protein; 349 AA.  
AC AAV92069;  
XX  
DT 01-AUG-2000 (first entry)  
XX  
DE Murine DKK-3.  
XX  
DM DKK-3; human rig-1-like 7-1 mRNA; chicken lens fiber protein; cleft 4;  
XX dkk-1; dickkopf-1; antagonist; wnt-8 signaling; morphogenesis;  
XX growth factor; cytosolic; sonic hedgehog; tissue differentiation.  
XX  
OS Mus sp.  
XX  
PN WO200018914-A2.  
XX  
PD 06-APR-2000.  
XX  
PF 17-SEP-1999; 99WO-US21647.  
XX  
PR 25-SEP-1998; 98US-0161241.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Baas MB, Sullivan JK, Theill LE, Wang D;  
XX WPI; 2000-291153/25.  
DR N-PSDB; AAA08838.  
PT New nucleic acid molecule encoding a biologically active DKK  
PT polypeptide, useful in treatment of cancer, e.g. mammary tumors and  
PT stem cell tumors  
XX  
PS Claim 18; Page 127-128; 143p; English.  
XX  
AAV92069-75 are novel mouse and human DKK polypeptides.  
CC The murine DKK-3 open reading frame has homology to human rig-1-like 7-1  
CC mRNA and to chicken lens fiber protein cleft 4 gene.  
CC DKK-1 is a human ortholog of dkk-1 (dickkopf-1), a novel gene identified  
CC in Xenopus and mouse, purportedly an antagonist of wnt-8 signaling.  
CC DKK-2, -3 and -4 are each related to DKK-1 by their cysteine pattern.  
CC DKK-1 is also involved in morphogenesis in the developing embryo, and  
CC therefore a growth factor. By inference DKK polypeptides are also  
CC growth factors. The DKK polypeptides are useful for treating cancer,  
CC e.g. mammary tumors, stem cell tumors, or other cancers in which the wnt

CC and/or sonic hedgehog (shh) signal transduction pathways are activated.  
CC They can also be used to enhance tissue differentiation, such as bone  
CC formation and hematopoietic cell formation.  
XX  
SQ Sequence 349 AA;  
Query Match 11.7%; Score 41; DB 21; Length 349;  
Best Local Similarity 100.0%; Pred. No. 3e-31;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 40 YPOEATLNEMFREVEIMEDTQHKLSAVEEMEAEEAAK 80  
DB 40 YPOEATLNEMFREVEIMEDTQHKLSAVEEMEAEEAAK 80  
RESULT 29  
AAU24777  
ID AAU24777 standard; Peptide; 14 AA.  
AC AAU24777;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Schizophrenia-Associated Protein Isoform (SPI) peptide #6.  
XX  
DM Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;  
XX neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.  
XX  
OS Homo sapiens.  
XX  
PN WO200162785-A2.  
XX  
PD 30-AUG-2001.  
XX  
PF 23-FEB-2001; 2001WO-GB00792.  
XX  
PR 24-FEB-2000; 2000GB-0004415.  
XX 28-NOV-2000; 2000US-0750395.  
XX  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX  
PI Herath HMC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;  
XX WPI; 2001-570624/64.  
XX  
DR 2001-570624/64.  
XX  
PT New schizophrenia associated protein isoforms and encoding nucleic acid  
PT molecule, useful for treatment, diagnosis and prognosis of  
PT schizophrenia and screening for potential drugs for treatment and new  
PT drug targets -  
XX  
PS Disclosure; Page 29; 148p; English.  
XX  
XX The sequence represents a schizophrenia-associated protein isoform (SPI).  
CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable  
CC in cerebrospinal fluid, serum or plasma and are useful markers of  
CC schizophrenia. The sequences can be used for treatment and diagnosis of  
CC schizophrenia, screening, prognosis, monitoring the results of therapy,  
CC identifying patients most likely to respond to a particular therapy and  
CC identification of new targets for drug treatment. SPI DNA is useful as a  
CC nucleic acid probe to detect the presence of nucleic acids or SPIs.  
XX  
SQ Sequence 14 AA;  
Query Match 4.0%; Score 14; DB 22; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.4e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 67 SAVEMEAEEAAK 80  
DB 1 SAVEMEAEEAAK 14  
RESULT 30



XX Homo sapiens.  
XX WO200169261-A2.  
XX  
XX 20-SEP-2001.  
XX  
XX 14-MAR-2001; 2001WO-GB01106.  
XX  
XX 15-MAR-2000; 2000GB-0006285.  
XX 24-NOV-2000; 2000GB-0028734.  
XX 28-NOV-2000; 2000US-0724391.  
XX  
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX Herath HMAc, Parekh RB, Rohlf C,  
XX WPI, 2001-557937/62.  
XX  
XX Screening, diagnosis or prognosis of vascular dementia (VD), useful for  
XX determining stage of VD and monitoring the effect of VD therapy,  
XX comprises analysing body fluid by 2-dimensional electrophoresis for  
XX features correlated with VD -  
XX  
XX Claim 6; Page 36; 15pp; English.  
XX  
XX The invention relates to screening, diagnosis or prognosis of Vascular  
XX Dementia (VD) in a subject comprising analysing body fluid from the  
XX subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of  
XX features containing at least one chosen feature whose relative abundance  
XX correlates with the presence, absence, stage or severity of VD or  
XX predicts the onset or course of VD, especially detecting in a sample of  
XX cerebrospinal fluid (CSF) from the subject one of 223 VD-associated  
XX protein isoforms (VPIs) (ABBS5601-ABBS6295) as fully defined in the  
XX specification. Detecting VD-associated features and VPI is useful for the  
XX screening, diagnosis or prognosis of VD, for determining the stage or  
XX severity of VD, for identifying a subject at risk of VD or for  
XX monitoring the effect of therapy administered to a subject having VD.  
XX Nucleic acids encoding a VPI or inhibiting the function of a VPI are  
XX useful for the treatment of VD and for gene therapy.  
XX  
SQ Sequence 12 AA;  
Query Match 3.4%; Score 12; DB 22; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00026;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 213 DCQPGICCAFOR 224  
DB 1 DCQPGICCAFOR 12  
RESULT 33  
ABBS2342 ID ABB52342 standard; Peptide; 12 AA.  
XX  
XX ABB52342;  
XX AC  
XX 08-FEB-2002 (first entry)  
XX  
XX Human API-121 tryptic digest peptide #2.  
XX  
XX Human; neuroprotective; nootropic; gene therapy; vaccine;  
XX Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;  
XX Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;  
XX Expression Reference Protein Isoform; ERPI; proteolysis.  
XX  
XX Homo sapiens.  
XX OS  
XX WO200175454-A2.  
XX PN  
XX 11-OCT-2001.  
XX PD  
XX

PF 03-APR-2001; 2001WO-US10908.  
XX  
XX 03-APR-2000; 2000US-194504P.  
XX 28-NOV-2000; 2000US-253647P.  
XX  
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX (PFIZ ) PFIZER INC.  
XX  
XX Durham KL, Friedman DL, Herath HMAc, Kimmel LH, Parekh RB;  
XX Potter DM, Rohlf C, Silber BW, Stiger TR, Sunderland PT;  
XX Townsend RR, White F, Williams SA;  
XX WPI, 2001-639384/73.  
XX  
XX Screening for Alzheimer's disease in a mammal, by making  
XX two-dimensional array of a feature whose relative abundance correlates  
XX with disease, and comparing with abundance of the feature in samples of  
XX healthy persons -  
XX  
XX Example; Page 34; 162pp; English.  
XX  
XX The invention relates to methods for the screening, diagnosis and  
XX prognosis of Alzheimer's disease. The methods involve the detection  
XX of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's  
XX Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,  
XX serum or plasma. The abundance of the AFs and APIs is then  
XX normalised to an Expression Reference Protein Isoform (ERPI) in  
XX order to determine whether a patient is suffering from, or has  
XX a predisposition to, Alzheimer's Disease. The relative abundance of  
XX the AFs and APIs correlates with the severity of Alzheimer's Disease.  
XX The present sequence is a peptide produced from an API by proteolysis.  
XX  
SQ Sequence 12 AA;  
Query Match 3.4%; Score 12; DB 22; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00026;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 213 DCQPGICCAFOR 224  
DB 1 DCQPGICCAFOR 12  
RESULT 34  
ABBS6098 ID ABB56098 standard; Peptide; 10 AA.  
XX  
XX ABB56098;  
XX AC  
XX 15-FEB-2002 (first entry)  
XX DT  
XX  
XX Vascular dementia-associated protein isoform (VPI) 298.  
XX  
XX Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;  
XX diagnosis; prognosis; Gene therapy.  
XX  
XX Homo sapiens.  
XX OS  
XX WO200169261-A2.  
XX PN  
XX 20-SEP-2001.  
XX  
XX 14-MAR-2001; 2001WO-GB01106.  
XX  
XX 15-MAR-2000; 2000GB-0006285.  
XX 24-NOV-2000; 2000GB-0028734.  
XX 28-NOV-2000; 2000US-0724391.  
XX  
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX Herath HMAc, Parekh RB, Rohlf C,  
XX WPI, 2001-557937/62.  
XX PD  
XX

XX Screening, diagnosis or prognosis of vascular dementia (VD), useful for  
 PT determining stage of VD and monitoring the effect of VD therapy.  
 PT comprises analysing body fluid by 2-dimensional electrophoresis for  
 PT features correlated with VD -  
 XX Claim 6; Page 36; 151pp; English.  
 CC The invention relates to screening, diagnosis or prognosis of Vascular  
 CC Dementia (VD) in a subject comprising analysing body fluid from the  
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of  
 CC features containing at least one chosen feature whose relative abundance  
 CC correlates with the presence, absence, stage or severity of VD or  
 CC predicts the onset or course of VD, especially detecting in a sample of  
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated  
 CC protein isoforms (VPIs) (ABBS5801-ABBS6295) as fully defined in the  
 CC specification. Detecting VD-associated features and VPI is useful for the  
 CC screening, diagnosis or prognosis of VD, for determining the stage or  
 CC severity of VD, for identifying a subject at risk of VD or for  
 CC monitoring the effect of therapy administered to a subject having VD.  
 CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are  
 CC useful for the treatment of VD and for gene therapy.

QY Sequence 10 AA; 2.9%; Score 10; DB 22; Length 10;  
 Query Match Best Local Similarity 100.0%; Pred. No. 0.02; Mismatches 0;  
 Matches 10; Conservative 0; Indels 0; Gaps 0;

QY 293 DDGDEILPR 302  
 DB 1 DDGDEILPR 10

RESULT 35  
 AAG80272  
 ID AAG80272 standard; Protein; 10 AA.

AC AAG80272;

DT 11-FEB-2002 (first entry)

XX Human DKK-3 protein derived tryptic peptide.

KM DKK-3; detection; schizophrenia; neuroleptic; vaccine; gene therapy;  
 KM neurologic defect; neuropsychiatric disorder; human; tryptic peptide.

OS Homo sapiens.

XX WO200163295-A2.

XX 30-AUG-2001.

PF 26-FEB-2001; 2001WO-IB00259.

XX 24-FEB-2000; 2000GB-0004412.

PR 24-FEB-2000; 2000GB-0004415.

PR 15-MAR-2000; 2000GB-0006285.

PR 24-NOV-2000; 2000GB-0028734.

PR 28-NOV-2000; 2000US-0724391.

PR 08-DEC-2000; 2000GB-0030050.

PR 12-DEC-2000; 2000US-0254830.

PR 28-DEC-2000; 2000US-0750395.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Heratch HWAC, Parekh RB, Rohlf C, Patel TP;

XX WPI; 2001-570652/64.

PT Diagnosing and monitoring Schizophrenia by detecting the presence of  
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein  
 PT isoforms in samples of cerebrospinal fluid -

XX Example 2; Fig 3; 91pp; English.

CC This invention describes a novel method for detecting the presence of  
 CC schizophrenia associated features (SFS) and schizophrenia associated  
 CC protein isoforms (SPIs) in samples, e.g. by electrophoresis, immunoassay  
 CC or hybridisation assay, for diagnosing and monitoring schizophrenia,  
 CC studying the effectiveness of treatments and for identifying potential  
 CC therapeutic agents. The products of the invention have neuroleptic  
 CC activity and can be used in vaccines or for gene therapy. The method (I)  
 CC is used: (1) for screening or diagnosis of schizophrenia and the relative  
 CC abundance of at least 1 chosen feature correlates with the presence or  
 CC absence of schizophrenia and for monitoring the effect of therapy  
 CC administered to a subject with schizophrenia and the relative abundance  
 CC of at least 1 chosen feature which correlates with the severity of  
 CC schizophrenia. The expression and activity of the SFS, SPIs and related  
 CC molecules (e.g. secondary messengers) are studied to diagnose  
 CC schizophrenia, monitor the progress of the disorder and the effectiveness  
 CC of treatment and as targets to identify and produce potential therapeutic  
 CC agents for the treatment of schizophrenia. The paucity of detectable  
 CC neurologic defects distinguishes neuropsychiatric disorders such as  
 CC schizophrenia from neurological disorders, where manifestations of  
 CC anatomical and biochemical changes have been identified in many cases.  
 CC Consequently the identification and characterisation of cellular and/or  
 CC molecular causative defects and neuropathies are necessary for improved  
 CC treatment of neuropsychiatric disorders. This sequence represents a  
 CC human DKK-3 protein derived tryptic peptide described in the method of  
 CC the invention.

QY Sequence 10 AA;

Query Match Best Local Similarity 100.0%; Score 10; DB 22; Length 10;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 DDGDEILPR 302  
 DB 1 DDGDEILPR 10

RESULT 36  
 ABB52202  
 ID ABB52202 standard; Peptide; 10 AA.

AC ABB52202;

DT 08-FEB-2002 (first entry)

XX Human API-153 tryptic digest peptide.

KM Human; neuroprotective; neuroleptic; gene therapy; vaccine;  
 KM Alzheimer's disease; Alzheimer's Disease-Associated Feature; API;  
 KM Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;  
 KM Expression Reference Protein Isoform; ERPI; proteolysis.

XX Homo sapiens.

XX WO200175454-A2.

XX 11-OCT-2001.

XX 03-APR-2001; 2001WO-US10908.

XX 03-APR-2000; 2000US-194504P.

XX 28-NOV-2000; 2000US-253647P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI (PRIZ) PRIZR INC.

XX Durham KU, Friedman DU, Heratch HWAC, Kimmel LH, Parekh RB;

PI Potter DM, Rohlf C, Silber BM, Stigler TR, Sunderland PT;

PI Townsend RR, White F, Williams SA;



```

DR WPI; 2001-639384/73.
PT Screening for Alzheimer's disease in a mammal, by making
PT two-dimensional array of a feature whose relative abundance correlates
PT with disease, and comparing with abundance of the feature in samples of
PT healthy persons
XX Example; Page 30; 162pp; English.
PS
XX
CC The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection
CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
CC serum or plasma. The abundance of the AFs and APIs is then
CC normalised to an Expression Reference Protein Isoform (ERPI) in
CC order to determine whether a patient is suffering from, or has
CC a predisposition to, Alzheimer's Disease. The relative abundance of
CC the AFs and APIs correlates with the severity of Alzheimer's Disease.
CC The present sequence is a peptide produced from an API by proteolysis.
XX
SQ Sequence 10 AA;
Query Match 2.9%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 293 DDDGELLPR 302
DB 1 DDDGELLPR 10
RESULT 37
ABBS2341
ID ABBS2341 standard; Peptide; 10 AA.
XX
AC ABBS2341;
XX
DT 08-FEB-2002 (first entry)
XX
DE Human API-121 tryptic digest peptide #1.
XX
KW Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KW Expression Reference Protein Isoform; ERPI; proteolysis.
XX
OS Homo sapiens.
XX
PN WO200175454-A2.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US10908.
XX
PR 03-APR-2000; 2000US-194504P.
PR 28-NOV-2000; 2000US-253647P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA (PFIZ ) PFIZER INC.
PI Durham KL, Friedman DL, Herath HMAC, Kimmel LH, Parekh RB;
PI Potter DM, Rolf C, Silber BM, Stiger TR, Sunderland PT;
PI Townsend RR, White F, Williams SA;
XX
DR WPI; 2001-639384/73.
XX
PT Screening for Alzheimer's disease in a mammal, by making
PT two-dimensional array of a feature whose relative abundance correlates
PT with disease, and comparing with abundance of the feature in samples of
PT healthy persons
XX Example; Page 34; 162pp; English.
XX

```

```

CC The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection
CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
CC serum or plasma. The abundance of the AFs and APIs is then
CC normalised to an Expression Reference Protein Isoform (ERPI) in
CC order to determine whether a patient is suffering from, or has
CC a predisposition to, Alzheimer's Disease. The relative abundance of
CC the AFs and APIs correlates with the severity of Alzheimer's Disease.
CC The present sequence is a peptide produced from an API by proteolysis.
XX
SQ Sequence 10 AA;
Query Match 2.9%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 293 DDDGELLPR 302
DB 1 DDDGELLPR 10
RESULT 38
ABBS2343
ID ABBS2343 standard; Peptide; 10 AA.
XX
AC ABBS2343;
XX
DT 08-FEB-2002 (first entry)
XX
DE Human API-122 tryptic digest peptide.
XX
KW Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KW Expression Reference Protein Isoform; ERPI; proteolysis.
XX
OS Homo sapiens.
XX
PN WO200175454-A2.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US10908.
XX
PR 03-APR-2000; 2000US-194504P.
PR 28-NOV-2000; 2000US-253647P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA (PFIZ ) PFIZER INC.
PI Durham KL, Friedman DL, Herath HMAC, Kimmel LH, Parekh RB;
PI Potter DM, Rolf C, Silber BM, Stiger TR, Sunderland PT;
PI Townsend RR, White F, Williams SA;
XX
DR WPI; 2001-639384/73.
XX
PT Screening for Alzheimer's disease in a mammal, by making
PT two-dimensional array of a feature whose relative abundance correlates
PT with disease, and comparing with abundance of the feature in samples of
PT healthy persons
XX Example; Page 34; 162pp; English.
XX

```

CC The present sequence is a peptide produced from an API by proteolysis.  
XX  
SQ Sequence 10 AA;  
Query Match 2.9%; Score 10; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 293 DDDGELLPR 302  
DB 1 DDDGELLPR 10  
RESULT 39  
AAU28428  
ID AAU28428 standard; Peptide; 10 AA.  
XX  
XX AAU28428;  
XX  
DT 03-JAN-2002 (first entry)  
XX  
XX DPI tryptic digest peptide #25.  
XX  
XX Human; depression associated protein isoform; tryptic digest peptide;  
XX DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;  
XX neuropsychiatric disorder; bipolar mood disorder; neuroleptic;  
XX manic-depressive illness; schizoaffective disorder.  
XX Homo sapiens.  
XX MO200162787-A1.  
XX  
XX 30-AUG-2001.  
XX  
XX 23-FEB-2001; 2001MO-GB00786.  
XX  
XX 24-FEB-2000; 2000GB-0004412.  
XX 08-DEC-2000; 2000GB-0030050.  
XX 12-DEC-2000; 2000US-0254830.  
XX  
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX  
XX Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;  
XX WPI; 2001-570626/64.  
XX  
XX Novel nucleic acid encoding a protein associated with bipolar affective  
XX disorder, which is used for diagnosis, prophylaxis and therapy of  
XX neuropsychiatric disorders, such as bipolar affective disorder -  
XX  
XX Disclosure; Page 31; 153pp; English.  
XX  
XX The present invention relates to the identification of depression  
XX associated protein isoforms (DPIs), particularly the tryptic digest  
XX peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)  
XX described are decreased in the cerebrospinal fluid (CSF) of BAD  
XX (bipolar affective disorder) subjects, whilst other DPIs  
XX (AAU28626-AAU28887) are increased in BAD subjects. Also described  
XX are peptide sequences identified from DPI-45 and DPI-213 and the  
XX nucleic acid sequence they are encoded by. The sequences of the  
XX invention are useful for clinical screening, diagnosis, prognosis,  
XX therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also  
XX known as bipolar mood disorder, BP), manic-depressive illnesses,  
XX attention deficit disorders, schizoaffective disorders, and unipolar  
XX affective disorders. The present sequence represents one of the DPI  
XX tryptic digest peptides of the present invention.  
XX  
XX Sequence 10 AA;  
SQ  
Query Match 2.9%; Score 10; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 293 DDDGELLPR 302  
DB 1 DDDGELLPR 10  
RESULT 41  
AAU28566  
ID AAU28566 standard; Peptide; 10 AA.

QY 293 DDDGELLPR 302  
DB 1 DDDGELLPR 10  
RESULT 40  
AAU28553  
ID AAU28553 standard; Peptide; 10 AA.  
XX  
XX AAU28553;  
XX  
DT 03-JAN-2002 (first entry)  
XX  
XX DPI tryptic digest peptide #150.  
XX  
XX Human; depression associated protein isoform; tryptic digest peptide;  
XX DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;  
XX neuropsychiatric disorder; bipolar mood disorder; neuroleptic;  
XX manic-depressive illness; schizoaffective disorder.  
XX Homo sapiens.  
XX MO200162787-A1.  
XX  
XX 30-AUG-2001.  
XX  
XX 23-FEB-2001; 2001MO-GB00786.  
XX  
XX 24-FEB-2000; 2000GB-0004412.  
XX 08-DEC-2000; 2000GB-0030050.  
XX 12-DEC-2000; 2000US-0254830.  
XX  
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX  
XX Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;  
XX WPI; 2001-570626/64.  
XX  
XX Novel nucleic acid encoding a protein associated with bipolar affective  
XX disorder, which is used for diagnosis, prophylaxis and therapy of  
XX neuropsychiatric disorders, such as bipolar affective disorder -  
XX  
XX Disclosure; Page 33; 153pp; English.  
XX  
XX The present invention relates to the identification of depression  
XX associated protein isoforms (DPIs), particularly the tryptic digest  
XX peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)  
XX described are decreased in the cerebrospinal fluid (CSF) of BAD  
XX (bipolar affective disorder) subjects, whilst other DPIs  
XX (AAU28626-AAU28887) are increased in BAD subjects. Also described  
XX are peptide sequences identified from DPI-45 and DPI-213 and the  
XX nucleic acid sequence they are encoded by. The sequences of the  
XX invention are useful for clinical screening, diagnosis, prognosis,  
XX therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also  
XX known as bipolar mood disorder, BP), manic-depressive illnesses,  
XX attention deficit disorders, schizoaffective disorders, and unipolar  
XX affective disorders. The present sequence represents one of the DPI  
XX tryptic digest peptides of the present invention.  
XX  
XX Sequence 10 AA;  
SQ  
Query Match 2.9%; Score 10; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 293 DDDGELLPR 302  
DB 1 DDDGELLPR 10  
RESULT 41  
AAU28566  
ID AAU28566 standard; Peptide; 10 AA.

```

XX AC AAU28566;
XX
XX DT 03-JAN-2002 (first entry)
XX DE DPI tryptic digest peptide #163.
XX
XX KM Human; depression associated protein isoform; tryptic digest peptide;
XX KM DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
XX KM neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
XX KM manic-depressive illness; schizoaffective disorder.
XX OS Homo sapiens.
XX PN WO200162787-A1.
XX PD 30-AUG-2001.
XX
XX PF 23-FEB-2001; 2001WO-GB00786.
XX
XX PR 24-FEB-2000; 2000GB-0004412.
XX PR 08-DEC-2000; 2000GB-0030050.
XX PR 12-DEC-2000; 2000US-0254830.
XX
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX PI Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
XX
XX DR WPI; 2001-570626/64.
XX
XX PT Novel nucleic acid encoding a protein associated with bipolar affective
XX PT disorder, which is used for diagnosis, prophylaxis and therapy of
XX PT neuropsychiatric disorders, such as bipolar affective disorder -
XX PS Disclosure; Page 34; 153pp; English.
XX
XX SQ The present invention relates to the identification of depression
XX CC associated protein isoforms (DPIs), particularly the tryptic digest
XX CC peptides of these proteins. Some of the DPIs (AAU24776-AAU28625)
XX CC described are decreased in the cerebrospinal fluid (CSF) of BAD
XX CC (bipolar affective disorder) subjects, whilst other DPIs
XX CC (AAU28626-AAU28887) are increased in BAD subjects. Also described
XX CC are peptide sequences identified from DPI-45 and DPI-213 and the
XX CC nucleic acid sequences they are encoded by. The sequences of the
XX CC invention are useful for clinical screening, diagnosis, prognosis,
XX CC therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also
XX CC known as bipolar mood disorder, BP), manic-depressive illnesses,
XX CC attention deficit disorders, schizoaffective disorders, and unipolar
XX CC affective disorders. The present sequence represents one of the DPI
XX CC tryptic digest peptides of the present invention.
XX
XX SQ Sequence 10 AA;
XX
XX Query Match 2.9%; Score 10; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred.No.0.02; Mismatches 0; Gaps 0;
XX Matches 10; Conservative 0; Indels 0;
XX
XX QY 293 DQDGEILLPR 302
XX |||||
XX 1 DQDGEILLPR 10
XX
XX Db 1 DQDGEILLPR 10
XX
XX RESULT 42
XX AAU24776
XX ID AAU24776 standard; Peptide; 10 AA.
XX
XX AC AAU24776;
XX
XX DT 18-DEC-2001 (first entry)
XX
XX DE Schizophrenia-associated Protein Isoform (SPI) peptide #5.
XX
XX KM Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
XX KM Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
XX KM Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

```

```

XX KM neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
XX
XX OS Homo sapiens.
XX PN WO200162785-A2.
XX PD 30-AUG-2001.
XX
XX PF 23-FEB-2001; 2001WO-GB00792.
XX
XX PR 24-FEB-2000; 2000GB-0004415.
XX PR 28-NOV-2000; 2000US-0750395.
XX
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX PI Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
XX
XX DR WPI; 2001-570624/64.
XX
XX PT New schizophrenia associated protein isoforms and encoding nucleic acid
XX PT molecules, useful for treatment, diagnosis and prognosis of
XX PT schizophrenia and screening for potential drugs for treatment and new
XX PT drug targets -
XX PS Disclosure; Page 29; 148pp; English.
XX
XX SQ The sequence represents a schizophrenia-associated protein isoform (SPI).
XX CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
XX CC in cerebrospinal fluid, serum or plasma and are useful markers of
XX CC schizophrenia. The sequences can be used for treatment and diagnosis of
XX CC schizophrenia, screening, prognosis, monitoring the results of therapy,
XX CC identifying patients most likely to respond to a particular therapy and
XX CC identification of new targets for drug treatment. SPI DNA is useful as a
XX CC nucleic acid probe to detect the presence of nucleic acids or SPIs.
XX
XX SQ Sequence 10 AA;
XX
XX Query Match 2.9%; Score 10; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred.No.0.02; Mismatches 0; Gaps 0;
XX Matches 10; Conservative 0; Indels 0;
XX
XX QY 293 DQDGEILLPR 302
XX |||||
XX 1 DQDGEILLPR 10
XX
XX Db 1 DQDGEILLPR 10
XX
XX RESULT 43
XX AAU25210
XX ID AAU25210 standard; Peptide; 10 AA.
XX
XX AC AAU25210;
XX
XX DT 18-DEC-2001 (first entry)
XX
XX DE Schizophrenia-associated Protein Isoform (SPI) peptide #439.
XX
XX KM Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
XX KM neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
XX
XX OS Homo sapiens.
XX PN WO200162785-A2.
XX PD 30-AUG-2001.
XX
XX PF 23-FEB-2001; 2001WO-GB00792.
XX
XX PR 24-FEB-2000; 2000GB-0004415.
XX PR 28-NOV-2000; 2000US-0750395.
XX
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX PI Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

```

XX WPI; 2001-570624/64.  
 XX  
 PT New schizophrenia associated protein isoforms and encoding nucleic acid  
 PT molecules, useful for treatment, diagnosis and prognosis of  
 PT schizophrenia and screening for potential drugs for treatment and new  
 PT drug targets -  
 PS Disclosure; Page 37; 148pp; English.  
 XX  
 CC The sequence represents a schizophrenia-associated protein isoform (SPI).  
 CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable  
 CC in cerebrospinal fluid, serum or plasma and are useful markers of  
 CC schizophrenia. The sequences can be used for treatment and diagnosis of  
 CC schizophrenia, screening, prognosis, monitoring the results of therapy,  
 CC identifying patients most likely to respond to a particular therapy and  
 CC identification of new targets for drug treatment. SPI DNA is useful as a  
 CC nucleic acid probe to detect the presence of nucleic acids or SPIs.  
 XX  
 SQ Sequence 10 AA;  
 QY 293 DODGEIILPR 302  
 DB 1 DODGEIILPR 10  
 RESULT 44  
 AAU25377  
 ID AAU25377 standard; Peptide; 10 AA.  
 AC AAU25377;  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Schizophrenia-Associated Protein Isoform (SPI) peptide #606.  
 XX  
 KW Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;  
 KW neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2001:62785-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 23-FEB-2001; 2001MO-GB00792.  
 XX  
 PR 24-FEB-2000; 2000GB-0004415.  
 PR 28-NOV-2000; 2000US-0750395.  
 XX  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 PI Herath HMAc, Parekh RB, Rohlf C, Terrett JA, Tyson XL;  
 DR WPI; 2001-570624/64.  
 XX  
 PT New schizophrenia associated protein isoforms and encoding nucleic acid  
 PT molecules, useful for treatment, diagnosis and prognosis of  
 PT schizophrenia and screening for potential drugs for treatment and new  
 PT drug targets -  
 PS Disclosure; Page 41; 148pp; English.  
 XX  
 CC The sequence represents a schizophrenia-associated protein isoform (SPI).  
 CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable  
 CC in cerebrospinal fluid, serum or plasma and are useful markers of  
 CC schizophrenia. The sequences can be used for treatment and diagnosis of  
 CC schizophrenia, screening, prognosis, monitoring the results of therapy,  
 CC identifying patients most likely to respond to a particular therapy and

CC identification of new targets for drug treatment. SPI DNA is useful as a  
 CC nucleic acid probe to detect the presence of nucleic acids or SPIs.  
 XX  
 SQ Sequence 10 AA;  
 QY 293 DODGEIILPR 302  
 DB 1 DODGEIILPR 10  
 RESULT 45  
 AAU26074  
 ID AAU26074 standard; Peptide; 10 AA.  
 AC AAU26074;  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Depression-Associated Protein Isoform DPI-6 #1.  
 XX  
 KW Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;  
 KW DPI; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;  
 KW CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;  
 KW attention deficient disorder; schizoaffective disorder;  
 KW unipolar affective disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2001:63294-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 23-FEB-2001; 2001MO-GB00791.  
 XX  
 PR 24-FEB-2000; 2000GB-0004412.  
 PR 08-DEC-2000; 2000GB-0030050.  
 PR 12-DEC-2000; 2000US-0254830.  
 XX  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 PI Herath HMAc, Parekh RB, Rohlf C;  
 DR WPI; 2001-582081/65.  
 XX  
 PT Preparation for diagnosing or treating bipolar affected disorder (BAD)  
 PT or unipolar depression, or for screening for modulators, comprises a  
 PT BAD-associated protein isoform -  
 PS Claim 8; Page 31; 163pp; English.  
 XX  
 CC The invention relates to a preparation comprising an isolated Bipolar  
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are  
 CC used to screen, diagnose or prognose of BAD or unipolar depression,  
 CC determine the stage or severity of BAD or unipolar depression, identify a  
 CC subject at risk of developing BAD or unipolar depression, or monitor the  
 CC effect of therapy in a subject. They are also used to screen for or  
 CC identify agents that interact with a DPI. These agents, antibodies  
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat  
 CC or prevent BAD or unipolar depression. Diseases that can be treated are  
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a  
 CC unipolar affective disorder. The DPIs are used in proteomics. The  
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of  
 CC BAD or unipolar depression overcomes the problems of using gene  
 CC expression analysis, such as not being able to obtain central nervous  
 CC system (CNS) tissue from a living patient under normal circumstances.  
 CC The present sequence is a DIP decreased in the CSF (cerebro-spinal  
 CC fluid) of subjects having BAD.  
 XX  
 SQ Sequence 10 AA;

Query Match 2.9%; Score 10; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 DQDGEILLPR 302  
Db 1 DQDGEILLPR 10

## RESULT 46

AAU26200  
ID AAU26200 standard; Peptide; 10 AA.

XX AAU26200;

DT 18-DEC-2001 (first entry)

DE Depression-Associated Protein Isoform DPI-186.

KM Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;  
KM DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;  
KM CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;  
KM attention deficient disorder; schizoaffective disorder;  
KM unipolar affective disorder.

XX Homo sapiens.

XX OS

XX WO200163294-A2.

PN 30-AUG-2001.

PF 23-FEB-2001; 2001WO-GB00791.

XX 24-FEB-2000; 2000GB-0004412.

PR 08-DEC-2000; 2000GB-0030050.

PR 12-DEC-2000; 2000US-0254830.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMAC, Parekh RB, Rohlf C;

DR WPI; 2001-582081/65.

PT Preparation for diagnosing or treating bipolar affected disorder (BAD)

PT or unipolar depression, or for screening for modulators, comprises a

PT BAD-associated protein isoform -

XX Claim 8; Page 33; 163pp; English.

CC The invention relates to a preparation comprising an isolated Bipolar  
CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are  
CC used to screen, diagnose or prognose of BAD or unipolar depression,  
CC determine the stage or severity of BAD or unipolar depression, identify a  
CC subject at risk of developing BAD or unipolar depression, or monitor the  
CC effect of therapy in a subject. They are also used to screen for or  
CC identify agents that interact with a DPI. These agents, antibodies  
CC against the DPIs, and nucleic acids encoding the DPIs are used to treat  
CC or prevent BAD or unipolar depression. Diseases that can be treated are  
CC attention deficient disorder, a schizoaffective disorder, a bipolar or a  
CC unipolar affective disorder. The DPIs are used in proteomics. The  
CC proteomic approach of using DPIs for screening, diagnosis or prognosis of  
CC BAD or unipolar depression overcomes the problems of using gene  
CC expression analysis, such as not being able to obtain central nervous  
CC system (CNS) tissue from a living patient under normal circumstances.  
CC The present sequence is a DIP decreased in the CSF (cerebro-spinal  
CC fluid) of subjects having BAD.

XX Sequence 10 AA;

Query Match 2.9%; Score 10; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 DQDGEILLPR 302  
Db 1 DQDGEILLPR 10

RESULT 47  
AAU26213  
ID AAU26213 standard; Peptide; 10 AA.

XX AAU26213;

DT 18-DEC-2001 (first entry)

DE Depression-Associated Protein Isoform DPI-192 #1.

KM Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;  
KM DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;  
KM CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;  
KM attention deficient disorder; schizoaffective disorder;  
KM unipolar affective disorder.

XX Homo sapiens.

XX OS

XX WO200163294-A2.

PN 30-AUG-2001.

PF 23-FEB-2001; 2001WO-GB00791.

XX 24-FEB-2000; 2000GB-0004412.

PR 08-DEC-2000; 2000GB-0030050.

PR 12-DEC-2000; 2000US-0254830.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMAC, Parekh RB, Rohlf C;

DR WPI; 2001-582081/65.

PT Preparation for diagnosing or treating bipolar affected disorder (BAD)

PT or unipolar depression, or for screening for modulators, comprises a

PT BAD-associated protein isoform -

XX Claim 8; Page 34; 163pp; English.

CC The invention relates to a preparation comprising an isolated Bipolar  
CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are  
CC used to screen, diagnose or prognose of BAD or unipolar depression,  
CC determine the stage or severity of BAD or unipolar depression, identify a  
CC subject at risk of developing BAD or unipolar depression, or monitor the  
CC effect of therapy in a subject. They are also used to screen for or  
CC identify agents that interact with a DPI. These agents, antibodies  
CC against the DPIs, and nucleic acids encoding the DPIs are used to treat  
CC or prevent BAD or unipolar depression. Diseases that can be treated are  
CC attention deficient disorder, a schizoaffective disorder, a bipolar or a  
CC unipolar affective disorder. The DPIs are used in proteomics. The  
CC proteomic approach of using DPIs for screening, diagnosis or prognosis of  
CC BAD or unipolar depression overcomes the problems of using gene  
CC expression analysis, such as not being able to obtain central nervous  
CC system (CNS) tissue from a living patient under normal circumstances.  
CC The present sequence is a DIP decreased in the CSF (cerebro-spinal  
CC fluid) of subjects having BAD.

XX Sequence 10 AA;

Query Match 2.9%; Score 10; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 DQDGEILLPR 302  
Db 1 DQDGEILLPR 10

RESULT 48  
 ID AAU15120 standard; Peptide; 10 AA.  
 AC AAU15120;  
 DT 24-OCT-2001 (first entry)  
 DE Schizophrenia-associated isoform peptide #5.  
 KW Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;  
 KW neurological disorder; neuropathy.  
 OS Homo sapiens.  
 PN WO200163293-A2.  
 PD 30-AUG-2001.  
 PF 23-FEB-2001; 2001WO-GB00783.  
 PR 24-FEB-2000; 2000GB-0004415.  
 PR 28-NOV-2000; 2000US-0750395.  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 PI Herath HMC, Parekh RB, Rohlf C;  
 PI WPI; 2001-502868/55.  
 DR WPI; 2001-502868/55.  
 PT Diagnosing and monitoring Schizophrenia by detecting the presence of  
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein  
 PT isoforms in samples of cerebrospinal fluid -  
 PS Claim 6; Page 29; 160pp; English.  
 XX The invention relates to methods and compositions for screening,  
 CC diagnosis and prognosis of Schizophrenia. The method involves detecting  
 CC the presence of Schizophrenia (SCH) Associated Features (SFS) and SCH  
 CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,  
 CC immunoblotting or hybridisation assay, for diagnosing and monitoring SCH,  
 CC studying the effectiveness of treatments and for identifying potential  
 CC therapeutic agents. The method is used for (1) screening or diagnosis of  
 CC SCH and the relative abundance of at least 1 chosen feature correlates  
 CC with the presence or absence of SCH; and (2) monitoring the effect of  
 CC therapy administered to a subject with SCH and the relative abundance of  
 CC at least 1 chosen feature which correlates with the severity of SCH.  
 CC The expression and activity of the SFS, SPIs and related molecules  
 CC (e.g. secondary messengers) are studied to diagnose SCH, monitor the  
 CC progress of the disorder and the effectiveness of treatment and as  
 CC targets to identify and produce potential therapeutic agents for the  
 CC treatment of SCH. The paucity of detectable neurologic defects  
 CC distinguishes neuropsychiatric disorders such as SCH from neurological  
 CC disorders, where manifestations of anatomical and biochemical changes  
 CC have been identified in many cases. Consequently the identification and  
 CC characterisation of cellular and/or molecular causative defects and  
 CC neuropathies are necessary for improved treatment of neuropsychiatric  
 CC disorders. AAU15114-AAU15762 represent the amino acid sequences of  
 CC schizophrenia-associated isoforms used in the method of the invention.  
 XX Sequence 10 AA;  
 SQ  
 Query Match 2.9%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 49  
 ID AAU15554 standard; Peptide; 10 AA.  
 AC AAU15554;  
 DT 24-OCT-2001 (first entry)  
 DE Schizophrenia-associated isoform peptide #439.  
 KW Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;  
 KW neurological disorder; neuropathy.  
 OS Homo sapiens.  
 PN WO200163293-A2.  
 PD 30-AUG-2001.  
 PF 23-FEB-2001; 2001WO-GB00783.  
 PR 24-FEB-2000; 2000GB-0004415.  
 PR 28-NOV-2000; 2000US-0750395.  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 PI Herath HMC, Parekh RB, Rohlf C;  
 PI WPI; 2001-502868/55.  
 DR WPI; 2001-502868/55.  
 PT Diagnosing and monitoring Schizophrenia by detecting the presence of  
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein  
 PT isoforms in samples of cerebrospinal fluid -  
 PS Claim 6; Page 38; 160pp; English.  
 XX The invention relates to methods and compositions for screening,  
 CC diagnosis and prognosis of Schizophrenia. The method involves detecting  
 CC the presence of Schizophrenia (SCH) Associated Features (SFS) and SCH  
 CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,  
 CC immunoblotting or hybridisation assay, for diagnosing and monitoring SCH,  
 CC studying the effectiveness of treatments and for identifying potential  
 CC therapeutic agents. The method is used for (1) screening or diagnosis of  
 CC SCH and the relative abundance of at least 1 chosen feature correlates  
 CC with the presence or absence of SCH; and (2) monitoring the effect of  
 CC therapy administered to a subject with SCH and the relative abundance of  
 CC at least 1 chosen feature which correlates with the severity of SCH.  
 CC The expression and activity of the SFS, SPIs and related molecules  
 CC (e.g. secondary messengers) are studied to diagnose SCH, monitor the  
 CC progress of the disorder and the effectiveness of treatment and as  
 CC targets to identify and produce potential therapeutic agents for the  
 CC treatment of SCH. The paucity of detectable neurologic defects  
 CC distinguishes neuropsychiatric disorders such as SCH from neurological  
 CC disorders, where manifestations of anatomical and biochemical changes  
 CC have been identified in many cases. Consequently the identification and  
 CC characterisation of cellular and/or molecular causative defects and  
 CC neuropathies are necessary for improved treatment of neuropsychiatric  
 CC disorders. AAU15114-AAU15762 represent the amino acid sequences of  
 CC schizophrenia-associated isoforms used in the method of the invention.  
 XX Sequence 10 AA;  
 SQ  
 Query Match 2.9%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



ID AAU15721 standard; Peptide, 10 AA.  
 XX  
 AC AAU15721;  
 XX  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Schizophrenia-associated isoform peptide #606.  
 XX  
 KW Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;  
 neuropsychiatric disorder; neuropathy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200163293-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 23-FEB-2001; 2001WO-GB00783.  
 XX  
 PR 24-FEB-2000; 2000GB-0004415.  
 PR 28-NOV-2000; 2000US-0750395.  
 XX  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX  
 PI Herach HMC, Parekh RB, Rohlf C;  
 DR WPI; 2001-502868/55.  
 XX  
 PT Diagnosing and monitoring Schizophrenia by detecting the presence of  
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein  
 PT Isoforms in samples of cerebrospinal fluid -  
 PS  
 PS Claim 6; Page 41; 160pp; English.  
 XX  
 CC The invention relates to methods and compositions for screening,  
 CC diagnosis and prognosis of Schizophrenia. The method involves detecting  
 CC the presence of Schizophrenia (SCH) Associated Features (SfAs) and SCH  
 CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,  
 CC immunoblotting or hybridisation assay, for diagnosing and monitoring SCH,  
 CC studying the effectiveness of treatments and for identifying potential  
 CC therapeutic agents. The method is used for (1) screening or diagnosis of  
 CC SCH and the relative abundance of at least 1 chosen feature correlates  
 CC with the presence or absence of SCH; and (2) monitoring the effect of  
 CC therapy administered to a subject with SCH and the relative abundance of  
 CC at least 1 chosen feature which correlates with the severity of SCH.  
 CC The expression and activity of the SfAs, SPIs and related molecules  
 CC (e.g. secondary messengers) are studied to diagnose SCH, monitor the  
 CC progress of the disorder and the effectiveness of treatment and as  
 CC targets to identify and produce potential therapeutic agents for the  
 CC treatment of SCH. The paucity of detectable neuronal defects  
 CC distinguishes neuropsychiatric disorders such as SCH from neurological  
 CC disorders, where manifestations of anatomical and biochemical changes  
 CC have been identified in many cases. Consequently the identification and  
 CC characterisation of cellular and/or molecular causative defects and  
 CC neuropathies are necessary for improved treatment of neuropsychiatric  
 CC disorders. AAU1514-AAU15762 represent the amino acid sequences of  
 CC schizophrenia-associated isoforms used in the method of the invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 2.9%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 293 DQDGEILPR 302  
 |||||  
 DB 1 DQDGEILPR 10

Search completed: February 21, 2004, 01:47:04  
 Job time : 95 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comphen Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2004, 01:45:36 / Search time 28 seconds

(without alignments)  
528.886 Million cell updates/sec

Title: US-10-063-671-8

Perfect score: 350

Sequence: 1 MORTALITICILLINAAVPTA.....ENALGPAAAAALLIGSEI 350

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched:

Word size: 6

Total number of hits satisfying chosen parameters: 2194

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database:

Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	350	100.0	350	4	US-09-161-241-9
2	41	11.7	349	4	US-09-161-241-8
3	9	2.6	109	4	US-09-325-932A-144
4	9	2.6	398	4	US-09-252-991A-19907
5	8	2.3	12	1	US-08-460-874A-46
6	8	2.3	12	2	US-08-388-883B-15
7	8	2.3	12	3	US-08-462-211A-46
8	8	2.3	20	3	US-08-935-009A-5
9	8	2.3	31	1	US-08-460-874A-12
10	8	2.3	31	1	US-08-460-874A-13
11	8	2.3	31	2	US-08-388-883B-12
12	8	2.3	31	2	US-08-388-883B-13
13	8	2.3	31	3	US-08-462-211A-12
14	8	2.3	31	3	US-08-462-211A-13
15	8	2.3	32	1	US-08-460-874A-15
16	8	2.3	32	1	US-08-388-883B-15
17	8	2.3	32	2	US-08-462-211A-15
18	8	2.3	40	2	US-08-388-883B-1
19	8	2.3	51	1	US-08-460-874A-17
20	8	2.3	51	2	US-08-388-883B-17
21	8	2.3	51	3	US-08-462-211A-17
22	8	2.3	92	4	US-09-366-887A-14
23	8	2.3	97	4	US-09-886-319A-21
24	8	2.3	156	4	US-09-646-028-4
25	8	2.3	162	1	US-08-460-874A-33
26	8	2.3	162	2	US-08-388-883B-33
27	8	2.3	162	3	US-08-462-211A-33

28	8	2.3	162	4	US-09-433-241A-4	Sequence 4, Appli
29	8	2.3	171	4	US-09-646-028-9	Sequence 9, Appli
30	8	2.3	300	3	US-08-765-856-2	Sequence 2, Appli
31	8	2.3	300	3	US-08-935-009A-2	Sequence 2, Appli
32	8	2.3	302	3	US-08-765-856-4	Sequence 4, Appli
33	8	2.3	302	3	US-08-935-009A-4	Sequence 4, Appli
34	8	2.3	303	4	US-08-252-991A-27884	Sequence 27884, A
35	8	2.3	332	2	US-08-405-175A-5	Sequence 5, Appli
36	8	2.3	344	3	US-09-110-116-4	Sequence 2, Appli
37	8	2.3	415	3	US-09-032-523-2	Sequence 2, Appli
38	8	2.3	428	4	US-09-252-991A-27213	Sequence 27213, A
39	8	2.3	435	4	US-09-252-991A-30846	Sequence 30846, A
40	8	2.3	435	4	US-08-433-241A-12	Sequence 12, Appli
41	8	2.3	503	3	US-08-382-556-10	Sequence 10, Appli
42	8	2.3	503	3	US-08-395-115-10	Sequence 10, Appli
43	8	2.3	503	4	US-08-436-265-10	Sequence 10, Appli
44	8	2.3	503	4	US-09-679-187-10	Sequence 10, Appli
45	8	2.3	521	3	US-08-999-689A-6	Sequence 6, Appli
46	8	2.3	521	3	US-08-956-322-4	Sequence 4, Appli
47	8	2.3	607	4	US-08-252-991A-30878	Sequence 30878, A
48	8	2.3	652	3	US-08-110-116-1	Sequence 1, Appli
49	8	2.3	652	3	US-08-956-322-2	Sequence 2, Appli
50	8	2.3	899	3	US-09-413-814-5	Sequence 5, Appli
51	8	2.3	1048	4	US-09-171-699-10	Sequence 10, Appli
52	8	2.3	1084	4	US-09-227-725A-3	Sequence 3, Appli
53	8	2.0	9	3	US-08-159-339A-163	Sequence 163, App
54	8	2.0	14	2	US-08-503-326B-42	Sequence 42, Appli
55	8	2.0	14	2	US-08-721-558B-42	Sequence 42, Appli
56	8	2.0	21	1	US-08-460-874A-35	Sequence 35, Appli
57	8	2.0	21	2	US-08-388-883B-35	Sequence 35, Appli
58	8	2.0	21	3	US-08-462-211A-35	Sequence 35, Appli
59	8	2.0	22	3	US-08-516-859A-103	Sequence 103, App
60	8	2.0	22	4	US-09-586-472-103	Sequence 103, App
61	8	2.0	22	4	US-09-528-706-103	Sequence 103, App
62	8	2.0	30	1	US-08-460-874A-14	Sequence 14, Appli
63	8	2.0	30	2	US-08-388-883B-14	Sequence 14, Appli
64	8	2.0	30	3	US-08-462-211A-14	Sequence 14, Appli
65	8	2.0	35	1	US-08-460-874A-9	Sequence 9, Appli
66	8	2.0	35	2	US-08-388-883B-9	Sequence 9, Appli
67	8	2.0	35	3	US-08-462-211A-9	Sequence 9, Appli
68	8	2.0	36	2	US-08-388-883B-16	Sequence 16, Appli
69	8	2.0	37	2	US-08-180-524-1	Sequence 1, Appli
70	8	2.0	37	2	US-08-180-524-8	Sequence 8, Appli
71	8	2.0	37	2	US-08-180-524-9	Sequence 9, Appli
72	8	2.0	37	2	US-08-975-166-1	Sequence 1, Appli
73	8	2.0	37	2	US-08-975-166-8	Sequence 8, Appli
74	8	2.0	37	2	US-08-975-166-9	Sequence 9, Appli
75	8	2.0	37	4	US-09-117-121-39	Sequence 39, Appli
76	8	2.0	37	4	US-09-117-121-42	Sequence 42, Appli
77	8	2.0	37	4	US-09-344-529-4	Sequence 4, Appli
78	8	2.0	38	2	US-07-814-220-1	Sequence 1, Appli
79	8	2.0	38	2	US-07-814-220-1	Sequence 1, Appli
80	8	2.0	39	4	US-09-117-121-38	Sequence 38, Appli
81	8	2.0	41	1	US-08-460-874A-16	Sequence 16, Appli
82	8	2.0	41	1	US-08-460-874A-18	Sequence 18, Appli
83	8	2.0	41	2	US-08-388-883B-18	Sequence 18, Appli
84	8	2.0	41	3	US-08-462-211A-16	Sequence 16, Appli
85	8	2.0	41	3	US-08-462-211A-18	Sequence 18, Appli
86	8	2.0	42	4	US-08-826-114-17	Sequence 17, Appli
87	8	2.0	54	4	US-09-117-121-30	Sequence 30, Appli
88	8	2.0	73	4	US-08-469-260A-33	Sequence 33, Appli
89	8	2.0	73	4	US-08-469-260A-33	Sequence 33, Appli
90	8	2.0	73	4	US-08-469-260A-33	Sequence 33, Appli
91	8	2.0	76	6	5273901-11	Patent No. 5273901
92	8	2.0	76	6	5482709-10	Patent No. 5482709
93	8	2.0	104	3	US-08-744-419-2	Sequence 2, Appli
94	8	2.0	127	4	US-09-252-991A-23654	Sequence 23654, A
95	8	2.0	128	4	US-09-732-210-1298	Sequence 1298, App
96	8	2.0	136	4	US-09-205-258-465	Sequence 465, App
97	8	2.0	137	4	US-09-205-258-308	Sequence 308, App
98	8	2.0	137	4	US-09-252-991A-21633	Sequence 21633, A
99	8	2.0	178	7	US-09-252-991A-17021	Sequence 17021, A
100	8	2.0	180	6	5273901-7	Patent No. 5273901

Line	Offset	Time	Source	Destination	Sequence	Length	Port	Protocol	Flags	Window	Checksum	Sequence	Length	Port	Protocol	Flags	Window	Checksum	Sequence
101	7	2.0	180	6	5482709-6	2.0	733	3	US-08-464-700-2	Sequence 2, Appl	174	7	2.0	733	3	US-08-464-700-2	Sequence 2, Appl	174	
102	7	2.0	201	3	US-09-220-528-116	2.0	738	4	US-09-328-352-4315	Sequence 4315, App	175	7	2.0	738	4	US-09-328-352-4315	Sequence 4315, App	175	
103	7	2.0	204	3	US-09-252-991A-25056	2.0	743	4	US-09-252-991A-25056	Sequence 28327, A	176	7	2.0	743	4	US-09-252-991A-25056	Sequence 28327, A	176	
104	7	2.0	205	4	US-09-252-991A-31167	2.0	760	1	US-08-195-152-2	Sequence 2, Appl	177	7	2.0	760	1	US-08-195-152-2	Sequence 2, Appl	177	
105	7	2.0	228	3	US-09-286-690-12	2.0	750	4	US-09-252-991A-27790	Sequence 27790, A	178	7	2.0	750	4	US-09-252-991A-27790	Sequence 27790, A	178	
106	7	2.0	244	4	US-09-173-300-53	2.0	792	2	US-08-678-039A-40	Sequence 40, Appl	179	7	2.0	792	2	US-08-678-039A-40	Sequence 40, Appl	179	
107	7	2.0	247	4	US-09-228-986-105	2.0	803	2	US-08-951-648-4	Sequence 4, Appl	180	7	2.0	803	2	US-08-951-648-4	Sequence 4, Appl	180	
108	7	2.0	248	4	US-09-134-001C-3394	2.0	803	3	US-09-174-437-4	Sequence 4, Appl	181	7	2.0	803	3	US-09-174-437-4	Sequence 4, Appl	181	
109	7	2.0	248	4	US-09-482-273-126	2.0	803	3	US-09-686-055A-4	Sequence 4, Appl	182	7	2.0	803	3	US-09-686-055A-4	Sequence 4, Appl	182	
110	7	2.0	249	4	US-09-173-300-47	2.0	812	1	US-08-446-194A-4	Sequence 4, Appl	183	7	2.0	812	1	US-08-446-194A-4	Sequence 4, Appl	183	
111	7	2.0	255	3	US-09-036-987A-21	2.0	816	4	US-09-266-225D-12	Sequence 12, Appl	184	7	2.0	816	4	US-09-266-225D-12	Sequence 12, Appl	184	
112	7	2.0	255	3	US-09-370-700-21	2.0	894	4	US-09-735-934A-4	Sequence 4, Appl	185	7	2.0	894	4	US-09-735-934A-4	Sequence 4, Appl	185	
113	7	2.0	255	3	US-09-603-207-21	2.0	894	4	US-10-060-332-4	Sequence 4, Appl	186	7	2.0	894	4	US-10-060-332-4	Sequence 4, Appl	186	
114	7	2.0	261	4	US-09-252-991A-21486	2.0	937	4	US-09-252-991A-31823	Sequence 31823, A	187	7	2.0	937	4	US-09-252-991A-31823	Sequence 31823, A	187	
115	7	2.0	261	4	US-08-690-095-1	2.0	952	4	US-09-252-991A-32183	Sequence 32183, A	188	7	2.0	952	4	US-09-252-991A-32183	Sequence 32183, A	188	
116	7	2.0	272	3	US-09-113-789-1	2.0	1004	3	US-08-916-352-2	Sequence 2, Appl	189	7	2.0	1004	3	US-08-916-352-2	Sequence 2, Appl	189	
117	7	2.0	272	3	US-09-252-991A-33395	2.0	1065	3	US-09-412-545-2	Sequence 2, Appl	190	7	2.0	1065	3	US-09-412-545-2	Sequence 2, Appl	190	
118	7	2.0	275	4	US-09-252-991A-28776	2.0	1323	1	US-08-026-1385-4	Sequence 4, Appl	191	7	2.0	1323	1	US-08-026-1385-4	Sequence 4, Appl	191	
119	7	2.0	301	3	US-08-829-525-24	2.0	1346	3	US-09-320-878-4	Sequence 4, Appl	192	7	2.0	1346	3	US-09-320-878-4	Sequence 4, Appl	192	
120	7	2.0	301	3	US-08-609-583A-24	2.0	1346	3	US-09-105-537-37	Sequence 37, Appl	193	7	2.0	1346	3	US-09-105-537-37	Sequence 37, Appl	193	
121	7	2.0	301	3	US-08-937-399-24	2.0	1346	4	US-09-141-908-5	Sequence 5, Appl	194	7	2.0	1346	4	US-09-141-908-5	Sequence 5, Appl	194	
122	7	2.0	301	4	US-09-310-367-24	2.0	1384	4	US-08-657-440-4	Sequence 4, Appl	195	7	2.0	1384	4	US-08-657-440-4	Sequence 4, Appl	195	
123	7	2.0	301	4	US-09-032-337-24	2.0	1626	2	US-08-826-134-2	Sequence 2, Appl	196	7	2.0	1626	2	US-08-826-134-2	Sequence 2, Appl	196	
124	7	2.0	301	4	US-09-464-231-24	2.0	1626	3	US-08-771-602D-2	Sequence 2, Appl	197	7	2.0	1626	3	US-08-771-602D-2	Sequence 2, Appl	197	
125	7	2.0	305	4	US-09-252-991A-19267	2.0	1626	3	US-09-232-446B-2	Sequence 2, Appl	198	7	2.0	1626	3	US-09-232-446B-2	Sequence 2, Appl	198	
126	7	2.0	307	4	US-09-252-991A-20828	2.0	1724	3	US-08-857-076-12	Sequence 12, Appl	199	7	2.0	1724	3	US-08-857-076-12	Sequence 12, Appl	199	
127	7	2.0	308	4	US-09-252-991A-21929	2.0	1820	3	US-07-998-289B-8	Sequence 8, Appl	200	7	2.0	1820	3	US-07-998-289B-8	Sequence 8, Appl	200	
128	7	2.0	309	3	US-08-508-761B-37	2.0	2100	2	US-08-808-793-23	Sequence 23, Appl	201	7	2.0	2100	2	US-08-808-793-23	Sequence 23, Appl	201	
129	7	2.0	309	4	US-09-252-991A-18568	2.0	2104	3	US-08-808-793-23	Sequence 19, Appl	202	7	2.0	2104	3	US-08-808-793-23	Sequence 19, Appl	202	
130	7	2.0	322	4	US-09-252-991A-25477	2.0	2104	2	US-08-772-512A-19	Sequence 4, Appl	203	7	2.0	2104	2	US-08-772-512A-19	Sequence 4, Appl	203	
131	7	2.0	325	2	US-08-107-676-30	2.0	2105	2	US-08-772-512A-4	Sequence 4, Appl	204	7	2.0	2105	2	US-08-772-512A-4	Sequence 4, Appl	204	
132	7	2.0	327	4	US-09-252-991A-22625	2.0	2105	2	US-08-808-793-3	Sequence 3, Appl	205	7	2.0	2105	2	US-08-808-793-3	Sequence 3, Appl	205	
133	7	2.0	335	4	US-09-252-991A-18555	2.0	2105	2	US-08-772-512A-3	Sequence 3, Appl	206	7	2.0	2105	2	US-08-772-512A-3	Sequence 3, Appl	206	
134	7	2.0	335	4	US-09-252-991A-18555	2.0	3782	3	US-09-105-537-4	Sequence 4, Appl	207	7	2.0	3782	3	US-09-105-537-4	Sequence 4, Appl	207	
135	7	2.0	382	4	US-09-328-352-8119	2.0	6396	4	US-09-410-551B-72	Sequence 72, Appl	208	7	2.0	6396	4	US-09-410-551B-72	Sequence 72, Appl	208	
136	7	2.0	407	2	US-08-765-875-2	2.0	8991	4	US-08-714-741-32	Sequence 32, Appl	209	7	2.0	8991	4	US-08-714-741-32	Sequence 32, Appl	209	
137	7	2.0	407	2	US-08-765-875-6	2.0	11877	4	US-09-105-537-6	Sequence 6, Appl	210	7	2.0	11877	4	US-09-105-537-6	Sequence 6, Appl	210	
138	7	2.0	407	3	US-08-795-671-2	2.0	6	2	US-08-837-305-6	Sequence 1, Appl	211	7	2.0	6	2	US-08-837-305-6	Sequence 1, Appl	211	
139	7	2.0	407	3	US-08-795-671-6	2.0	6	3	US-08-611-395-9	Sequence 3, Appl	212	7	2.0	6	3	US-08-611-395-9	Sequence 3, Appl	212	
140	7	2.0	407	3	US-09-454-540-2	2.0	6	3	US-08-748-073-2	Sequence 2, Appl	213	7	2.0	6	3	US-08-748-073-2	Sequence 2, Appl	213	
141	7	2.0	407	4	US-09-454-540-6	2.0	7	4	US-08-877-605-143	Sequence 143, App	214	7	2.0	7	4	US-08-877-605-143	Sequence 143, App	214	
142	7	2.0	423	4	US-09-073-009-142	2.0	8	3	US-08-963-168C-24	Sequence 24, Appl	215	7	2.0	8	3	US-08-963-168C-24	Sequence 24, Appl	215	
143	7	2.0	431	3	US-09-381-681-3	2.0	215	6	US-08-963-168C-26	Sequence 26, Appl	216	7	2.0	215	6	US-08-963-168C-26	Sequence 26, Appl	216	
144	7	2.0	434	2	US-08-710-249-4	2.0	217	6	US-08-425-069-12	Sequence 12, Appl	217	7	2.0	217	6	US-08-425-069-12	Sequence 12, Appl	217	
145	7	2.0	434	4	US-09-220-157A-4	2.0	218	6	US-08-317-844B-12	Sequence 12, Appl	218	7	2.0	218	6	US-08-317-844B-12	Sequence 12, Appl	218	
146	7	2.0	436	4	US-09-252-991A-20220	2.0	219	6	US-08-336-385-12	Sequence 12, Appl	219	7	2.0	219	6	US-08-336-385-12	Sequence 12, Appl	219	
147	7	2.0	441	3	US-09-191-136-31	2.0	220	6	US-08-159-339A-129	Sequence 129, App	220	7	2.0	220	6	US-08-159-339A-129	Sequence 129, App	220	
148	7	2.0	482	1	US-07-792-885A-1	2.0	221	6	US-08-159-339A-151	Sequence 151, App	221	7	2.0	221	6	US-08-159-339A-151	Sequence 151, App	221	
149	7	2.0	482	1	US-08-142-439A-7	2.0	222	6	US-08-159-339A-152	Sequence 152, App	222	7	2.0	222	6	US-08-159-339A-152	Sequence 152, App	222	
150	7	2.0	482	2	US-08-669-477-7	2.0	223	6	US-08-159-339A-153	Sequence 153, App	223	7	2.0	223	6	US-08-159-339A-153	Sequence 153, App	223	
151	7	2.0	485	3	US-09-320-878-10	2.0	224	6	US-08-159-339A-154	Sequence 154, App	224	7	2.0	224	6	US-08-159-339A-154	Sequence 154, App	224	
152	7	2.0	485	3	US-09-105-537-10	2.0	225	6	US-08-159-339A-155	Sequence 155, App	225	7	2.0	225	6	US-08-159-339A-155	Sequence 155, App	225	
153	7	2.0	485	4	US-09-141-908-23	2.0	226	6	US-08-159-339A-156	Sequence 156, App	226	7	2.0	226	6	US-08-159-339A-156	Sequence 156, App	226	
154	7	2.0	485	4	US-09-657-440-10	2.0	227	6	US-08-159-339A-157	Sequence 157, App	227	7	2.0	227	6	US-08-159-339A-157	Sequence 157, App	227	
155	7	2.0	497	4	US-09-125-642C-14	2.0	228	6	US-08-159-339A-158	Sequence 158, App	228	7	2.0	228	6	US-08-159-339A-158	Sequence 158, App	228	
156	7	2.0	505	1	US-08-221-750A-5	2.0	229	6	US-08-159-339A-159	Sequence 159, App	229	7	2.0	229	6	US-08-159-339A-159	Sequence 159, App	229	
157	7	2.0	513	2	US-08-459-346-19	2.0	230	6	US-08-159-339A-160	Sequence 160, App	230	7	2.0	230	6	US-08-159-339A-160	Sequence 160, App	230	
158	7	2.0	513	2	US-07-989-847-8	2.0	231	6	US-08-159-339A-161	Sequence 161, App	231	7	2.0	231	6	US-08-159-339A-161	Sequence 161, App	231	
159	7	2.0	513	2	US-08-889-419-19	2.0	232	6	US-08-159-339A-162	Sequence 162, App	232	7	2.0	232	6	US-08-159-339A-162	Sequence 162, App	232	
160	7	2.0	513	3	US-08-469-411-8	2.0	233	6	US-08-159-339A-163	Sequence 163, App	233	7	2.0	233	6	US-08-159-339A-163	Sequence 163, App	233	
161	7	2.0	513	3	US-08-402-542-19	2.0	234	6	US-08-159-339A-164	Sequence 164, App	234	7	2.0	234	6	US-08-159-339A-164	Sequence 164, App	234	
162	7	2.0	513	5	PCT-US93-07189-19	2.0	235	6	US-08-159-339A-165	Sequence 165, App	235	7	2.0	235	6	US-08-159-339A-165	Sequence 165, App	235	
163	7	2.0	513	6	PCT-US93-07189-19	2.0	236	6	US-08-159-339A-166	Sequence 166, App	236	7	2.0	236	6	US-08-159-339A-166	Sequence 166, App	236	
164	7	2.0	533	1	US-07-952-800-2	2.0	237	6											

247	6	1.7	10	2	US-08-545-151-15	Sequence 15, Appl	320	6	1.7	18	4	US-09-598-419-18	Sequence 18, Appl
248	6	1.7	10	2	US-08-458-887-9	Sequence 9, Appl	321	6	1.7	18	6	5472691-5	Patent No. 5472691
249	6	1.7	10	3	US-08-159-339A-149	Sequence 149, App	322	6	1.7	19	2	US-08-837-305-3	Sequence 3, Appl
250	6	1.7	10	3	US-08-159-339C-150	Sequence 150, App	323	6	1.7	19	3	US-08-848-880-8	Sequence 8, Appl
251	6	1.7	10	3	US-08-159-339C-150	Sequence 25, Appl	324	6	1.7	19	5	PCT-US92-04537-4	Sequence 4, Appl
252	6	1.7	10	4	US-09-314-135-2	Patent No. 5169933	325	6	1.7	20	1	US-08-150-331-26	Sequence 26, Appl
253	6	1.7	10	4	5169933-19	Patent No. 5169933	326	6	1.7	20	1	US-08-440-861-26	Sequence 26, Appl
254	6	1.7	10	6	5169933-41	Patent No. 5169933	327	6	1.7	20	1	US-08-440-861-27	Sequence 27, Appl
255	6	1.7	10	6	5169933-41	Patent No. 5169933	328	6	1.7	20	1	US-08-399-566-70	Sequence 70, Appl
256	6	1.7	11	2	US-07-814-220-5	Sequence 5, Appl	329	6	1.7	20	2	US-07-814-220-27	Sequence 27, Appl
257	6	1.7	11	2	US-07-814-220-6	Sequence 6, Appl	330	6	1.7	20	2	US-07-814-221-27	Sequence 27, Appl
258	6	1.7	11	2	US-07-814-220-6	Sequence 8, Appl	331	6	1.7	20	4	US-08-569-284-48	Sequence 48, Appl
259	6	1.7	11	2	US-07-814-220-11	Sequence 11, Appl	332	6	1.7	20	6	5422425-10	Patent No. 5422425
260	6	1.7	11	2	US-07-814-221-5	Sequence 5, Appl	333	6	1.7	20	6	5422425-11	Patent No. 5422425
261	6	1.7	11	2	US-07-812-421-6	Sequence 6, Appl	334	6	1.7	21	1	US-08-425-069-5	Sequence 5, Appl
262	6	1.7	11	2	US-07-812-421-8	Sequence 8, Appl	335	6	1.7	21	2	US-07-814-220-24	Sequence 24, Appl
263	6	1.7	11	2	US-07-812-421-11	Sequence 11, Appl	336	6	1.7	21	2	US-07-812-21-24	Sequence 24, Appl
264	6	1.7	11	3	US-09-208-966-53	Sequence 53, Appl	337	6	1.7	21	2	US-08-317-844B-5	Sequence 5, Appl
265	6	1.7	12	1	US-07-992-288-7	Sequence 7, Appl	338	6	1.7	21	3	US-08-848-580-9	Sequence 9, Appl
266	6	1.7	12	1	US-08-433-854-43	Sequence 43, Appl	339	6	1.7	21	3	US-08-556-978B-43	Sequence 43, Appl
267	6	1.7	12	1	US-08-433-854-43	Sequence 43, Appl	340	6	1.7	21	5	PCT-US92-04537-5	Sequence 5, Appl
268	6	1.7	12	1	US-08-174-745A-43	Sequence 43, Appl	341	6	1.7	22	1	US-07-989-764-6	Sequence 6, Appl
269	6	1.7	12	2	US-08-195-947-43	Sequence 43, Appl	342	6	1.7	22	1	US-07-989-764-6	Sequence 6, Appl
270	6	1.7	12	2	US-08-433-885-43	Sequence 43, Appl	343	6	1.7	23	1	US-07-826-528A-11	Sequence 11, Appl
271	6	1.7	12	2	US-08-433-908B-43	Sequence 43, Appl	344	6	1.7	23	3	US-07-927-91-7	Sequence 7, Appl
272	6	1.7	12	2	US-09-058-459-37	Sequence 37, Appl	345	6	1.7	23	3	US-08-556-978B-49	Sequence 49, Appl
273	6	1.7	12	3	US-09-127-926-37	Sequence 37, Appl	346	6	1.7	24	3	US-08-556-978B-55	Sequence 55, Appl
274	6	1.7	12	3	US-08-410-614-43	Sequence 43, Appl	347	6	1.7	24	4	US-09-206-576-6	Sequence 6, Appl
275	6	1.7	12	4	US-08-728-742A-34	Sequence 34, Appl	348	6	1.7	25	1	US-08-425-069-38	Sequence 38, Appl
276	6	1.7	12	4	US-08-728-742A-65	Sequence 65, Appl	349	6	1.7	25	2	US-07-814-220-33	Sequence 33, Appl
277	6	1.7	13	4	US-08-788-822A-15	Sequence 15, Appl	350	6	1.7	25	2	US-07-812-421-33	Sequence 33, Appl
278	6	1.7	13	4	US-08-706-054A-12	Sequence 12, Appl	351	6	1.7	25	2	US-08-317-844B-38	Sequence 38, Appl
279	6	1.7	13	4	US-09-313-299-12	Sequence 12, Appl	352	6	1.7	25	3	US-08-641-873-15	Sequence 15, Appl
280	6	1.7	13	5	PCT-US94-10257A-3	Sequence 3, Appl	353	6	1.7	25	6	5169933-42	Patent No. 5169933
281	6	1.7	13	5	PCT-US93-04121-38	Sequence 38, Appl	354	6	1.7	26	2	US-08-700-442A-15	Sequence 15, Appl
282	6	1.7	13	5	PCT-US93-04121-50	Sequence 50, Appl	355	6	1.7	26	3	US-08-920-610-10	Sequence 10, Appl
283	6	1.7	13	5	PCT-US93-04121-52	Sequence 52, Appl	356	6	1.7	26	3	US-08-831-028-15	Sequence 15, Appl
284	6	1.7	13	5	PCT-US93-04121-54	Sequence 54, Appl	357	6	1.7	27	1	US-08-475-989-39	Sequence 39, Appl
285	6	1.7	13	5	PCT-US93-04121-60	Sequence 60, Appl	358	6	1.7	27	1	US-08-425-069-51	Sequence 51, Appl
286	6	1.7	14	1	US-08-340-203A-14	Sequence 14, Appl	359	6	1.7	27	1	US-08-425-069-56	Sequence 56, Appl
287	6	1.7	14	2	US-08-503-226B-40	Sequence 40, Appl	360	6	1.7	27	2	US-08-475-985-59	Sequence 59, Appl
288	6	1.7	14	2	US-08-452-427-14	Sequence 14, Appl	361	6	1.7	27	2	US-08-475-985-29	Sequence 29, Appl
289	6	1.7	14	2	US-07-814-220-30	Sequence 30, Appl	362	6	1.7	27	2	US-08-317-844B-51	Sequence 51, Appl
290	6	1.7	14	2	US-07-812-421-30	Sequence 30, Appl	363	6	1.7	27	2	US-08-317-844B-56	Sequence 56, Appl
291	6	1.7	14	3	US-09-085-407-14	Sequence 14, Appl	364	6	1.7	27	2	US-08-317-844B-59	Sequence 59, Appl
292	6	1.7	14	3	US-08-721-458B-40	Sequence 40, Appl	365	6	1.7	27	3	US-08-256-839-89	Sequence 29, Appl
293	6	1.7	14	3	US-09-058-562-31	Sequence 31, Appl	366	6	1.7	27	3	US-08-556-978B-29	Sequence 29, Appl
294	6	1.7	16	1	US-08-366-953A-35	Sequence 35, Appl	367	6	1.7	27	3	US-08-556-978B-92	Sequence 92, Appl
295	6	1.7	16	2	US-08-308-494A-2	Sequence 2, Appl	368	6	1.7	28	1	US-08-053-131-98	Sequence 98, Appl
296	6	1.7	17	1	US-07-591-988B-3	Sequence 3, Appl	369	6	1.7	28	1	US-08-645-641-98	Sequence 98, Appl
297	6	1.7	17	1	US-07-591-988B-5	Sequence 5, Appl	370	6	1.7	28	1	US-08-425-069-40	Sequence 40, Appl
298	6	1.7	17	1	US-07-591-988B-6	Sequence 6, Appl	371	6	1.7	28	1	US-08-425-069-43	Sequence 43, Appl
299	6	1.7	17	1	US-07-591-988B-7	Sequence 7, Appl	372	6	1.7	28	1	US-07-853-008B-98	Sequence 98, Appl
300	6	1.7	17	1	US-08-164-618-4	Sequence 4, Appl	373	6	1.7	28	2	US-08-096-762-98	Sequence 98, Appl
301	6	1.7	17	1	US-08-164-618-5	Sequence 5, Appl	374	6	1.7	28	2	US-08-700-442A-14	Sequence 14, Appl
302	6	1.7	17	1	US-08-164-618-6	Sequence 6, Appl	375	6	1.7	28	2	US-08-700-442A-16	Sequence 16, Appl
303	6	1.7	17	1	US-08-006-037-3	Sequence 3, Appl	376	6	1.7	28	2	US-08-308-665-98	Sequence 98, Appl
304	6	1.7	17	1	US-08-006-037-5	Sequence 5, Appl	377	6	1.7	28	2	US-07-814-220-36	Sequence 36, Appl
305	6	1.7	17	1	US-08-006-037-6	Sequence 6, Appl	378	6	1.7	28	2	US-07-812-421-36	Sequence 36, Appl
306	6	1.7	17	1	US-08-006-037-7	Sequence 7, Appl	379	6	1.7	28	2	US-08-317-844B-40	Sequence 40, Appl
307	6	1.7	17	2	US-08-413-490-63	Sequence 63, Appl	380	6	1.7	28	2	US-08-317-844B-43	Sequence 43, Appl
308	6	1.7	17	3	US-09-146-269-63	Sequence 63, Appl	381	6	1.7	28	3	US-08-848-580-10	Sequence 10, Appl
309	6	1.7	17	3	US-09-146-269-63	Sequence 63, Appl	382	6	1.7	28	3	US-08-831-028-14	Sequence 14, Appl
310	6	1.7	17	4	US-09-553-042-63	Sequence 63, Appl	383	6	1.7	28	3	US-08-831-028-16	Sequence 16, Appl
311	6	1.7	17	5	PCT-US93-13037-63	Sequence 63, Appl	384	6	1.7	28	3	US-08-556-978B-72	Sequence 72, Appl
312	6	1.7	18	1	US-08-240-112-33	Sequence 33, Appl	385	6	1.7	28	5	PCT-US92-04537-6	Sequence 6, Appl
313	6	1.7	18	1	US-08-443-890-33	Sequence 33, Appl	386	6	1.7	28	5	PCT-US92-04537-98	Sequence 98, Appl
314	6	1.7	18	2	US-09-017-205-41	Sequence 41, Appl	387	6	1.7	29	1	US-08-425-069-51	Sequence 51, Appl
315	6	1.7	18	4	US-08-590-888-60	Sequence 60, Appl	388	6	1.7	29	1	US-08-209-747-42	Sequence 42, Appl
316	6	1.7	18	4	US-09-556-877-18	Sequence 18, Appl	389	6	1.7	29	1	US-08-460-874A-19	Sequence 19, Appl
317	6	1.7	18	4	US-09-288-594A-18	Sequence 18, Appl	390	6	1.7	29	2	US-08-458-298-42	Sequence 42, Appl
318	6	1.7	18	4	US-09-620-412C-18	Sequence 18, Appl	391	6	1.7	29	2	US-08-388-883B-19	Sequence 19, Appl
319	6	1.7	18	4	US-09-410-568-18	Sequence 18, Appl	392	6	1.7	29	2	US-08-317-844B-31	Sequence 31, Appl

[illegible]

QY 121 NOTGVVFEFTVTSVSGDEGRSHCEIIDDCGSPMYQFASFOYTCQPCGQMLCTR 180  
DB 121 NOTGVVFEFTVTSVSGDEGRSHCEIIDDCGSPMYQFASFOYTCQPCGQMLCTR 180  
QY 181 DSBCCDOLCVMGCHTKMTRGSGGTICDQRCQGLCCAFQGLFPVCTPLPVEGEL 240  
DB 181 DSBCCDOLCVMGCHTKMTRGSGGTICDQRCQGLCCAFQGLFPVCTPLPVEGEL 240  
QY 241 CHPAARLIDLITWELPDPALDRCASGLLCQPHSHSLVYVCKPTFGSRDQGEILL 300  
DB 241 CHPAARLIDLITWELPDPALDRCASGLLCQPHSHSLVYVCKPTFGSRDQGEILL 300  
QY 301 PREVPDEYGVSGFMEEYRQELDLERSLVEEVALGSPAAAAALLGGEI 350  
DB 301 PREVPDEYGVSGFMEEYRQELDLERSLVEEVALGSPAAAAALLGGEI 350  
RESULT 2  
US-09-161-241-8  
Sequence 8, Application US/09161241  
Patent No. 6344541  
GENERAL INFORMATION:  
APPLICANT: Bass, Michael B  
APPLICANT: Sullivan, John K  
APPLICANT: Theill, Lars E  
APPLICANT: Wang, Daquan  
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES  
FILE REFERENCE: A-548  
CURRENT APPLICATION NUMBER: US/09/161,241  
CURRENT FILING DATE: 1998-09-25  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 349  
TYPE: PRT  
ORGANISM: Mouse  
US-09-161-241-8  
Query Match 11.7%; Score 41; DB 4; Length 349;  
Best Local Similarity 100.0%; Pred. No. 1.7e-31;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 40 YPOEATINEMPREVELMEDTQHKLSAAYEMEAEEBAAK 80  
DB 40 YPOEATINEMPREVELMEDTQHKLSAAYEMEAEEBAAK 80  
RESULT 3  
US-09-325-932A-144  
Sequence 144, Application US/09325932A  
Patent No. 6451604  
GENERAL INFORMATION:  
APPLICANT: Flinn, Barry  
APPLICANT: Lasham, Annette  
TITLE OF INVENTION: Compositions affecting programmed cell  
TITLE OF INVENTION: death and their use in the modification of forestry plant devel  
FILE REFERENCE: 1022  
CURRENT APPLICATION NUMBER: US/09/325,932A  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 206  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 144  
LENGTH: 109  
TYPE: PRT  
ORGANISM: Eucalyptus grandis  
US-09-325-932A-144  
Query Match 2.6%; Score 9; DB 4; Length 109;  
Best Local Similarity 100.0%; Pred. No. 0.49;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 337 PAAAAAALL 345  
|||||

DB 17 PAAAAAALL 25  
RESULT 4  
US-09-252-991A-19907  
Sequence 19907, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc U. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 19907  
LENGTH: 398  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-19907  
Query Match 2.6%; Score 9; DB 4; Length 398;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 336 EPPAAAAALL 344  
|||||  
DB 53 EPPAAAAALL 61  
RESULT 5  
US-08-460-874A-46  
Sequence 46, Application US/08460874A  
Patent No. 5744298  
GENERAL INFORMATION:  
APPLICANT: Stuber, Werner  
APPLICANT: Mieczorek, Leszek  
APPLICANT: Zieglmaier, Robert  
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
TITLE OF INVENTION: and the Use Thereof  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner.  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington,  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,874A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/936,219  
FILING DATE: 27-AUG-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4128684.7  
FILING DATE: 29-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Forman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 05552-1210-04000



TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-460-874A-46

Query Match 2.3%; Score 8; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.55;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26  
DB 5 TAPAPAPT 12

RESULT 6  
US-08-388-883B-46  
Sequence 46, Application US/08388883B  
Patent No. 585185  
GENERAL INFORMATION:  
APPLICANT: ST BER, Werner  
APPLICANT: WIECZOREK, Leszek  
APPLICANT: ZIEGELMAIER, Robert  
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
TITLE OF INVENTION: and the Use Thereof  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner L.L.P.  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington,  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,883B  
FILING DATE: 13-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/300,305  
FILING DATE: 23-FEB-1994  
PRIOR APPLICATION DATA: US 07/936,219  
FILING DATE: 27-AUG-1992  
APPLICATION NUMBER: DE P4128684.7  
FILING DATE: 29-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Forman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 5552-1210-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-388-883B-46  
Query Match 2.3%; Score 8; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.55;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26  
DB 5 TAPAPAPT 12

RESULT 7  
US-08-462-211A-46  
Sequence 46, Application US/08462211A  
Patent No. 614393  
GENERAL INFORMATION:  
APPLICANT: Stuber, Werner  
APPLICANT: WIECZOREK, Leszek  
APPLICANT: ZIEGELMAIER, Robert  
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
TITLE OF INVENTION: and the Use Thereof  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner L.L.P.  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington,  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,211A  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/388,883  
FILING DATE: 13-FEB-1995  
PRIOR APPLICATION DATA: US 08/300,305  
FILING DATE: 23-FEB-1994  
PRIOR APPLICATION DATA: US 07/936,219  
FILING DATE: 27-AUG-1992  
APPLICATION NUMBER: DE P4128684.7  
FILING DATE: 29-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Forman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 5552.1210-03000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-462-211A-46  
Query Match 2.3%; Score 8; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.55;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8  
US-08-935-009A-5  
QY 19 TAPAPAPT 26  
DB 5 TAPAPAPT 12

Sequence 5, Application US/08935009A  
Patent No. 617241  
GENERAL INFORMATION:  
APPLICANT: Maine, Gregory T.  
TITLE OF INVENTION: USE OF PEPTIDES TO IMPROVE  
SPECIFICITY OF AN ENZYME IMMUNOASSAY FOR  
TITLE OF INVENTION: THE DETECTION OF HERPESVIRUS SPECIFIC IGM ANTIBODY  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/935,009A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Weinstein, David L.  
REGISTRATION NUMBER: 28,128  
REFERENCE/DOCKET NUMBER: 6186-US-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-6182  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6177241e  
US-08-935-009A-5

Query Match 2.3%; Score 8; DB 3; Length 20;  
Best Local Similarity 100.0%; Fred. No. 0.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26  
DB 9 TAPAPAPT 16

RESULT 9  
US-08-460-874A-12  
Sequence 12, Application US/08460874A  
Patent No. 5744298  
GENERAL INFORMATION:  
APPLICANT: Stuber, Werner  
APPLICANT: Mieczorek, Leszek  
APPLICANT: Ziegelmaler, Robert  
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
TITLE OF INVENTION: and the Use Thereof  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington,  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,874A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/936,219  
FILING DATE: 27-AUG-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4128684.7  
FILING DATE: 29-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Forman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 05552-1210-04000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-460-874A-12

Query Match 2.3%; Score 8; DB 1; Length 31;  
Best Local Similarity 100.0%; Fred. No. 1.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26  
DB 21 TAPAPAPT 28

RESULT 10  
US-08-460-874A-13  
Sequence 13, Application US/08460874A  
Patent No. 5744298  
GENERAL INFORMATION:  
APPLICANT: Stuber, Werner  
APPLICANT: Mieczorek, Leszek  
APPLICANT: Ziegelmaler, Robert  
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
TITLE OF INVENTION: and the Use Thereof  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington,  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,874A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/936,219  
FILING DATE: 27-AUG-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4128684.7

FILING DATE: 29-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Forman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 05552-1210-04000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-460-874A-13

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26  
Db 18 TAPAPAPT 25

RESULT 11  
US-08-388-883B-12  
Sequence 12, Application US/0838883B  
Patent No. 5859185  
GENERAL INFORMATION:  
APPLICANT: ST BER, Werner  
APPLICANT: WIECZOREK, Leszek  
APPLICANT: ZIEGELMAIER, Robert  
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner L.L.P.  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington,  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,883B  
FILING DATE: 13-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/300,305  
FILING DATE: 23-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/936,219  
FILING DATE: 27-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4128684.7  
FILING DATE: 29-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Forman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 5552-1210-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-388-883B-12

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26  
Db 21 TAPAPAPT 28

RESULT 12  
US-08-388-883B-13  
Sequence 13, Application US/0838883B  
Patent No. 5859185  
GENERAL INFORMATION:  
APPLICANT: ST BER, Werner  
APPLICANT: WIECZOREK, Leszek  
APPLICANT: ZIEGELMAIER, Robert  
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner L.L.P.  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington,  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,883B  
FILING DATE: 13-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/300,305  
FILING DATE: 23-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/936,219  
FILING DATE: 27-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4128684.7  
FILING DATE: 29-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Forman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 5552-1210-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-388-883B-13

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26  
Db 18 TAPAPAPT 25



COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,874A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/936,219  
FILING DATE: 27-AUG-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4128684.7  
FILING DATE: 29-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fortman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 05552-1210-04000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-460-874A-15

Query Match 2.3%; Score 8; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 TAPAPPT 26  
Db 16 TAPAPPT 23

RESULT 16  
US-08-388-883B-15  
Sequence 15, Application US/0838883B  
Patent No. 5859185  
GENERAL INFORMATION:  
APPLICANT: ST BER, Werner  
APPLICANT: WIECZOREK, Leszek  
APPLICANT: ZIEGELMAIER, Robert  
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
NUMBER OF INVENTION: and the Use Thereof  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner L.L.P.  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington,  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,883B  
FILING DATE: 13-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/300,305  
FILING DATE: 23-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/936,219

FILING DATE: 27-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4128684.7  
FILING DATE: 29-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fortman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 5552-1210-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-388-883B-15

Query Match 2.3%; Score 8; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 TAPAPPT 26  
Db 16 TAPAPPT 23

RESULT 17  
US-08-462-211A-15  
Sequence 15, Application US/08462211A  
Patent No. 6143493  
GENERAL INFORMATION:  
APPLICANT: Stuber, Werner  
APPLICANT: WIECZOREK, Leszek  
APPLICANT: ZIEGELMAIER, Robert  
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
NUMBER OF INVENTION: and the Use Thereof  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner L.L.P.  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington,  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,211A  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/388,883  
FILING DATE: 13-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/300,305  
FILING DATE: 23-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/936,219  
FILING DATE: 27-AUG-1992  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: DE P4128684.7  
FILING DATE: 29-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fortman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 5552-1210-03000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-462-211A-15

Query Match  
Best Local Similarity 100.0%; Score 8; DB 3; Length 32;  
Pred. No. 1.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 TAPAPAPT 26  
Db 16 TAPAPAPT 23

RESULT 18  
US-08-388-883B-1  
; Sequence 1, Application US/0838883B  
; Patent No. 5859185  
; GENERAL INFORMATION:  
; APPLICANT: ST BER, Werner  
; APPLICANT: WIECZOREK, Leszek  
; APPLICANT: ZIEGELMAIER, Robert  
; TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
; TITLE OF INVENTION: and the Use Thereof  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &  
; ADDRESSEE: Dunner L.L.P.  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington,  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,883B  
; FILING DATE: 13-FEB-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/300,305  
; FILING DATE: 23-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/936,219  
; FILING DATE: 27-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P4128684.7  
; FILING DATE: 29-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Forman, David S.  
; REGISTRATION NUMBER: 33,694  
; REFERENCE/DOCKET NUMBER: 5552-1210-02000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 1  
; OTHER INFORMATION: /note= "Some or all amino acids in

OTHER INFORMATION: the regions spanning 0-14 may be absent"  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 22  
; OTHER INFORMATION: /note= "Some or all amino acids in  
; OTHER INFORMATION: the regions 22-40 may be absent."  
US-08-388-883B-1

Query Match  
Best Local Similarity 100.0%; Score 8; DB 2; Length 40;  
Pred. No. 1.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 TAPAPAPT 26  
Db 30 TAPAPAPT 37

RESULT 19  
US-08-460-874A-17  
; Sequence 17, Application US/08460874A  
; Patent No. 5744298  
; GENERAL INFORMATION:  
; APPLICANT: Stuber, Werner  
; APPLICANT: WIECZOREK, Leszek  
; APPLICANT: ZIEGELMAIER, Robert  
; TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
; TITLE OF INVENTION: and the Use Thereof  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington,  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,874A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/936,219  
; FILING DATE: 27-AUG-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P4128684.7  
; FILING DATE: 29-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Forman, David S.  
; REGISTRATION NUMBER: 33,694  
; REFERENCE/DOCKET NUMBER: 05552-1210-04000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 51 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-460-874A-17

Query Match  
Best Local Similarity 100.0%; Score 8; DB 1; Length 51;  
Pred. No. 2.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 TAPAPAPT 26  
Db 19 TAPAPAPT 26



Db 35 TAPAPAPT 42

## RESULT 20

US-08-388-883B-17  
Sequence 17, Application US/0838883B  
Patent No. 5859185  
GENERAL INFORMATION:  
APPLICANT: ST BER, Werner  
APPLICANT: WIECZOREK, Leszek  
APPLICANT: ZIEGELMAIER, Robert  
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
TITLE OF INVENTION: and the Use Thereof  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner L.L.P.  
STREET: 1300 I Street, N.W., Suite 700  
City: Washington,  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,883B  
FILING DATE: 13-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/300,305  
FILING DATE: 23-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/936,219  
FILING DATE: 27-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4128684.7  
FILING DATE: 29-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Foreman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 5552-1210-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 51 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-388-883B-17

Query Match 2.3%; Score 8; DB 2; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26  
Db 35 TAPAPAPT 42

RESULT 21  
US-08-462-211A-17  
Sequence 17, Application US/08462211A  
Patent No. 6143493  
GENERAL INFORMATION:  
APPLICANT: Stuber, Werner  
APPLICANT: WIECZOREK, Leszek  
APPLICANT: Zieglmaier, Robert  
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor

TITLE OF INVENTION: and the Use Thereof  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner L.L.P.  
STREET: 1300 I Street, N.W., Suite 700  
City: Washington,  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,211A  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/388,883  
FILING DATE: 13-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/300,305  
FILING DATE: 23-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/936,219  
FILING DATE: 27-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4128684.7  
FILING DATE: 29-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Foreman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 5552-1210-03000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 51 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-462-211A-17

Query Match 2.3%; Score 8; DB 3; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26  
Db 35 TAPAPAPT 42

RESULT 22  
US-09-366-887A-14  
Sequence 14, Application US/09366887A  
Patent No. 6403782  
GENERAL INFORMATION:  
APPLICANT: LUSTER, ANDREW D.  
APPLICANT: LEDER, PHILIP  
APPLICANT: ROTHENBERG, MARC  
APPLICANT: GARCIA, EDUARDO  
TITLE OF INVENTION: EOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT  
FILE REFERENCE: 00383/025002  
CURRENT APPLICATION NUMBER: US/09/366,887A  
PRIOR FILING DATE: 1999-08-04  
PRIOR APPLICATION NUMBER: 60/000,449  
PRIOR FILING DATE: 1995-06-22  
PRIOR APPLICATION NUMBER: 08/522,713  
PRIOR FILING DATE: 1995-09-01  
PRIOR APPLICATION NUMBER: 08/522,713  
PRIOR FILING DATE: 1998-06-16

```

; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-366-887A-14

Query Match
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTLCCLL 13
   |||||
Db 5 ATTLCCLL 12

RESULT 23
US-09-886-319A-21
; Sequence 21, Application US/09886319A
; Patent No. 6586185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jörn-Peter
; APPLICANT: Regendogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the diagnosis or treatment of skin disorders and wound
; TITLE OF INVENTION: Healing and for the identification of pharmacologically
; FILE REFERENCE: 50125/014002
; CURRENT APPLICATION NUMBER: US/09/886,319A
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 10030149.5
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-886-319A-21

Query Match
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTLCCLL 13
   |||||
Db 5 ATTLCCLL 12

RESULT 24
US-09-646-028-4
; Sequence 4, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Bitagyn, Alva
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 156
```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-4

Query Match
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTLCCLL 13
   |||||
Db 5 ATTLCCLL 12

RESULT 25
US-08-460-874A-33
; Sequence 33, Application US/08460874A
; Patent No. 5744298
; GENERAL INFORMATION:
; APPLICANT: Stuber, Werner
; APPLICANT: Mieczorek, Leszek
; APPLICANT: Ziegelmayer, Robert
; TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
; TITLE OF INVENTION: and the Use Thereof
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington,
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,874A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/936,219
; FILING DATE: 27-AUG-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P4128684.7
; FILING DATE: 29-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Forman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-460-874A-33

Query Match
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26
   |||||
Db 59 TAPAPAPT 66
```

RESULT 26  
US-08-388-883B-33  
Sequence 33, Application US/0838883B  
Patent No. 5859185  
GENERAL INFORMATION:  
APPLICANT: ST BER, Werner  
APPLICANT: WIECZOREK, Leszek  
APPLICANT: ZIEGELMAIER, Robert  
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
TITLE OF INVENTION: and the Use Thereof  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner L.L.P.  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington,  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,883B  
FILING DATE: 13-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/300,305  
FILING DATE: 23-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/936,219  
FILING DATE: 27-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4128684.7  
FILING DATE: 29-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Forman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 5552-1210-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 162 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-388-883B-33

Query Match 2.3%; Score 8; DB 2; Length 162;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26  
DB 59 TAPAPAPT 66

RESULT 27  
US-08-462-211A-33  
Sequence 33, Application US/08462211A  
Patent No. 6143493  
GENERAL INFORMATION:  
APPLICANT: Studer, Werner  
APPLICANT: WIECZOREK, Leszek  
APPLICANT: ZIEGELMAIER, Robert  
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
TITLE OF INVENTION: and the Use Thereof  
NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner L.L.P.  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington,  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,211A  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/388,883  
FILING DATE: 13-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/300,305  
FILING DATE: 23-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/936,219  
FILING DATE: 27-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P4128684.7  
FILING DATE: 29-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Forman, David S.  
REGISTRATION NUMBER: 33,694  
REFERENCE/DOCKET NUMBER: 5552-1210-03000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 162 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-462-211A-33

Query Match 2.3%; Score 8; DB 3; Length 162;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26  
DB 59 TAPAPAPT 66

RESULT 28  
US-09-433-241A-4  
Sequence 4, Application US/09433241A  
Patent No. 6525244  
GENERAL INFORMATION:  
APPLICANT: Allen, Steve  
APPLICANT: Falco, Carl  
APPLICANT: Rafalecki, Antoni  
TITLE OF INVENTION: Plant Histidinol-Phosphate Aminotransferase Homologs  
FILE REFERENCE: BB1256 US NA  
CURRENT APPLICATION NUMBER: US/09/433,241A  
CURRENT FILING DATE: 1999-11-04  
PRIOR APPLICATION NUMBER: 60/107,273  
PRIOR FILING DATE: 1998-11-05  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 4  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Oryza sp.  
FEATURE:

NAME/KEY: UNSURE  
LOCATION: (88)  
OTHER INFORMATION: Xaa = ANY AMINO ACID  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (136)  
OTHER INFORMATION: Xaa = ANY AMINO ACID  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (137)  
OTHER INFORMATION: Xaa = ANY AMINO ACID  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (138)  
OTHER INFORMATION: Xaa = ANY AMINO ACID  
US-09-433-241A-4

Query Match 2.3%; Score 8; DB 4; Length 162;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 EPAAAAA 343  
|||  
55 EPAAAAA 62

RESULT 29  
US-09-646-028-9  
Sequence 9, Application US/09646028  
Patent No. 6562347  
GENERAL INFORMATION:  
APPLICANT: Kwak, Larry  
APPLICANT: Birsayn, Atya  
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF  
FILE REFERENCE: 14014.0316/P  
CURRENT APPLICATION NUMBER: US/09/646,028  
CURRENT FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: 60/077,745  
PRIOR FILING DATE: 1998-03-12  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 9  
LENGTH: 171  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
US-09-646-028-9

Query Match 2.3%; Score 8; DB 4; Length 171;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTLCULL 13  
|||  
5 ATTLCULL 12

RESULT 30  
US-08-765-856-2  
Sequence 2, Application US/08765856  
Patent No. 6074817  
GENERAL INFORMATION:  
APPLICANT: Landini, Maria P.  
APPLICANT: Ripalti, Alessandro  
APPLICANT: Maine, Gregory T.  
APPLICANT: Flanders, Richard T.  
TITLE OF INVENTION: RECOMBINANT MONO AND POLY ANTIGENS TO DETECT CYTOMEGALOVIRUS-9  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road

CITY: Abbott Park  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,856  
FILING DATE: 27-DEC-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/IT95/00073  
FILING DATE: 15-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Weinstein, David L.  
REGISTRATION NUMBER: 28,128  
REFERENCE/DOCKET NUMBER: 5750.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (847) 937-6182  
TELEFAX: (847) 938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-765-856-2

Query Match 2.3%; Score 8; DB 3; Length 300;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26  
|||  
241 TAPAPAPT 248

RESULT 31  
US-08-935-009A-2  
Sequence 2, Application US/08935009A  
Patent No. 6177241  
GENERAL INFORMATION:  
APPLICANT: Maine, Gregory T.  
TITLE OF INVENTION: USE OF PEPTIDES TO IMPROVE  
TITLE OF INVENTION: SPECIFICITY OF AN ENZYME IMMUNOASSAY FOR  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/935,009A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Weinstein, David L.  
REGISTRATION NUMBER: 28,128

REFERENCE/DOCKET NUMBER: 6186.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-6182  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-935-009A-2

Query Match 2.3%; Score 8; DB 3; Length 300;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26  
DB 241 TAPAPAPT 248

RESULT 32  
US-08-765-856-4  
Sequence 4, Application US/08765856  
Patent No. 6074817  
GENERAL INFORMATION:  
APPLICANT: Landini, Maria P.  
APPLICANT: Ripalci, Alessandro  
APPLICANT: Maine, Gregory T.  
APPLICANT: Flanders, Richard T.  
TITLE OF INVENTION: RECOMBINANT MONO AND POLY ANTIGENS TO DETECT CYTOMEGALOVIRUS-8  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,856  
FILING DATE: 27-DEC-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/IT95/00073  
FILING DATE: 15-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Weinstein, David L.  
REGISTRATION NUMBER: 28,128  
REFERENCE/DOCKET NUMBER: 5730.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (847) 937-6182  
TELEFAX: (847) 938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 302 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-765-856-4

Query Match 2.3%; Score 8; DB 3; Length 302;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26

DB 9 TAPAPAPT 16

RESULT 33  
US-08-935-009A-4  
Sequence 4, Application US/08935009A  
Patent No. 6177241  
GENERAL INFORMATION:  
APPLICANT: Maine, Gregory T.  
TITLE OF INVENTION: USE OF PEPTIDES TO IMPROVE  
SPECIFICITY OF AN ENZYME IMMUNOASSAY FOR  
THE DETECTION OF HERPESVIRUS SPECIFIC IGM ANTIBODY  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/935,009A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Weinstein, David L.  
REGISTRATION NUMBER: 28,128  
REFERENCE/DOCKET NUMBER: 6186.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-937-6182  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 302 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-935-009A-4

Query Match 2.3%; Score 8; DB 3; Length 302;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TAPAPAPT 26  
DB 9 TAPAPAPT 16

RESULT 34  
US-09-252-991A-27884  
Sequence 27884, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 27884  
LENGTH: 303  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-27884

Query Match 2.3%; Score 8; DB 4; Length 303;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 PTAPAP 25  
Db 156 PTAPAP 163

## RESULT 35

US-08-405-175A-5  
Sequence 5, Application US/08405175A

GENERAL INFORMATION:  
PATENT NO. 5885772  
APPLICANT: Aderem, Alan A.  
APPLICANT: Chen, Jiamin  
APPLICANT: Chang, Sandy  
TITLE OF INVENTION: METHOD FOR THE DETECTION OF ANENCEPHALY  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/405.175A  
FILING DATE: 16-MAR-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-121A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 467-5800  
TELEFAX: 201 343-1684

TELEX: 133521  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 332 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: Predicted primary structure of human MARCKS  
HYPOTHETICAL: NO  
US-08-405-175A-5

Query Match 2.3%; Score 8; DB 2; Length 332;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 GEPAAP 342  
Db 88 GEPAAP 95

RESULT 36  
US-09-110-116-4  
Sequence 4, Application US/09110116

PATENT NO. 6013479  
GENERAL INFORMATION:  
APPLICANT: Xu, Hong  
APPLICANT: Cohan, Victoria L.  
APPLICANT: Stuart, Susan G.  
TITLE OF INVENTION: HUMAN EMRL-LIKE G PROTEIN COUPLED  
FILE REFERENCE: PF-0550 US  
CURRENT APPLICATION NUMBER: US/09/110.116  
CURRENT FILING DATE: 1998-07-02  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 344  
TYPE: PRT  
ORGANISM: HOMO SAPIENS  
FEATURE:  
OTHER INFORMATION: 2935597, GenBank  
US-09-110-116-4

Query Match 2.3%; Score 8; DB 3; Length 344;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LUCILAA 15  
Db 69 LUCILAA 76

## RESULT 37

US-09-032-523-2  
Sequence 2, Application US/09032523

GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl  
APPLICANT: Baugh, Mariah  
TITLE OF INVENTION: HUMAN PROTEINASE MOLECULES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032.523  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0479 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 415 amino acids  
TYPE: amino acid  
STRANDEDNESS: single



TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: RATEROT02  
CLONE: 947429  
US-09-032-523-2

Query Match 2.3%; Score 8; DB 3; Length 415;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LCLTAA 16  
10 LCLTAA 17

RESULT 38  
US-09-252-991A-27213  
Sequence 27213, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 27213  
LENGTH: 417  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-27213

Query Match 2.3%; Score 8; DB 4; Length 417;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 AAAAALL 345  
308 AAAAALL 315

RESULT 39  
US-09-252-991A-30846  
Sequence 30846, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 30846  
LENGTH: 428  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-30846

Query Match 2.3%; Score 8; DB 4; Length 428;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLLAAAVP 18

DB 184 LLLAAAVP 191

RESULT 40  
US-09-433-241A-12  
Sequence 12, Application US/09433241A  
Patent No. 6525244  
GENERAL INFORMATION:  
APPLICANT: Allen, Steve  
APPLICANT: Falco, Steve  
APPLICANT: Rafalski, Antoni  
TITLE OF INVENTION: Plant Histidinol-Phosphate Aminotransferase Homologs  
FILE REFERENCE: Bb1256 US NA  
CURRENT APPLICATION NUMBER: US/09/433,241A  
PRIOR FILING DATE: 1999-11-04  
PRIOR APPLICATION NUMBER: 60/107,273  
PRIOR FILING DATE: 1998-11-05  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 12  
LENGTH: 435  
TYPE: PRT  
ORGANISM: Oryza sativa  
US-09-433-241A-12

Query Match 2.3%; Score 8; DB 4; Length 435;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 EPAAAAA 343  
57 EPAAAAA 64

RESULT 41  
US-09-382-256-10  
Sequence 10, Application US/09382256A  
Patent No. 6207814  
GENERAL INFORMATION:  
APPLICANT: MIYAZONO, Kohel  
TEN DIKE, Peter  
FRANZEN, Petra  
YAMASHITA, Hidetoshi  
HELDIN, Carl-Henrik  
TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS  
HAVING SERINE THREONINE KINASE DOMAINS,  
AND THEIR USE  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski L.L.P.  
STREET: 666 Fifth Avenue  
CITY: New York City  
STATE: New York  
COUNTRY: USA  
ZIP: 10103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/382,256A  
FILING DATE: 24-Aug-1999  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/02367  
FILING DATE: No. 6207814ember 17, 1993  
APPLICATION NUMBER: GB 9224057.1  
FILING DATE: No. 6207814ember 17, 1992  
APPLICATION NUMBER: GB 9304677.9  
FILING DATE: March 8, 1993  
APPLICATION NUMBER: GB 9304680.3

FILING DATE: March 8, 1993  
APPLICATION NUMBER: 9311047.6  
FILING DATE: May 28, 1993  
APPLICATION NUMBER: 9313763.6  
FILING DATE: July 2, 1993  
APPLICATION NUMBER: 9316099.2  
FILING DATE: August 3, 1993  
APPLICATION NUMBER: 321344.5  
FILING DATE: October 15, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6207814man D. Hanson  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5298.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 318-3000  
TELEFAX: (212) 752-5958  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 503 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-382-256-10

Query Match 2.3%; Score 8; DB 3; Length 503;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 AAAAAALL 345  
DB 21 AAAAAALL 28

RESULT 42  
US-09-395-115-10  
Sequence 10, Application US/09395115  
Patent No. 6271365  
GENERAL INFORMATION:  
APPLICANT: Miyazono, Kohel; DiJke, Peter Ten;  
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik  
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins  
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felife & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/395.115  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/436.265  
FILING DATE: 30-October-1995  
APPLICATION NUMBER: PCT/GB93/02367  
FILING DATE: 17-No. 6271365ember-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9224057.1  
FILING DATE: 17-No. 6271365ember-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9304677.9  
FILING DATE: 8-March-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9304680.3  
FILING DATE: 8-March-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9311047.6  
FILING DATE: 28-May-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9313763.6  
FILING DATE: 2-July-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9136099.2  
FILING DATE: 3-August-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9321344.5  
FILING DATE: 15-October-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohel, Vineet  
REGISTRATION NUMBER: 37,003  
REFERENCE/DOCKET NUMBER: LUD 5298  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 503 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-395-115-10

Query Match 2.3%; Score 8; DB 3; Length 503;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 AAAAAALL 345  
DB 21 AAAAAALL 28

RESULT 43  
US-08-436-265-10  
Sequence 10, Application US/08436265  
Patent No. 6316217  
GENERAL INFORMATION:  
APPLICANT: Miyazono, Kohel; DiJke, Peter Ten;  
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik  
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins  
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felife & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436.265  
FILING DATE: 30-October-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/02367  
FILING DATE: 17-No. 6316217ember-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9224057.1  
FILING DATE: 17-No. 6316217ember-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9304677.9  
FILING DATE: 8-March-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9304680.3  
FILING DATE: 8-March-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9311047.6  
FILING DATE: 28-May-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9313763.6  
FILING DATE: 2-July-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9136099.2  
FILING DATE: 3-August-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9321344.5  
FILING DATE: 15-October-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohlet, Vineet  
REGISTRATION NUMBER: 37,003  
REFERENCE/DOCKET NUMBER: LUD 5298  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 503 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-436-265-10

Query Match 2.3%; Score 8; DB 4; Length 503;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 AAAAAALL 345  
DB 21 AAAAAALL 28

RESULT 44  
US-09-679-187-10  
Sequence 10, Application US/09679187  
Patent No. 6331621  
GENERAL INFORMATION:  
APPLICANT: Miyazono, Kohel; Dilke, Peter Teni;  
APPLICANT: Frazer, Peter; Yamashita, Hidetoshi; Heldin, Carl-Henrik  
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins  
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Pelfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/679,187  
FILING DATE: 03-OCT-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,265  
FILING DATE: 30-October-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GS93/02367  
FILING DATE: 17-No. 6331621member-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9224057.1  
FILING DATE: 17-No. 6331621member-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9304677.9  
FILING DATE: 8-March-1993  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 9304680.3  
FILING DATE: 8-March-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9311047.6  
FILING DATE: 28-May-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9313763.6  
FILING DATE: 2-July-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9136099.2  
FILING DATE: 3-August-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9321344.5  
FILING DATE: 15-October-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohlet, Vineet  
REGISTRATION NUMBER: 37,003  
REFERENCE/DOCKET NUMBER: LUD 5298  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 503 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-679-187-10

Query Match 2.3%; Score 8; DB 4; Length 503;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 AAAAAALL 345  
DB 21 AAAAAALL 28

RESULT 45  
US-08-999-689A-6  
Sequence 6, Application US/08999689A  
Patent No. 6541615  
GENERAL INFORMATION:  
APPLICANT: ULARICH, AXEL  
APPLICANT: KHATTONENKOV, ALEXEI  
APPLICANT: CHEN, ZHENGJUN  
TITLE OF INVENTION: SIRD PROTEINS AND USES THEREOF  
FILE REFERENCE: 038602/0548  
CURRENT APPLICATION NUMBER: US/08/999,689A  
CURRENT FILING DATE: 1997-11-14  
PRIOR APPLICATION NUMBER: 60/030,964  
PRIOR FILING DATE: 1996-11-15  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 6  
TYPE: PRT  
LENGTH: 503  
ORGANISM: Homo sapiens  
US-08-999-689A-6

Query Match 2.3%; Score 8; DB 4; Length 503;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LUCCLIAA 15  
DB 14 LUCCLIAA 21

RESULT 46  
US-08-956-322-4  
Sequence 4, Application US/08956322  
Patent No. 6277977

GENERAL INFORMATION:  
APPLICANT: SATHE, GANESH  
APPLICANT: MAO, JOYCE  
TITLE OF INVENTION: CDNA CLONE HAP0167 THAT ENCODES  
TITLE OF INVENTION: A HUMAN 7-TRANSMEMBRANE RECEPTOR  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RATNER & PRESTIA  
STREET: P.O. BOX 980  
CITY: VALLEY FORGE  
STATE: PA  
COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,322  
FILING DATE: 23-OCT-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/049,329  
FILING DATE: 11-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: PRESTIA, PAUL F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: CH-70075  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 521 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-956-322-4

Query Match 2.3%; Score 8; DB 3; Length 521;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LILCLILAA 15  
Db 237 LILCLILAA 244

RESULT 47  
US-09-252-991A-30878  
Sequence 30878, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-07-27  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 30878  
LENGTH: 607  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-30878

Query Match 2.3%; Score 8; DB 4; Length 607;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 333 ALGEPAAA 340  
Db 279 ALGEPAAA 286

RESULT 48  
US-09-110-116-1  
Sequence 1, Application US/09110116  
Patent No. 6013479  
GENERAL INFORMATION:  
APPLICANT: Xu, Hong  
APPLICANT: Cohan, Victoria L.  
APPLICANT: Stuart, Susan G.  
TITLE OF INVENTION: HUMAN EMRI-LIKE G PROTEIN COUPLED  
TITLE OF INVENTION: RECEPTOR  
FILE REFERENCE: PR-0550 US  
CURRENT APPLICATION NUMBER: US/09/110,116  
CURRENT FILING DATE: 1998-07-02  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 652  
TYPE: PRT  
ORGANISM: HOMO SAPIENS  
FEATURE:  
OTHER INFORMATION: 429905, EOSINOT03  
US-09-110-116-1

Query Match 2.3%; Score 8; DB 3; Length 652;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LILCLILAA 15  
Db 368 LILCLILAA 375

RESULT 49  
US-08-956-322-2  
Sequence 2, Application US/08956322  
Patent No. 6277977  
GENERAL INFORMATION:  
APPLICANT: SATHE, GANESH  
APPLICANT: MAO, JOYCE  
TITLE OF INVENTION: CDNA CLONE HAP0167 THAT ENCODES  
TITLE OF INVENTION: A HUMAN 7-TRANSMEMBRANE RECEPTOR  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RATNER & PRESTIA  
STREET: P.O. BOX 980  
CITY: VALLEY FORGE  
STATE: PA  
COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,322  
FILING DATE: 23-OCT-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/049,329  
FILING DATE: 11-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: PRESTIA, PAUL F  
REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GH-70075  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 652 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-956-322-2

Query Match 2.3%; Score 8; DB 3; Length 652;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LIGLILAA 15  
Db 368 LIGLILAA 375

RESULT 50  
US-09-413-814-5  
Sequence 5, Application US/09413814  
Patent No. 6225064  
GENERAL INFORMATION:  
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH  
APPLICANT: Bristol-Myers Squibb, Co.  
APPLICANT: Beyer, Stefan  
APPLICANT: Bloeker, Heilmut  
APPLICANT: Brandt, Petra  
APPLICANT: Cino, Paul M  
APPLICANT: Dougherty, Brian A  
APPLICANT: Goldberg, Steven L  
APPLICANT: Hoffe, Gerhard  
APPLICANT: Mueller, Joachim  
APPLICANT: Reichenbach, Hans  
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polypeptide or  
FILE OF INVENTION: heteropolypeptide compounds  
FILE REFERENCE: PCT/US 99/23535  
CURRENT APPLICATION NUMBER: US/09/413,814  
CURRENT FILING DATE: 1999-10-07  
EARLIER APPLICATION NUMBER: DE 198 46 493.2  
EARLIER FILING DATE: 1998-10-09  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 5  
LENGTH: 899  
TYPE: PRT  
ORGANISM: Sorangium cellulosum  
US-09-413-814-5

Query Match 2.3%; Score 8; DB 3; Length 899;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 EPPAAAAA 343  
Db 882 EPPAAAAA 889

Search completed: February 21, 2004, 01:52:15  
Job time : 39 secs